

ALIGNMENTS

RESULT 1

PC2280
 prolylendopeptidase-inhibiting peptide - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
 C:Accession: PC2280
 R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
 Biochem. Biophys. Res. Commun. 202, 809-815, 1994
 A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
 A:Reference number: PC2280; PMID:94324971; PMID:8048952
 C:Accession: PC2280
 A:Molecule type: protein
 A:Residues: 1-18 <OHM>
 A:Experimental source: brain
 C:Superfamily: cytoskeletal keratin

Query Match 71.4%; Score 5; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
 |||||
 Db 2 PPLP 6

RESULT 2

S71299
 ICL2 protein - Paramecium tetraurelia (fragment)
 C:Species: Paramecium tetraurelia
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C:Accession: S71299
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A:Title: Characterization of centrin genes in Paramecium.
 A:Reference number: S71298; PMID:96248429; PMID:8665928
 C:Accession: S71299
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 A:Experimental source: strain d4-2
 C:Genetics:
 A:Genetic code: SGCS

Query Match 57.1%; Score 4; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
 |||||
 Db 2 QPPP 5

RESULT 3

A60856
 inhibin alpha chain - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: A60856
 R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wattenhall
 J. Endocrinol. 113, 213-221, 1987
 A:Title: Isolation of inhibin from ovine follicular fluid.
 A:Reference number: A60856; PMID:87224684; PMID:3585232
 C:Accession: A60856
 A:Molecule type: protein
 A:Residues: 1-13 <LEV>
 C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
 C:Superfamily: inhibin
 C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 57.1%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPLP 7
 |||||
 Db 3 PPLP 6

RESULT 4

S11129
 phosphoprotein, bone - chicken (fragment)
 C:Species: Gallus gallus (Chicken)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 25-Oct-1996
 C:Accession: S11129
 R:Mikuni-Takagaki, Y.; Glimcher, M.J.
 Biochem. J. 268, 585-591, 1990
 A:Title: Post-translational processing of chicken bone phosphoproteins. Identification
 A:Reference number: S11127; PMID:90303246; PMID:2363696
 C:Accession: S11129
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <MIK>
 C:Keywords: phosphoprotein

Query Match 57.1%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
 |||||
 Db 5 PPPL 8

RESULT 5

B39109
 hypothetical 1.5K protein - hepatitis C virus
 N:Alternate names: hypothetical protein 2
 C:Species: hepatitis C virus
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
 C:Accession: B39109; JQ1585
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Teko
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identifica
 A:Reference number: A39109; PMID:91156678; PMID:1705704
 C:Accession: B39109
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-15 <HAN>
 A:Cross-references: GB:M58406
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992
 A:Title: Cloning and sequencing of the structural region and expression of putative
 A:Reference number: JQ1584; PMID:92300349; PMID:1318944
 C:Accession: JQ1585
 A:Molecule type: genomic RNA
 A:Residues: 1-15 <KUM>
 A:Experimental source: strain U.K.

Query Match 57.1%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 |||||
 Db 9 PPLP 12

RESULT 6

E58503
 superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)
 N:Alternate names: 21.3K bladder and kidney stone protein
 C:Species: unidentified bacterium
 C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999
 C:Accession: E58503

R;Binette, J.P.; Binette, M.B.
 Submitted to the Protein Sequence Database, October 1996
 A;Description: The proteins of kidney and gallbladder stones.
 A;Reference number: A58501
 A;Accession: E58503
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <BN>
 A;Experimental source: human bladder and kidney stones
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; oxidoreductase

Query Match 57.1%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 6 PPLP 9

RESULT 7
 T44453
 acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
 C;Species: Pseudomonas aeruginosa
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T44453
 R;Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
 J. Bacteriol. 180, 5559-5566, 1998
 A;Title: Molecular characterization and regulation of an operon encoding a system for the
 A;Reference number: 222777; MUID:99008987; PMID:9791103
 A;Accession: T44453
 A;Status: preliminary; translated from GE/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-20 <NIS>
 A;Cross-references: EMBL:AF012637; NID:92668593; PIDN:AAC71069.1; PID:92668594
 A;Experimental source: strain PAOI

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 10 PPLP 13

RESULT 8
 PC2030
 tumor-derived adhesion factor - human (fragment)
 N;Alternate names: 30K protein
 C;Species: Homo sapiens (man)
 C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jan-2000
 C;Accession: PC2030
 R;Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.; Ume
 Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994
 A;Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder ca
 A;Reference number: PC2030; MUID:94161713; PMID:8117260
 A;Accession: PC2030
 A;Molecule type: protein
 A;Residues: 1-20 <AKA>
 A;Experimental source: cell line EJ-1
 C;Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 15 PPLP 18

RESULT 9
 PT0283
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0283
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0283
 A;Molecule type: DNA
 A;Residues: 1-7 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotrimer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 Db 5 QPP 7

RESULT 10
 SI0783
 enamelin f - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: SI0783
 R;Strawich, E.; Glincher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
 A;Reference number: SI0780; MUID:90336641; PMID:2379503
 A;Accession: SI0783
 A;Molecule type: protein
 A;Residues: 1-8 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 Db 2 PLP 4

RESULT 11
 PC2171
 triacylglycerol lipase (BC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fr
 C;Species: Rhizopus niveus
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C;Accession: PC2171
 R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.
 Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994
 A;Title: Purification, characterization, and crystallization of two types of lipase f
 A;Reference number: PC2171; MUID:94319059; PMID:7765029
 A;Accession: PC2171
 A;Molecule type: protein
 A;Residues: 1-10 <KOH>
 A;Experimental source: cell line EJ-1
 C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.
 C;Keywords: carboxylic ester hydrolase

Query Match 42.9%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 Db 6 PPL 8

RESULT 12

C39745
sphingomyelinase - Rhodococcus sp. (fragment)
C:Species: Rhodococcus sp.
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: C39745
R:Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidas. Evidence using these activator proteins.
A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: C39745
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ITO>

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
DB 3 PLP 5

RESULT 13

A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
C:Accession: A36454; A61630
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A:Reference number: A36454; MUID:90367888; PMID:2394318
A:Accession: A36454
A:Molecule type: protein
A:Residues: 1-10 <BOR>
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A:Reference number: A61630; MUID:93357794; PMID:8353526
A:Accession: A61630
A:Molecule type: protein
A:Residues: 1-10 <BO2>
A:Note: none of the amino acids is modified
C:Function:
A:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep
C:Keywords: hormone

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
DB 5 PPP 7

RESULT 14

YHRT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coele
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein

A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
een found in mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
A:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutan
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
DB 1 QPP 3

RESULT 15

YHHU
morphogenetic neuropeptide - human
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from c
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical str
C:Comment: This peptide was first isolated from nerve cells of hydra and was called i
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
A:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neur
P:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st

Query Match 42.9%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
DB 1 QPP 3

RESULT 16

YHBO
morphogenetic neuropeptide - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: C01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from c
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: C01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Molecule type: protein

A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head

malian intestine and hypothalamus.
 C:Superfamily: unassigned animal peptides
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropep
 F:/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 17

YHXAE

morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)

N:Alternate names: head activator

C:Species: Anthopleura elegantissima

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: A93900; A01427

R:Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A:Reference number: A93900

A:Accession: A93900

A:Molecule type: protein

A:Residues: 1-11 <SCH>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head
 n mammalian intestine and hypothalamus.

C:Superfamily: unassigned animal peptides

C:Keywords: growth factor; hormone; neuropeptide; pyrrolidone carboxylic acid

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 18

YHJFHV

morphogenetic neuropeptide - Hydra attenuata

N:Alternate names: head activator

C:Species: Hydra attenuata

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: B93900; A01427

R:Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A:Reference number: A93900

A:Accession: B93900

A:Molecule type: protein

A:Residues: 1-11 <SCH>

R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A:Title: Synthesis of a new neuropeptide, the head activator from hydra.

A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis

A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head

n mammalian intestine and hypothalamus.
 C:Superfamily: unassigned animal peptides
 C:Keywords: growth factor; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 1 QPP 3

RESULT 19

D45900

complement C3b receptor type 2 - mouse (clone 12) (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: D45900

R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.

J. Immunol. 144, 3581-3591, 1990

A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2

A:Reference number: A45900; MUID:90229754; PMID:2139460

A:Accession: D45900

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-11 <KUR>

Query Match 42.9%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
 ||||
 Db 9 QPP 11

RESULT 20

S70337

napin small chain S2 - Swedish turnip (fragment)

C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)

C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C:Accession: S70337

R:Neumann, G.M.; Condrion, R.; Thomas, I.; Polya, G.M.

Biochim. Biophys. Acta 1295, 23-33, 1996

A:Title: Purification and sequencing of multiple forms of Brassica napus seed napin

A:Reference number: S70336; MUID:96283790; PMID:8679670

A:Accession: S70337

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <NEU>

Query Match 42.9%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPP 3
 ||||
 Db 3 QPP 5

RESULT 21

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: PN0663

R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retain

A:Reference number: PN0662; MUID:94156881; PMID:8113213

A:Accession: PN0663

A:Molecule type: protein
A:Residues: 1-12 <YOS>

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 3 PLP 5

RESULT 22

B39690
neural cell adhesion molecule, cardiac splice form +,-,- rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-12 <REY>
A:Cross-references: GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 42.9%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 23

B39690
neural cell adhesion molecule, cardiac splice form +,-,- rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <REY>
A:Cross-references: GB:M63970
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like domain
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 24

S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152

R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, F.E.B.S. Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of *Phyllomedusa bicolor*
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein
A:Residues: 1-13 <WIG>
A:Experimental source: skin
C:Superfamily: unassigned animal peptides

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 7 PPP 9

RESULT 25

A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
A:Accession: A05174
R:Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C:Superfamily: unassigned animal peptides
C:Keywords: pyroglutamic acid; skin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 7 PPP 9

RESULT 26

S03716
2S albumin large chain (1 and 2) nrl - rape (fragments)
N:Alternate names: 2S albumin large chain nrl
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S03716; S09718; S09717
R:Nonsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
F.E.B.S. Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed protein
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S03716
A:Molecule type: protein
A:Residues: 1-9;10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9;10-13 <MO3>
A:Experimental source: seed

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 8 PPP 10

RESULT 27

184603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I84603
R:Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A:Reference number: I45884; MUID:87213162; PMID:3579900
A:Accession: I84603
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13

A:Cross-references: GB:M26144; NID:g951194; PIDN:AAA74588.1; PID:g951195
C:Genetics:
A:Gene: GDB:DNTT
A:Cross-references: GDB:119100; OMIM:187410
A:Map position: 10q23-10q24

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 9 PLP 11

RESULT 28

G61458
Ig lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; PLO159
R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-assc
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: G61458
A:Molecule type: protein
A:Residues: 1-13

C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycop
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
Db 6 QPP 8

RESULT 29

A86126
hypothetical protein Z5883 [imported] - Escherichia coli (strain O157:H7, substrain ED19
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86126
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86126
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-13 <STO>
A:Cross-references: GB:AB005174; NID:g12519285; PIDN:AAG59469.1; GSPDB:GN00145; UMG:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5883

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOP 3
|||
Db 1 MOP 3

RESULT 30

S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
C:Species: Pisaster ochraceus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S12904
R:Saungera, J.S.; Abersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated
A:Reference number: S12904; MUID:91032186; PMID:1699809
A:Accession: S12904
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SAN>
C:Keywords: phosphotransferase

Query Match 42.9%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 8 PPP 10

RESULT 31

PQ0545
capsid protein VP19C - human herpesvirus 1 (fragment)
C:Species: human herpesvirus 1
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PQ0545
R:Davidson, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of her
A:Reference number: PQ0544; MUID:93019027; PMID:1328483
A:Accession: PQ0545
A:Molecule type: protein
A:Residues: 1-15 <DAV>
A:Experimental source: strain 17
C:Genetics:
A:Gene: UL38
C:Keywords: capsid protein

Query Match 42.9%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 5 PLP 7

RESULT 32

PT0037
light harvesting complex chain III/b, photosystem I - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: PT0037; PS0205

R;Uchiyama, Y.; Tsugita, A.
 Submitted to JIPID, June 1991
 A;Reference number: PS0189
 A;Accession: PT0037
 A;Molecule type: protein
 A;Residues: 1-15 <UCH>

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 ||||
 Db 8 PPP 10

RESULT 33

PA0060
 Protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0060
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 Submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A;Reference number: PA0051
 A;Accession: PA0060
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 ||||
 Db 4 PLP 6

RESULT 34

B61457
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
 C;Accession: B61457
 R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
 J. Protozool. 36, 562-567, 1989
 A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
 A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457
 A;Molecule type: protein
 A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGCS

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 7 PPL 9

RESULT 35

A60221
 apolipoprotein A-I - common carp (fragment)

C;Species: Cyprinus carpio (common carp)
 C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993
 C;Accession: A60221
 R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.
 J. Neurochem. 55, 1237-1243, 1990

A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve
 A;Reference number: A60221; MUID:90376100; PMID:2118944
 A;Accession: A60221
 A;Molecule type: protein
 A;Residues: 1-15 <HAR>
 A;Note: protein from plasma and from optic nerve yielded the same sequence
 C;Keywords: lipid binding; lipoprotein

Query Match 42.9%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 ||||
 Db 2 QPP 4

RESULT 36

I57530

gene c-fms protein - mouse (fragment)

C;Species: Mus sp. (mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-May-1997
 C;Accession: I57530
 R;Yue, X.; Favot, P.; Dunn, T.L.; Cassidy, A.I.; Hume, D.A.
 Mol. Cell. Biol. 13, 3191-3201, 1993

A;Title: Expression of mRNA encoding the macrophage colony-stimulating factor recept
 A;Reference number: I57530; MUID:93268269; PMID:8497248

A;Accession: I57530

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-16 <RES>

A;Cross-references: GB:S62219; NID:g386001

C;Genetics:

A;Gene: C-fms

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homo

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 5 PPL 7

RESULT 37

S57517

T cell receptor beta chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57517

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversifi

A;Reference number: S57494

A;Accession: S57517

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <BUR>

A;Cross-references: EMBL:Z49924; NID:g887480; PIDN:CAA90170.1; PID:g887481

C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 ||||
 Db 5 PPL 7

RESULT 38

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
 C:Accession: JH0517
 R:Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
 Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
 A:Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
 A:Reference number: JH0515; MUID:92109718; PMID:1722398
 A:Accession: JH0517
 A:Molecule type: protein
 A:Residues: 1-16 <COL>
 A:Experimental source: serum

Query Match 42.9%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 39

S57991
 hydroxyproline-rich protein - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata
 C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jan-2000

R:Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.
 submitted to the EMBL Data Library, March 1995
 A:Description: Use of differential display to identify novel Sesbania rostrata genes enb
 A:Reference number: S57991
 A:Accession: S57991
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-17 <GOO>
 A:Cross-references: EMBL:248673; NID:g899484; PID:g899485
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 10 PPP 12

RESULT 40

S59481
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)
 C>Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998

R:Wojtaszek, P.; Tretlowan, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to differ
 A:Reference number: S59481; MUID:96011753; PMID:7548825
 A:Accession: S59481
 A:Molecule type: protein
 A:Residues: 1-17 <WOJ>
 C:Keywords: glycoprotein; hydroxyproline
 F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 8 PPP 10

RESULT 41

S10786
 enamelin, 26K - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)
 C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C:Accession: S10786
 R:Strawich, E.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990

A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
 A:Reference number: S10780; MUID:90336641; PMID:2379503
 A:Accession: S10786
 A:Molecule type: protein
 A:Residues: 1-17 <STR>
 C:Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
 |||
 Db 3 QPP 5

RESULT 42

S04229
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)

A:Alternate names: glycosylasparaginase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C:Accession: S04229
 R:Tollersrud, O.K.; Aronson Jr., N.N.
 Biochem. J. 260, 101-108, 1989

A:Title: Purification and characterization of rat liver glycosylasparaginase.
 A:Reference number: S04228; MUID:89374025; PMID:2775174
 A:Accession: S04229
 A:Molecule type: protein
 A:Residues: 1-18 <TOL>
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
 C:Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 |||
 Db 3 PLP 5

RESULT 43

I52614
 u-plasminogen activator receptor precursor - human (fragment)

C:Species: Homo sapiens (man)
 C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 R:Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.
 Blood 86, 624-635, 1995
 A:Title: A conserved TATA-less proximal promoter drives basal transcription from the
 A:Reference number: I52614; MUID:95329719; PMID:7605992
 A:Accession: I52614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-18 <RES>
 A:Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989
 C:Genetics:
 A:Gene: UPAR
 C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 42.9%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
|||
Db 4 PPL 6

RESULT 44

C56211
progesterone receptor-related protein p23 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C:Accession: C56211

R:Johnson, J.L.; Beito, T.G.; Krco, C.J.; Toft, D.O.

Mol. Cell. Biol. 14, 1956-1963, 1994

A:Title: Characterization of a novel 23-kilodalton protein of inactive progesterone receptor

A:Reference number: A56211; MUID:94158868; PMID:8114727

A:Accession: C56211

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <JOH>

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10

C:Keywords: steroid hormone receptor

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
|||
Db 1 MQP 3

RESULT 45

A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002

C:Accession: A54195

R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase

A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <ESM>

A:Experimental source: rectal gland

A:Note: sequence extracted from NCBI backbone (NCBIP:149363)

C:Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 8 PPP 10

RESULT 46

S60633
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion

C:Species: mitochondrion Artemia sp. (brine shrimp)

A:Variety: strain La Mata

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002

C:Accession: S60633

R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.

J. Mol. Evol. 38, 156-168, 1994

A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic populations

A:Reference number: S60624; MUID:94223692; PMID:8169960

A:Accession: S60633

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-19 <PER>

C:Keywords: hydrolase

C:Keywords: hydrolase

A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211
A:Experimental source: strain La Mata
A:Note: the source is designated as Artemia parthenogenetica
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Genetics:

A:Gene: ATP8

A:Genome: mitochondrion

A:Genetic code: SGC4

C:Superfamily: H+-transporting ATP synthase protein 8

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
|||
Db 6 PPL 8

RESULT 47

G56819

PS I complex subunit 6 - cucumber (fragment)

C:Species: Cucumis sativus (cucumber)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: G56819

R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-146, 1991

A:Title: Characterization of genes that encode subunits of cucumber PS I complex by

A:Reference number: A56819; MUID:91355209; PMID:1883835

A:Accession: G56819

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <IWA>

A:Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 48

S59486
cell wall protein, 22K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S59486

R:Wojtaszek, P.; Iretrowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to diff

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59486

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <WOU>

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
|||
Db 3 QPP 5

RESULT 49

A37968

neural surface protein Bravo - chicken (fragment)

C:Species: Gallus gallus (chicken)

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997

C;Accession: A37968; A36345
 R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 112, 1049, 1991
 A;Reference number: A37968; MUID:91154309; PMID:1999455
 A;Contents: extratum
 A;Accession: A37968
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19
 R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
 J. Cell Biol. 111, 3067-3096, 1990
 A;Title: Topologically restricted appearance in the developing chick retinotectal system
 A;Reference number: A36345; MUID:91100421; PMID:2269667
 A;Accession: A36345
 A;Molecule type: protein
 A;Residues: 1-7,9-19 <DE2>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 2 QPP 4
 |||
 Db 15 QPP 17

RESULT 50

PH1352
 Ig heavy chain DJ region (clone C100-115) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1352
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1352
 A;Molecule type: DNA
 A;Residues: 1-19 <WAS>
 A;Note: the authors translated the stop codon for residue 2 as X
 C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 51

S50018
 hyaluronidase - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
 C;Accession: S50018
 R;Gacasa, P.; Civill, N.D.; Harrison, R.A.P.
 Biochem. J. 303, 335-336, 1994
 A;Title: PH-20 and sperm hyaluronidase: a conceptual conundrum in mammalian fertilization
 A;Reference number: S50018; MUID:95031981; PMID:7945261
 A;Accession: S50018
 A;Molecule type: protein
 A;Residues: 1-19 <GAC>

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 4 PPL 6
 |||
 Db 5 PPL 7

RESULT 52

S25715
 hypothetical protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S25715; S21390
 R;Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
 Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992
 A;Title: Identification of murine homologues of the Drosophila Son of sevenless gene.
 A;Reference number: S25714; MUID:92335328; PMID:1631150
 A;Accession: S25715
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <BOW>
 A;Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133
 R;Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.
 submitted to the EMBL Data Library, January 1992
 A;Description: Identification of murine homologues of the Drosophila Son of sevenless
 A;Reference number: S21390
 A;Accession: S21390
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <BO2>
 A;Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133

Query Match 42.9%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
 |||
 Db 2 PPP 4

RESULT 53

S29817
 cytochrome P450 2C23 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
 C;Accession: S29817
 R;Marie, S.; Roussel, F.; Cresteil, T.
 Biochim. Biophys. Acta 1172, 124-130, 1993
 A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
 A;Reference number: S29817; MUID:93176794; PMID:7679925
 A;Accession: S29817
 A;Molecule type: mRNA
 A;Residues: 1-20 <MAR>
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 42.9%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 5 PLP 7
 |||
 Db 4 PLP 6

RESULT 54

D42842
 antifungal 2S storage albumin large chain - radish (fragment)
 C;Species: Raphanus sativus (radish)
 C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C;Accession: D42842
 R;Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderley
 J. Biol. Chem. 267, 15301-15309, 1992
 A;Title: Analysis of two novel classes of plant antifungal proteins from radish (Raph
 A;Reference number: A42842; MUID:92348373; PMID:1639777
 A;Accession: D42842
 A;Status: preliminary

A:Reference number: A42267; MUID:92156146; PMID:1740450
A:Accession: A42267
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <KAW>
A:Cross-references: GB:M81866

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 13 PPP 15

RESULT 58

A31516
lestin, galactose/N-acetylgalactosamine-specific - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: A31516
R:Fi, M.; Kawasaki, T.; Yamashina, I.
Biochem. Biophys. Res. Commun. 155, 720-725, 1988
A:Title: Structural similarity between the macrophage lectin specific for galactose
A:Reference number: A31516; MUID:88339956; PMID:3421964
A:Accession: A31516
A:Molecule type: protein
A:Residues: 1-20 <IIX>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 16 PPP 18

RESULT 59

A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C:Accession: A32039
R:Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fac
A:Reference number: A32039; MUID:89123285; PMID:2563371
A:Accession: A32039
A:Molecule type: protein
A:Residues: 1-4 <HOR>
A:Experimental source: brain
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
|||
Db 2 PL 3

RESULT 60

HOROHA
proctolin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01644
R:Starratt, A.N.; Brown, B.E.

A:Molecule type: protein
A:Residues: 1-20 <TER>
A:Experimental source: seed
A>Note: sequence extracted from NCBI backbone (NCBIP:109925)
C:Superfamily: wheat alpha-amylase inhibitor

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
|||
Db 8 PPL 10

RESULT 55

S65605
dimeric protein (BDP) - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: S65605
R:Garcia-Casado, G.; Armentia, A.; Sanchez-Monge, R.; Sanchez, L.M.; Lopez-Otin, C.; Sal
FEBS Lett. 364, 36-40, 1995
A:Title: A major baker's asthma allergen from rye flour is considerably more active than
A:Reference number: S65604; MUID:95269763; PMID:7750539
A:Accession: S65605
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAR>

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
|||
Db 18 PLP 20

RESULT 56

S46479
retinoid-X-receptor-gamma - chicken
C:Species: Gallus gallus (chicken)
C>Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C:Accession: S46479
R:Seleiro, E.A.P.; Darling, D.; Brickell, P.M.
Biochem. J. 301, 283-288, 1994
A:Title: The chicken retinoid-X-receptor-gamma gene gives rise to two distinct species c
A:Reference number: S46478; MUID:94311845; PMID:8037682
A:Accession: S46479
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <SEL>
A:Cross-references: GB:S72435; MID:9619294; PIDN:AAB31348.1; PID:9619295

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
|||
Db 1 MQP 3

RESULT 57

A42267
J-kappa recombination sequence-binding protein RBP-2N - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: A42267; S23798
R:Kawauchi, M.; Oka, C.; Shibayama, S.; Koromilas, A.E.; Matsunami, N.; Hanaguchi, Y.; H
J. Biol. Chem. 267, 4016-4022, 1992
A:Title: Geromic organization of mouse J-kappa recombination signal binding protein (RBF

Life Sci. 17, 1253-1256, 1975
 A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
 A;Reference number: A93048; MUID:7607408; PMID:576
 A;Accession: A01644
 A;Molecule type: protein
 A;Residues: 1-5 <STA>
 A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.
 R;O'Shea, M.; Adams, M.E.
 Science 213, 567-569, 1981
 A;Title: Pentapeptide (proctolin) associated with an identified neuron.
 A;Reference number: A94260; MUID:81225865; PMID:6113690
 A;Contents: annotation; biological source
 A;Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.
 C;Superfamily: proctolin
 C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 6 LP 7
 ||
 Db 3 LP 4

RESULT 61

JN0860
 C;Title: dipeptidase A inhibitory peptide C107 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0860
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
 A;Reference number: JN0859; MUID:94060036; PMID:7764272
 A;Accession: JN0860
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: intestine
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory activity.
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 6 LP 7
 ||
 Db 2 LP 3

RESULT 62

E42364
 C;Title: flagellar protein flir - Salmonella typhimurium (fragment)
 C;Species: Salmonella typhimurium
 C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
 C;Accession: E42364
 R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
 J. Bacteriol. 173, 3564-3572, 1991
 A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion
 A;Reference number: E42364; MUID:91258342; PMID:1646201
 A;Accession: E42364
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <VOG>
 A;Cross-references: GB:M62408

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 6 LP 7
 ||
 Db 4 LP 5

RESULT 63

B37988
 C;Title: acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C;Species: Physarum polycephalum
 C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 C;Accession: B37988
 R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990
 A;Title: Purification and characterization of a novel intracellular acid proteinase
 A;Reference number: A37988; MUID:91060608; PMID:2246266
 A;Accession: B37988
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 3 PP 4
 ||
 Db 3 PP 4

RESULT 64

A60411
 C;Title: proctolin - Atlantic horseshoe crab
 C;Species: Limulus polyphemus (Atlantic horseshoe crab)
 C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
 C;Accession: A60411
 R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, P. J. Biol. Chem. 265, 205-211, 1990
 A;Title: Identification of proctolin in the central nervous system of the horseshoe crab
 A;Reference number: A60411; MUID:90287800; PMID:2356151
 A;Accession: A60411
 A;Molecule type: protein
 A;Residues: 1-5 <GRO>
 C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horseshoe crab.
 C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 6 LP 7
 ||
 Db 3 LP 4

RESULT 65

I67345
 C;Title: MHC H2-K-k cell surface glycoprotein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I67345
 R;Archibald, A.L.; Thompson, N.A.; Kvist, S.
 EMBO J. 5, 957-965, 1986
 A;Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the H2-K-k gene
 A;Reference number: I67345; MUID:86247587; PMID:3013627
 A;Accession: I67345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M26859; NID:9199439; PIDN:AAA39612.1; PID:G387458

Query Match 28.6%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 6 LP 7
 ||
 Db 3 LP 4

QY 6 LP 7
 ||
 Db 3 LP 4

Query Match 28.6%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 1 LP 2

RESULT 66

A35039
 Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: A35039
 R:Bennett, V.D.; Adams, S.L.
 J. Biol. Chem. 265, 2223-2230, 1990
 A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 2(I) collagen gene
 A:Reference number: A35039; MUID:90130479; PMID:1688851
 A:Accession: A35039
 A:Molecule type: mRNA
 A:Residues: 1-6 <BEN>
 A:Cross-references: GB:M33382; NID:g211043
 A:Note: This ORF is not translated in GenBank entry CHKA21CG
 C:Comment: This sequence is the translation of a cartilage specific alternative transcript
 C:Keywords: alternative splicing; cartilage

Query Match 28.6%; Score 2; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 4 LP 5

RESULT 67

A61081
 Cryptophyllin, basic - Rohde's leaf frog
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C:Accession: A61081
 R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
 Int. J. Pept. Protein Res. 33, 391-395, 1989
 A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containing peptide
 A:Reference number: A61081
 A:Accession: A61081
 A:Molecule type: protein
 A:Residues: 1-7 <MON>
 C:Comment: The biological activity of this peptide was not determined.
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; hydroxyproline; skin
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
 ||
 Db 2 PP 3

RESULT 68

PC1316
 large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)
 C:Species: Tachypleus tridentatus
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1316
 R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993
 A:Title: Separation of large and small granules from horseshoe crab (Tachypleus tridentatus)

A:Reference number: PC1309; MUID:94110249; PMID:8282718
 A:Accession: PC1316
 A:Molecule type: protein
 A:Residues: 1-7 <SHI>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 3 QP 4

RESULT 69

B39040
 Calsequestrin, fast skeletal muscle - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
 C:Accession: B39040
 R:Gala, S.E.; Jones, L.R.
 J. Biol. Chem. 266, 391-398, 1991
 A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by calmodulin
 A:Reference number: A39040; MUID:91093153; PMID:1983907
 A:Accession: B39040
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <CAL>
 C:Keywords: phosphoprotein; skeletal muscle

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 6 LP 7

RESULT 70

I48105
 dihydrofolate reductase - Chinese hamster (fragment)
 C:Species: Cricetus griseus (Chinese hamster)
 C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C:Accession: I48105
 R:Aizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
 Biochemistry 25, 6228-6236, 1986
 A:Title: Nucleotide sequence and nuclelease hypersensitivity of the Chinese hamster dihydrofolate reductase
 A:Reference number: I48105; MUID:87076541; PMID:3024702
 A:Accession: I48105
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
 ||
 Db 4 PL 5

RESULT 71

I48086
 DNA topoisomerase II alpha - Chinese hamster (fragment)
 C:Species: Cricetus griseus (Chinese hamster)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48086
 R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
 J. Biol. Chem. 270, 25850-25858, 1995

A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster
 A:Reference number: I48086; MUID:96029684; PMID:7592770
 A:Accession: I48086
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
 ||
 Db 5 PL 6

RESULT 72

S66442
 Glutathione S-transferase P - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 A:Accession: S66442
 R:Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
 Eur. J. Biochem. 232, 106-110, 1995
 A:Title: Identification of the electrophilic substrate-binding site of glutathione S-transferase P from Rattus norvegicus
 A:Reference number: S66442; MUID:96048035; PMID:7556138
 A:Accession: S66442
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NIS>

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 2 LP 3

RESULT 73

A39690
 neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 A:Accession: A39690
 R:Reyes, A.A.; Small, S.J.; Akesson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA from Rattus norvegicus
 A:Reference number: A39690; MUID:91141516; PMID:1996115
 A:Accession: A39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-7 <REY>
 A:Cross-references: GB:M63970
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 1 QP 2

RESULT 74

A58718
 carnocin UI49 - Carnobacterium sp. (fragment)
 C:Species: Carnobacterium sp.
 C:Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 A:Accession: A58718

R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
 Appl. Environ. Microbiol. 58, 1417-1422, 1992
 A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobacterium strain
 A:Reference number: A58718; MUID:92321768; PMID:1622206
 A:Accession: A58718
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <STO>
 C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
 ||
 Db 5 QP 6

RESULT 75

S45648
 Na+-transporting ATP synthase (EC 3.6.1.1-) alpha chain - Acetobacterium woodii (fragment)
 N:Alternate names: ATPase alpha chain
 C:Species: Acetobacterium woodii
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 A:Accession: S45648
 R:Reidlinger, J.; Mueller, V.
 Eur. J. Biochem. 223, 275-283, 1994
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification of its subunits
 A:Reference number: S45648; MUID:94307271; PMID:8033902
 A:Accession: S45648
 A:Molecule type: protein
 A:Residues: 1-374-7 <REI>
 A:Experimental source: DSM 1030
 C:Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
 ||
 Db 3 LP 4

Search completed: November 25, 2003, 18:28:11
 Job time : 7.44149 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 3.383 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-1
Perfect score: 7
Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 3 | 42.9 | 10 | 1 | TMOF_AEDAE |
| 2 | 3 | 42.9 | 11 | 1 | MORN_HUMAN |
| 3 | 3 | 42.9 | 11 | 1 | TIN4_HOPTI |
| 4 | 3 | 42.9 | 12 | 1 | TIN2_HOPTI |
| 5 | 3 | 42.9 | 12 | 1 | TIN3_HOPTI |
| 6 | 3 | 42.9 | 13 | 1 | TY13_PHYRO |
| 7 | 3 | 42.9 | 14 | 1 | ECDC_LYMDI |
| 8 | 3 | 42.9 | 15 | 1 | AFIL_MALPA |
| 9 | 3 | 42.9 | 15 | 1 | PRP_MYCBO |
| 10 | 3 | 42.9 | 16 | 1 | IBPI_PIG |
| 11 | 3 | 42.9 | 17 | 1 | APID_BOMPA |
| 12 | 3 | 42.9 | 19 | 1 | PSAE_CUCSA |
| 13 | 2 | 28.6 | 5 | 1 | PRCT_PERAM |
| 14 | 2 | 28.6 | 6 | 1 | TRPI_PSEPU |
| 15 | 2 | 28.6 | 6 | 1 | VP19_HSV1K |
| 16 | 2 | 28.6 | 7 | 1 | LANC_CARUI |
| 17 | 2 | 28.6 | 7 | 1 | MNPI_LEPDE |
| 18 | 2 | 28.6 | 7 | 1 | TPFY_PACDA |
| 19 | 2 | 28.6 | 7 | 1 | UF04_MOUSE |
| 20 | 2 | 28.6 | 7 | 1 | UN06_PINPS |
| 21 | 2 | 28.6 | 8 | 1 | ALL5_CALVO |
| 22 | 2 | 28.6 | 8 | 1 | ALL6_CYDPO |
| 23 | 2 | 28.6 | 8 | 1 | COW2_CONFU |
| 24 | 2 | 28.6 | 8 | 1 | NPB_BOVIN |
| 25 | 2 | 28.6 | 8 | 1 | PKP2_PERAM |
| 26 | 2 | 28.6 | 9 | 1 | AL10_CARMA |
| 27 | 2 | 28.6 | 9 | 1 | COXE_THUOB |
| 28 | 2 | 28.6 | 9 | 1 | FAR3_PENNO |
| 29 | 2 | 28.6 | 9 | 1 | FAR4_PENNO |
| 30 | 2 | 28.6 | 9 | 1 | FAR9_ASCSU |
| 31 | 2 | 28.6 | 9 | 1 | PRF1_SARBU |
| 32 | 2 | 28.6 | 9 | 1 | KNL3_BOMVA |
| 33 | 2 | 28.6 | 9 | 1 | LMT3_LOEMI |
| 34 | 2 | 28.6 | 9 | 1 | OXYA_SQUAC |
| 35 | 2 | 28.6 | 9 | 1 | XYT_RABIT |
| 36 | 2 | 28.6 | 9 | 1 | RS10_SERVA |
| 37 | 2 | 28.6 | 9 | 1 | RT33_BOVIN |
| 38 | 2 | 28.6 | 9 | 1 | UPA3_HUMAN |
| 39 | 2 | 28.6 | 9 | 1 | YBFR_AZOVI |
| 40 | 2 | 28.6 | 10 | 1 | AH3_FRUSE |
| 41 | 2 | 28.6 | 10 | 1 | BP22_BOTIN |
| 42 | 2 | 28.6 | 10 | 1 | BP22_BOTJA |
| 43 | 2 | 28.6 | 10 | 1 | BP28_BOTIN |
| 44 | 2 | 28.6 | 10 | 1 | BP2_VIPAS |
| 45 | 2 | 28.6 | 10 | 1 | BRK_ONCMY |
| 46 | 2 | 28.6 | 10 | 1 | CATB_SHEEP |
| 47 | 2 | 28.6 | 10 | 1 | FAR6_PANRE |
| 48 | 2 | 28.6 | 10 | 1 | GON1_ALLMI |
| 49 | 2 | 28.6 | 10 | 1 | GON1_ONCKE |
| 50 | 2 | 28.6 | 10 | 1 | GONL_SQUAC |
| 51 | 2 | 28.6 | 10 | 1 | NO40_TOBAC |
| 52 | 2 | 28.6 | 10 | 1 | NS1_MYCTU |
| 53 | 2 | 28.6 | 10 | 1 | PSBF_CAPAN |
| 54 | 2 | 28.6 | 10 | 1 | TEMK_RANTE |
| 55 | 2 | 28.6 | 10 | 1 | TKL2_LOEMI |
| 56 | 2 | 28.6 | 10 | 1 | UPA2_HUMAN |
| 57 | 2 | 28.6 | 10 | 1 | UPA5_HUMAN |
| 58 | 2 | 28.6 | 10 | 1 | URE3_MORMO |
| 59 | 2 | 28.6 | 11 | 1 | BP23_BOTIN |
| 60 | 2 | 28.6 | 11 | 1 | BP24_BOTIN |
| 61 | 2 | 28.6 | 11 | 1 | BP28_AKSHA |
| 62 | 2 | 28.6 | 11 | 1 | BP2_AKHP |
| 63 | 2 | 28.6 | 11 | 1 | BRK_MEGFL |
| 64 | 2 | 28.6 | 11 | 1 | EPG_CLOPA |
| 65 | 2 | 28.6 | 11 | 1 | LADD_ONCMY |
| 66 | 2 | 28.6 | 11 | 1 | LPW_THETH |
| 67 | 2 | 28.6 | 11 | 1 | PQOC_PSEFL |
| 68 | 2 | 28.6 | 11 | 1 | TKN1_PSEGU |
| 69 | 2 | 28.6 | 11 | 1 | TKN2_PSEGU |
| 70 | 2 | 28.6 | 11 | 1 | TKN3_PSEGU |
| 71 | 2 | 28.6 | 11 | 1 | TKN4_PSEGU |
| 72 | 2 | 28.6 | 11 | 1 | TKN5_PSEGU |
| 73 | 2 | 28.6 | 11 | 1 | TKN5_PSEGU |
| 74 | 2 | 28.6 | 12 | 1 | FAR7_PENMO |
| 75 | 2 | 28.6 | 12 | 1 | FARI_CALVO |
| 76 | 2 | 28.6 | 12 | 1 | FIFI_SARBU |
| 77 | 2 | 28.6 | 12 | 1 | GRAR_RANRU |
| 78 | 2 | 28.6 | 12 | 1 | HS9A_RAT |
| 79 | 2 | 28.6 | 12 | 1 | NUDM_CANFA |
| 80 | 2 | 28.6 | 12 | 1 | PPK4_PERAM |
| 81 | 2 | 28.6 | 12 | 1 | RS19_TOBBP |
| 82 | 2 | 28.6 | 12 | 1 | TKN2_KASMA |
| 83 | 2 | 28.6 | 12 | 1 | TM2A_METMA |
| 84 | 2 | 28.6 | 13 | 1 | ACT7_SOYBN |
| 85 | 2 | 28.6 | 13 | 1 | AH4_FRUSE |
| 86 | 2 | 28.6 | 13 | 1 | BP21_BOTJA |
| 87 | 2 | 28.6 | 13 | 1 | BRK_PARID |
| 88 | 2 | 28.6 | 13 | 1 | CRBL_ICASP |
| 89 | 2 | 28.6 | 13 | 1 | CRBL_VESAN |
| 90 | 2 | 28.6 | 13 | 1 | CRBL_VESCR |
| 91 | 2 | 28.6 | 13 | 1 | CRBL_VESLE |
| 92 | 2 | 28.6 | 13 | 1 | CRBL_VESMA |
| 93 | 2 | 28.6 | 13 | 1 | CRBL_VESTR |
| 94 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 95 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 96 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 97 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 98 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 99 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |
| 100 | 2 | 28.6 | 13 | 1 | CRBL_VESXA |

RESULT 1

ALIGNMENTS

P42999 squalus aca
P32878 oryctolagus
O69336 seriatia ma
P82926 bos taurus
P30089 homo sapien
P25825 azotobacter
P29261 prunus sero
P01022 bothrops ja
P30426 bothrops in
P31351 vipera aspi
Q99prz1 oncorhynch
P82305 ovnis aries
P82660 panagrellus
P37041 alligator m
P20167 oncorhynch
P27429 squalus aca
P55962 nicotiana t
P81135 mycobacteri
Q03367 capsicum an
P56923 rana tempor
P16224 locusta mig
P30088 homo sapien
P30091 homo sapien
P17339 morganelia
P30423 bothrops in
P30424 bothrops in
P01021 agkistrodon
P04562 agkistrodon
P12797 megascollia
P81350 clostridium
P81018 oncorhynch
P05624 thermus the
P55173 pseudomonas
P42866 pseudophryn
P08612 uperoleia r
P42987 pseudophryn
P42988 pseudophryn
P42989 pseudophryn
P42990 pseudophryn
P01323 eledone mos
P83322 penaeus mon
P41869 calliphora
P83349 sarcophaga
P40754 rana rugosa
P82995 rattus norv
P54713 canis famli
Q52619 periplaneta
P08614 kassina mac
P08614 kassina mac
P15937 glycine max
P29262 prunus sero
P01020 bothrops ja
P42717 parapolybia
P17233 vespa anali
P17233 vespa anali
P01518 vespa crabr
P17235 vespa lew
P17232 vespa manda
P17231 vespa tropi
P17234 vespa xanth
P1832 rana esculie
P82098 litoria rub
P54963 homo sapien
P14478 oryctolagus
P28525 hordeum vul

TMOF_AEDAE ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RX STRAIN=Vero beach; TISSUE=Ovary;
RC MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RX STRAIN=Vero beach; TISSUE=Ovary;
RC MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236DOA7777776DC7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 5 PPP 7

RESULT 2
ID MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human).
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).

[2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82950803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHET.
DR PIR; A93900; YHAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; --
KW Growth factor; Cell cycle; Mitosis; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 1 QPP 3

RESULT 3
ID TIN4 HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.

```

FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 4
TIN2_HOPI
ID TIN2_HOPI STANDARD; PRT; 12 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX TISSUE=Skin secretion;
RC PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B. SUBTILIS, E. COLI,
CC S. AUREUS, M. LUTEUS, P. PUTIDA AND S. CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 5
TIN3_HOPI
ID TIN3_HOPI STANDARD; PRT; 12 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX TISSUE=Skin secretion;
RC PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana

```

```

RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B. SUBTILIS, E. COLI,
CC S. AUREUS, M. LUTEUS, P. PUTIDA AND S. CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
7 PLP 9

RESULT 6
TIN3_PHYRO
ID TIN3_PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A21222773 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 7
ECDC_LYMDI
ID ECDC_LYMDI STANDARD; PRT; 14 AA.
AC P80940;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis edysiotropin peptide C (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;

```



```

RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 5 PPL 7
Db 9 PPL 11

RESULT 8
AFIL_MALPA STANDARD; PRT; 15 AA.
AC P83141;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Antifungal protein 1 large subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OC NCBI_TaxID=145753;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RL parviflora).";
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC NOT F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO: GO:0003799; F:antifungal peptide activity; IDA.
KW Fungicide; Antibiotic.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1783 MW; 2CB3079F53CC70F9 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 PPL 6
Db 8 PPL 10

RESULT 9
PRP_MYCBO STANDARD; PRT; 15 AA.
AC P80149;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE Proline-rich protein (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;

```

```

RX MEDLINE=93281750; PubMed=8506381;
RA Romain F., Audier J., Pescher P., Marchal G.A.;
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
RT type hypersensitivity reactions only in guinea pigs immunized with
RT living mycobacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
CC REACTIONS IN GUINEA PIGS.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
Db 7 PPP 9

RESULT 10
IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109719; PubMed=1722398;
RA Coleman W.E., Pan X.-C.E., Ehterton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 IGFBP domain.
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR000716; Thyroglobulin_1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 PPP 5
Db 7 PPP 9

RESULT 11
APID_BOMPA STANDARD; PRT; 17 AA.
ID APID_BOMPA
AC P81464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

```

```

DT 15-SBP-2003 (Rel. 42, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN [1]_TaxID=65598;
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=9219367;
RA MEDLINE=97362903;
RX Rees J.A., Montatte M., Bulet P.;
RT "Novel antibacterial peptides isolated from a European bumblebee,
RT Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
CC InterPro: IPR004828; Apidaecin.
DR Pfam: PF00807; Apidaecin; 1.
KW Insect immunity; Antibiotic; Hemolymph.
SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 8 PPP 10

RESULT 12
PSAE_CUUSA STANDARD; PRT; 19 AA.
AC P42047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5
DE kDa protein) (PS I subunit 6) (Fragment).
GN PSAB.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid 1; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]_TaxID=3659;
RP SEQUENCE.
RC TISSUE=Cotyledon; PubMed=1883835;
RX MEDLINE=91355209;
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing.";
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: Stabilizes the interaction between psac and the PSI
CC core, assists the docking of the ferredoxin to PSI and interacts
CC with ferredoxin-NADP oxidoreductase (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.
DR PIR; G56819; G56819.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NONTER 19
FT SEQUENCE 19 AA; 1810 MW; A93E8BDD089FB738 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
DB 6 PPP 8

RESULT 13
PRACT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach), and
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]_TaxID=6978, 6850, 6759;
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]_TaxID=76074708, 576;
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]_TaxID=81225865, 6113690;
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]_TaxID=90287800, 2356151;
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 3 LP 4

RESULT 14
TRPI_PSEPU STANDARD; PRT; 6 AA.
ID TRPI_PSEPU
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

```


TISSUE=Head;
MEDLINE=95380343; PubMed=7651886;
RA Spittels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotonic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata";
RL Peptides 16:365-374(1998);
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC Neuropeptide; Amidation.
KW MOD RES 7
FT SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PL 6
DB 5 PL 6
RESULT 18
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (pdt-1)
OS Pachymedusa dactylor (Giant mexican leaf frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
CC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RA TISSUE=Skin secretion;
RA Chen T.B., Orr D.P., Shaw C.;
RT "pachymedusa dactylor tryptophyllin-1 (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra...; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3
FT MOD RES 3
FT MOD RES 3
FT SEQUENCE 7 AA; 794 MW; 7772D37BC776350 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PP 4
DB 2 PP 3
RESULT 19
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RC MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PP 4
DB 3 PP 4
RESULT 20
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RC MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON TER 1
FT NON TER 7
FT SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;
SQ
Query Match 28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 LP 7
DB 5 LP 6
RESULT 21
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) ([Hyp3]Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCB1_TaxID=27454;
RN [1]
RN SEQUENCE
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RA "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RN CHARACTERIZATION, AND HYDROXYLATION.
RP TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RA "[Hyp3]Met-callistatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393;
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 2 PP 3

RESULT 22
ALL6_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCB1_TaxID=82600;
RN [1]
RN SEQUENCE.
RP TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RA "Lepidopteran peptides of the allatostatin superfamily.";
RT Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 5 LP 6

RESULT 24
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RN SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;
RA "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Db 1 LP 2

RESULT 23
COM2_CONPU STANDARD; PRT; 8 AA.
ID COM2_CONPU
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCB1_TaxID=41690;
RN [1]
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388939; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RA "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732C5B8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 5 LP 6

RESULT 24
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RN SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;
RA "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
||

Db 4 QP 5

RESULT 25

PPK2 PERAM
ID -PPK2 PERAM STANDARD; PRT; 8 AA.
AC P82632;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
||

Db 2 PP 3

RESULT 26

AL10 CARMA
ID -AL10 CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoides; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

RA "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
||

Db 3 QP 4

RESULT 27

COXE THUOB
ID -COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
||

Db 3 QP 4

RESULT 28

FAR3 PENMO
ID -FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE FMRamide-like neuropeptide FLP3 (AOPSMRLRF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=VALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1105 MW; CDD107340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 29
FAR4 PENMO
ID FAR4 PENMO STANDARD; PRT; 9 AA.
AC P8319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=VALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 2 QP 3

RESULT 30
FAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF9.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
DB 6 PL 7

RESULT 31
FRF1_SARBU
ID FRF1_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
protein-coupled FMRamide receptor."
Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 1 QP 2

```

RESULT 32

KNL3_BOMVA
ID_KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McLean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
arterial smooth muscle and constriction of intestinal smooth
muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4

DB 2 PP 3

RESULT 33

LMT3_LOCFI
ID_LMT3_LOCFI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
IV, two additional neuropeptides of Locusta migratoria: members of the
locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3

DB 3 QP 4

RESULT 34

ID_OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
RL Bur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6

DB 7 PL 8

RESULT 35

OXYT_RABIT
ID_OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oxytocin cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus),
OS Balaenoptera physalus (Finback whale) (Common rorqual), and
OS Tachyglossus aculeatus (Australian echidna), and
OS Hydrolagus colliiei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=7215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).


```

RN RP SEQUENCE.
RC SPECIES=H.amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RL neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
[3]
RN RP SEQUENCE.
RC SPECIES=B.physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
[4]
RN RP SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophysial hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
[5]
RN RP SEQUENCE.
RC SPECIES=H.collicia;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophysial hormone in the holocephalian
RT elasmobranch fish, Hydroloagus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1
FT MOD RES 9 9 AMIDATION.
FT SEQ SEQUENCE 9 AA; 1010 MW; 17P8376EB456D04B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
Db 7 PL 8

RESULT 36
RS10 SERVA STANDARD; PRT; 9 AA.
AC O68936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RPSJ.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity). BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL; AF058451; AAC14294.1; -
DR HAMAP; MF_00508; -; 1.
DR InterPro; IPR001848; Ribosomal_S10.
DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
KW Ribosomal protein.
FT NON TER 9
FT SEQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
Db 1 MQ 2

RESULT 37
RT33 BOVIN STANDARD; PRT; 9 AA.
AC P82928;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=Liver;
RP SEQ SEQUENCE.
RC MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON TER 1
FT NON TER 9
FT SEQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
Db 5 QP 6

RESULT 38
UPA3 HUMAN STANDARD; PRT; 9 AA.
ID UPA3 HUMAN
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)

```

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RA MEDLINE=93092937; PubMed=1459037;
 RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1056 MW; 2672B1BAF769C737 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
 ||
 Db 2 PL 3

RESULT 39
 YBFR AZOVI
 ID YBFR AZOVI STANDARD; PRT; 9 AA.
 AC P25825;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in bfr 3' region (Fragment).
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196129; PubMed=1549605;
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
 RA Stiefel E.I.;
 RT "Unification of the ferritin family of proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M83692; AAA22122.1; -;
 DR FTR; B41983; B41983.
 KW Hypothetical protein.
 FT NON_TER 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
 ||
 Db 3 PP 4

RESULT 40
 AH3_PRUSE
 ID AH3_PRUSE STANDARD; PRT; 10 AA.
 AC P29261;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
 DE isozyme II) (AH II) (Fragment).
 OS Prunus serotina (Black cherry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-290(1992).
 CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
 CC glucose.
 CC -!- SUBUNIT: Monomer.
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
 CC EMBRYONAL TISSUES.
 CC -!- PTM: GLYCOSYLATED.
 CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
 ||
 Db 3 PP 4

RESULT 41
 BPP2_BOTIN
 ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR FTR; B37196; B37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1
 FT MOD_RES 1
 FT MOD_RES 1
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

```

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 42
BPP2 BOTJA
ID_BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A01255; XAVI6B.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 43
BPP8 BOTIN
ID_BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RA "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";
RT J. Protein Chem. 9:221-227(1990).
RL

```

```

CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; H37196; H37196.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 44
BPP VIPAS
ID_BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A60377; XASNPC.
DR Hypotensive agent; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PP 4
DB      9 PP 10

RESULT 45
BRK ONCMY
ID_BRK_ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.

```

```

RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RL trout plasma.";
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
Db 3 PP 4

RESULT 46
CATB_SHEEP
ID CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSB.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; SHP00T_acsite.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LP 7
Db 1 LP 2

```

```

RESULT 47
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRFamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 5 QP 6

RESULT 48
GON1_ALLMI
ID GON1_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 4, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 8 QP 9

RESULT 49
GON3_ONCKE
ID GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-RH III) (Luliberin III).
GN GNRH3.
OS Onchorynchus keta (Chum salmon), and
OS Clupea pallasi (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 30724;
RN [1]
RP SEQUENCE.
RC SPECIES=O.keta; PubMed=6341999;
RX MEDLINE=83195140; PubMed=6341999;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A21114; A21114.
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 10
FT MOD_RES 10 10
FT AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 8 LP 9

RESULT 50
GONL_SQUAC
ID GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH) (Luliberin).
OS Squaleus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Squala; Squaloidei; Squalidae; Squaleus.
NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A46030; A46030.
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR PROSITE: PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 10
FT MOD_RES 10 10
FT AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
DB 8 LP 9

RESULT 51
NO40_TOBAC
ID NO40_TOBAC STANDARD; PRT; 10 AA.
AC P55962;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40 homolog.
GN ENOD40.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRL;
RX MEDLINE=96320417; PubMed=8662527;
RA van de Sande K., Pawlowski K., Czaja I., Wieneke U., Schell J.,
RA Schmidt J., Waiden R., Matvienko M., Weillink J., van Kammen A.,
RA Franssen H., Bisseling T.;
RT "Modification of phytohormone response by a peptide encoded by ENOD40 of legumes and a nonlegume.";
RL Science 273:370-373(1996).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT GROWTH REGULATOR THAT ALTERS PHYTHORMONE RESPONSES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; X98716; CAA67267.1; -.
KW Modulation.
SQ SEQUENCE 10 AA; 1173 MW; 2A3248E05DDB1AB3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
Db 1 MQ 2

RESULT 52
NS1_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE
RC STRAIN=H37Rv;
RA Prasad H.K., Annappurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PL 6
Db 4 PL 5

RESULT 53
PSBF_CAPAN STANDARD; PRT; 10 AA.
ID PSBF_CAPAN
AC Q03567;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; lamiids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts."
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbE / psbF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X65570; CAA46539.1; -.
DR PIR; S28055; S28055.
DR HAMAP; MF_00643; -; 1.
DR InterPro; IPR006216; Cyt_b559.
DR PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1
FT TRANSMEM <1 5 BY SIMILARITY.
FT DOMAIN 6 10 LUMENAL (POTENTIAL).
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D69DC5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQ 2
Db 5 MQ 6

RESULT 54
TEMK_RANTE STANDARD; PRT; 10 AA.
ID TEMK_RANTE
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
Db 2 LP 3

RESULT 55
TKL2_LOCM1 STANDARD; PRT; 10 AA.
ID TKL2_LOCM1
AC P16224;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C86557 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PL 6
 DB 2 PL 3
 RESULT 56
 ID UP2A2 HUMAN STANDARD; PRT; 10 AA.
 AC P30088;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30088; HUMAN.
 FT NON TER 1 1
 FT VARIANT 9 9 G -> Y.
 FT 1
 FT 9 /FTID=VAR_000002.
 FT 10
 FT 10
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB7777587 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PP 4
 DB 5 PP 6
 RESULT 57
 ID UP2A5 HUMAN STANDARD; PRT; 10 AA.
 AC P30091;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON TER 1 1
 FT VARIANT 9 9 G -> Y.
 FT 1
 FT 9 /FTID=VAR_000002.
 FT 10
 FT 10
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QP 3
 DB 3 QP 4
 RESULT 58
 ID URE3 MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.B.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences.";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON TER 10 10
 FT 10
 FT 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCE077771A7 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQ 2
 DB 1 MQ 2

```

RESULT 59
BPP3 BOTIN
ID _BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 4 PP 5

RESULT 60
BPP4 BOTIN
ID _BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBF13C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 4 PP 5

RESULT 61
BPPB AGKHA
ID _BPPB_AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffi.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LP 7
Db 3 LP 4

RESULT 62
BPP AGKHP
ID _BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.

```


Tip operon leader peptide.
TREL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG."
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X07744; CAA30565.1; -.
DR Tryptophan biosynthesis; Leader peptide.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LP 7
Db 3 LP 4

RESULT 67
PQQ_PSEFL STANDARD; PRT; 11 AA.
ID PQQ_PSEFL
AC P56173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Coenzyme PQQ synthesis protein C (fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CHAO;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "R5-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
mutational inactivation of the genes results in overproduction of the
antibiotic pyoluteorin."
RL Appl. Environ. Microbiol. 61:3856-3864(1995).
CC -!- FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE (PQQ)
BIOSYNTHESIS
CC -!- SIMILARITY: TO OTHER BACTERIAL PQQC.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X87299; CAA60734.1; -.

DR PIR; S58244; S58244.
KW PQQ.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LP 6
Db 5 LP 6

RESULT 68
TKNI_PSEGU STANDARD; PRT; 11 AA.
ID TKNI_PSEGU
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN (1)
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B60409; B60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 11 11
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 1 Qp 2

RESULT 69
TKNI_UPERU STANDARD; PRT; 11 AA.
ID TKNI_UPERU
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (wrinkled toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Edean R.;
 RT "Structure of uperolein, a physalaemin-like endcapeptide occurring
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 KX MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;
 QY Query Match 28.6%; Score 2; DB 1; Length 11;
 Db Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 2 QP 3
 Db 1 QP 2
 RESULT 70
 TKN2 PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: D60409; D60409.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 KX MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;
 QY Query Match 28.6%; Score 2; DB 1; Length 11;
 Db Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 2 QP 3
 Db 1 QP 2
 RESULT 72
 TKN4 PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;
 QY Query Match 28.6%; Score 2; DB 1; Length 11;
 Db Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 2 QP 3
 Db 1 QP 2
 RESULT 71
 TKN3 PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: D60409; D60409.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 KX MOD RES 1 1
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;
 QY Query Match 28.6%; Score 2; DB 1; Length 11;
 Db Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 2 QP 3
 Db 1 QP 2
 RESULT 72
 TKN4 PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
ON NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR, E60409; E60409.
DR InterPro: IPR003580; Protachykinin.
DR Pfam: PF02202; Tachykinin.
DR SMART, SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
DR Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db 1 QP 2

RESULT 73
TKNS_PSEGU ID TKNS_PSEGU STANDARD; PRT; 11 AA.
AC P42390;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
ON NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR, F60409; F60409.

DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART, SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
DR Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db 1 QP 2

RESULT 74
TKN_ELEMO ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC P01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musk octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
ON NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
RT endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR, A01561; EOOC.
DR PIR, B01561; EOOC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro: IPR002040; Tachykinin.
DR Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
DR PROSITE; PS00267; TACHYKININ; 1.
DR 3D-structure.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QP 3
Db 1 QP 2

RESULT 75
FAR7_PENMO ID FAR7_PENMO STANDARD; PRT; 12 AA.
AC P83322;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRamide-like neuropeptide FLP7 (GYRKPFGNSIF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
Db 5 PP 6

Search completed: November 25, 2003, 18:17:21
Job time : 5.3883 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 16.867 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: listing first 100 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 4 | 57.1 | 18 | 12 | Q84129 influenza |
| 2 | 4 | 57.1 | 19 | 4 | Q9UC80 homo sapien |
| 3 | 4 | 57.1 | 20 | 2 | O50180 pseudomonas |
| 4 | 4 | 57.1 | 20 | 4 | Q9UCA8 |
| 5 | 4 | 57.1 | 20 | 12 | Q912B4 human eryth |
| 6 | 3 | 42.9 | 9 | 2 | P83157 |
| 7 | 3 | 42.9 | 9 | 5 | Q9TWV0 |
| 8 | 3 | 42.9 | 9 | 10 | Q9S8J8 |
| 9 | 3 | 42.9 | 9 | 10 | P82429 |
| 10 | 3 | 42.9 | 9 | 16 | Q935G1 |
| 11 | 3 | 42.9 | 10 | 8 | Q8SHA8 |
| 12 | 3 | 42.9 | 10 | 11 | Q9QVF7 |
| 13 | 3 | 42.9 | 10 | 11 | Q8VHM9 |
| 14 | 3 | 42.9 | 10 | 12 | Q9Q0W9 |
| 15 | 3 | 42.9 | 10 | 12 | Q8V70 |
| 16 | 3 | 42.9 | 10 | 12 | Q9Q0W1 polyomaviru |

| | | | | | |
|----|---|------|----|----|--------------------|
| 17 | 3 | 42.9 | 10 | 12 | Q8JV68 |
| 18 | 3 | 42.9 | 10 | 12 | Q9Q0V9 |
| 19 | 3 | 42.9 | 10 | 12 | Q9Q0W7 |
| 20 | 3 | 42.9 | 10 | 12 | Q8JV66 |
| 21 | 3 | 42.9 | 10 | 12 | Q9Q0V7 |
| 22 | 3 | 42.9 | 10 | 12 | Q8JV82 |
| 23 | 3 | 42.9 | 10 | 12 | Q8JV76 |
| 24 | 3 | 42.9 | 10 | 12 | P90391 tomato yell |
| 25 | 3 | 42.9 | 10 | 12 | Q8JV74 |
| 26 | 3 | 42.9 | 10 | 12 | Q9Q0W5 |
| 27 | 3 | 42.9 | 10 | 12 | Q9Q0X3 |
| 28 | 3 | 42.9 | 10 | 12 | Q9Q0X5 |
| 29 | 3 | 42.9 | 10 | 12 | Q9Q0W3 |
| 30 | 3 | 42.9 | 10 | 12 | Q8JV80 |
| 31 | 3 | 42.9 | 10 | 12 | Q9Q0X1 |
| 32 | 3 | 42.9 | 10 | 12 | Q9Q0X9 |
| 33 | 3 | 42.9 | 10 | 12 | Q8JV72 |
| 34 | 3 | 42.9 | 11 | 4 | Q8IVG8 |
| 35 | 3 | 42.9 | 11 | 10 | P82436 |
| 36 | 3 | 42.9 | 11 | 13 | Q8UTP1 |
| 37 | 3 | 42.9 | 12 | 2 | Q8KZ86 |
| 38 | 3 | 42.9 | 12 | 4 | Q9BZ49 |
| 39 | 3 | 42.9 | 12 | 4 | Q9NTQ2 |
| 40 | 3 | 42.9 | 12 | 10 | Q93X21 |
| 41 | 3 | 42.9 | 12 | 10 | P82328 |
| 42 | 3 | 42.9 | 13 | 4 | Q14182 |
| 43 | 3 | 42.9 | 13 | 8 | Q9T569 |
| 44 | 3 | 42.9 | 13 | 11 | Q88176 |
| 45 | 3 | 42.9 | 13 | 12 | Q67604 |
| 46 | 3 | 42.9 | 13 | 16 | Q8X4F5 |
| 47 | 3 | 42.9 | 14 | 10 | P82326 |
| 48 | 3 | 42.9 | 15 | 6 | Q9TR14 |
| 49 | 3 | 42.9 | 15 | 10 | Q9S8N8 |
| 50 | 3 | 42.9 | 15 | 10 | Q40562 |
| 51 | 3 | 42.9 | 15 | 10 | Q40563 |
| 52 | 3 | 42.9 | 15 | 10 | P82439 |
| 53 | 3 | 42.9 | 16 | 4 | Q9NN22 |
| 54 | 3 | 42.9 | 16 | 5 | Q9TNW7 |
| 55 | 3 | 42.9 | 16 | 6 | Q9BGG8 |
| 56 | 3 | 42.9 | 16 | 6 | Q9TQZ7 |
| 57 | 3 | 42.9 | 16 | 10 | Q8RVF4 |
| 58 | 3 | 42.9 | 16 | 12 | Q83967 |
| 59 | 3 | 42.9 | 16 | 12 | Q83960 |
| 60 | 3 | 42.9 | 16 | 12 | Q84055 |
| 61 | 3 | 42.9 | 17 | 4 | Q96P96 |
| 62 | 3 | 42.9 | 17 | 4 | Q14001 |
| 63 | 3 | 42.9 | 17 | 6 | Q9TR22 |
| 64 | 3 | 42.9 | 17 | 6 | Q9TR78 |
| 65 | 3 | 42.9 | 17 | 6 | Q9TRU8 |
| 66 | 3 | 42.9 | 17 | 10 | Q49225 |
| 67 | 3 | 42.9 | 17 | 10 | Q41400 |
| 68 | 3 | 42.9 | 17 | 13 | Q9P839 |
| 69 | 3 | 42.9 | 18 | 4 | Q16244 |
| 70 | 3 | 42.9 | 18 | 4 | Q9UCT9 |
| 71 | 3 | 42.9 | 18 | 4 | Q8NFB4 |
| 72 | 3 | 42.9 | 18 | 4 | Q9H1I3 |
| 73 | 3 | 42.9 | 18 | 6 | Q9TQR9 |
| 74 | 3 | 42.9 | 18 | 10 | Q9S915 |
| 75 | 3 | 42.9 | 18 | 11 | Q9JIB9 |
| 76 | 3 | 42.9 | 18 | 13 | Q8QFT3 |
| 77 | 3 | 42.9 | 19 | 2 | Q9R8V1 |
| 78 | 3 | 42.9 | 19 | 4 | Q9UCL3 |
| 79 | 3 | 42.9 | 19 | 4 | Q9UCK6 |
| 80 | 3 | 42.9 | 19 | 8 | Q31687 |
| 81 | 3 | 42.9 | 19 | 10 | Q947T4 |
| 82 | 3 | 42.9 | 19 | 10 | P82941 |
| 83 | 3 | 42.9 | 19 | 12 | Q8UY03 |
| 84 | 3 | 42.9 | 19 | 12 | Q8UXY5 |
| 85 | 3 | 42.9 | 19 | 12 | Q8UY00 |
| 86 | 3 | 42.9 | 19 | 12 | Q8UXZ1 |
| 87 | 3 | 42.9 | 19 | 12 | Q8UXZ7 |
| 88 | 3 | 42.9 | 19 | 12 | Q8UXZ9 |
| 89 | 3 | 42.9 | 19 | 12 | Q8UY02 |

| | |
|--------|--------------|
| Q8JV68 | polyomaviru |
| Q9Q0V9 | polyomaviru |
| Q9Q0W7 | polyomaviru |
| Q8JV66 | polyomaviru |
| Q9Q0V7 | polyomaviru |
| Q8JV82 | polyomaviru |
| Q8JV76 | polyomaviru |
| P90391 | tomato yell |
| Q8JV74 | polyomaviru |
| Q9Q0W5 | polyomaviru |
| Q9Q0X3 | polyomaviru |
| Q9Q0X5 | polyomaviru |
| Q9Q0W3 | polyomaviru |
| Q8JV80 | polyomaviru |
| Q9Q0X1 | polyomaviru |
| Q9Q0X9 | polyomaviru |
| Q8JV72 | polyomaviru |
| Q8IVG8 | homo sapien |
| P82436 | nicotiana t |
| Q8UTP1 | xenopus lae |
| Q8KZ86 | acinetobact |
| Q9BZ49 | homo sapien |
| Q9NTQ2 | homo sapien |
| Q93X21 | zea mays {m |
| P82328 | pisum sativ |
| Q14182 | homo sapien |
| Q9T569 | zea mays {m |
| Q88176 | mus musculus |
| Q67604 | squash leaf |
| Q8X4F5 | escherichia |
| P82326 | pisum sativ |
| Q9TR14 | bos taurus |
| Q9S8N8 | hordeum vul |
| Q40562 | nicotiana t |
| Q40563 | nicotiana t |
| P82439 | nicotiana t |
| Q9NN22 | homo sapien |
| Q9TNW7 | toxoplasma |
| Q9BGG8 | sorex arane |
| Q9TQZ7 | bos taurus |
| Q8RVF4 | zea mays {m |
| Q83967 | influenzavi |
| Q83960 | influenzavi |
| Q84055 | influenzavi |
| Q96P96 | homo sapien |
| Q14001 | homo sapien |
| Q9TR22 | bos taurus |
| Q9TR78 | didelphis m |
| Q9TRU8 | bos taurus |
| Q49225 | glycine max |
| Q41400 | sesbania ro |
| Q9P839 | carassius a |
| Q16244 | homo sapien |
| Q9UCT9 | homo sapien |
| Q8NFB4 | homo sapien |
| Q9H1I3 | homo sapien |
| Q9TQR9 | mammuthus p |
| Q9S915 | tritium tu |
| Q9JIB9 | mus musculus |
| Q8QFT3 | gallus gall |
| Q9R8V1 | pseudomonas |
| Q9UCL3 | homo sapien |
| Q9UCK6 | homo sapien |
| Q31687 | artemia par |
| Q947T4 | oryza sativ |
| P82941 | hordeum vul |
| Q8UY03 | hepatitis c |
| Q8UXY5 | hepatitis c |
| Q8UY00 | hepatitis c |
| Q8UXZ1 | hepatitis c |
| Q8UXZ7 | hepatitis c |
| Q8UXZ9 | hepatitis c |
| Q8UY02 | hepatitis c |

90 Q69099 herpes simp
 91 Q8uxz4 hepatitis c
 92 Q8uy07 hepatitis c
 93 Q8uxz3 hepatitis c
 94 Q8uy04 hepatitis c
 95 Q8uxz6 hepatitis c
 96 Q8prt0 gallus gall
 97 Q91380 gallus gall
 98 Q9prn4 petromyzon
 99 Q9ps40 carassius a
 100 Q90rf8 human immun

ALIGNMENTS

RESULT 1
 Q84129 PRELIMINARY; PRT; 18 AA.
 AC Q84129;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
 8), COOH terminus of NS1 (Fragment).
 DE Influenzavirus A.
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=197911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83303830; PubMed=6612993;
 RA Parvin J.D., Young J.F., Palese P.;
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural
 RT proteins of influenza a virus isolates.";
 RL Virology 128:512-517(1983).
 DR ENBL; K00959; AAA43541.1; -;
 DR InterPro; IPR000256; Flu_NS1.
 DR Pfam; PF00600; Flu_NS1; 1.
 FT NON TER 1
 Q9 SEQUENCE 18 AA; 2105 MW; 87174BD420FFBEEF CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 11 PPLP 14

RESULT 2
 Q9UC80 PRELIMINARY; PRT; 19 AA.
 AC Q9UC80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
 [Mn/Fel] (Fragment)).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95215817; PubMed=7701298;
 RA Binette J.P., Binette M.B.;
 RT "Sequencing of proteins extracted from stones.";
 RL Scanning Microsc. 8:233-239(1994).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).

CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 19 AA; 2116 MW; A0D0DAB848EE7894 CRC64;

Query Match 57.1%; Score 4; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 5 PPLP 8

RESULT 3
 O50180 PRELIMINARY; PRT; 20 AA.
 AC O50180;
 DT 01-JAN-1999 (TrEMBLrel. 09, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Acetyl-CoA synthetase (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=99008987; PubMed=9791103;
 RA Nishijyo I., Park S.W., Lu C.D., Itoh Y., Abdeial A.T.;
 RT "Molecular characterization and regulation of an operon encoding a
 RT system for transport of arginine and ornithine and the ArgR regulatory
 RT protein in Pseudomonas aeruginosa.";
 RL J. Bacteriol. 180:5559-5566(1998).
 DR EMBL; AF012537; AAC71069.1; -;
 DR InterPro; IPR000873; AMP-bind.
 DR PROSITE; PS00455; AMP BINDING; PARTIAL.
 FT NON TER 1
 Q9 SEQUENCE 20 AA; 2097 MW; 58E35ED36990522D CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
 Db 10 PPLP 13

RESULT 4
 Q9UCA8 PRELIMINARY; PRT; 20 AA.
 AC Q9UCA8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Tumor-derived adhesion factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94161713; PubMed=8117260;
 RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
 RA Yasumitsu H., Umeda M., Miyazaki K.;
 RT "Cell adhesion activity of a 30-kDa major secreted protein from human
 RT bladder carcinoma cells.";
 RL Biochem. Biophys. Res. Commun. 198:1046-1053(1994).
 SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AE8D CRC64;

Query Match 57.1%; Score 4; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
 Db 15 PPLP 18
 ||||
 ||||

RESULT 5
 Q912B4 PRELIMINARY; PRT; 20 AA.
 AC Q912B4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 7.5-kDa nonstructural protein (Fragment).
 GN 7.5-KDA.
 OS Human erythrovirus V9.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
 OX NCBI_TaxID=72197;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=R234;
 RA Nguyen Q.T.;
 RT "Molecular cloning and sequencing of a novel human erythrovirus
 genome: new species beside B19 in the genus Erythrovirus.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249875; CAC80689.1; -;
 KW Nonstructural protein.
 FT NON_TER 1 20
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 1977 MW; F00971E8578CE490 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6
 Db 4 PPPL 7
 ||||
 ||||

RESULT 6
 P83157 PRELIMINARY; PRT; 9 AA.
 AC P83157;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apce S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 DR InterPro; IPR001189; SODismutase.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Iron; Metal-binding.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 Db 6 PLP 8
 ||||
 ||||

RESULT 7
 Q9TWV0 PRELIMINARY; PRT; 9 AA.
 ID Q9TWV0
 AC Q9TWV0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Antho-RPAMIDE-NEUROPEPTIDE.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones.";
 RL Peptides 13:851-857(1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 Db 5 PLP 7
 ||||
 ||||

RESULT 8
 Q9S8J8 PRELIMINARY; PRT; 9 AA.
 AC Q9S8J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORYZATENSIN=BIODACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95102521; PubMed=7804141;
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 peptide with ileum-contracting and immunomodulating activities derived
 from rice albumin.";
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
 DR Gramene; Q9S8J8; -;
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
 Db 6 PLP 8
 ||||
 ||||

RESULT 9

| | | | | | | | | | |
|------------|------------|--------------|-----------|------------|----|--------|----|------|----|
| BEST LOCAL | SIMILARITY | 100.0% | FREQ. NO. | 0.38703, | | | | | |
| MATCHES | 3: | Conservative | 0: | Mismatches | 0; | Indels | 0; | Gaps | 0; |

RESULT 13

Q8VHM9 PRELIMINARY; PRT; 10 AA.
 ID Q8VHM9
 AC Q8VHM9
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Interferon receptor 2a' (Fragment).
 GN IFNAR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The genomic structure and expression patterns of the gene encoding
 RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
 RT "The organization, transcriptional regulation and chromosomal
 RT localization of the locus encoding the gene for the murine type I
 RT interferon receptor, Ifnar2.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF440786; AAL40944.1; -.
 KW Receptor.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 1 1
 1 1139 MW; 322A36A771A32763 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 |||
 Db 2 PPL 4

RESULT 14

Q9QOW9 PRELIMINARY; PRT; 10 AA.
 ID Q9QOW9
 AC Q9QOW9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UME3;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119350; AAF24106.1; -.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 1 1
 1 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 15

Q8JUV70 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV70
 AC Q8JUV70
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA 5;
 RX MEDLINE=21465052; PubMed=11591397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304387; AAM97804.1; -.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 1 1
 1 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 16

Q9QOW1 PRELIMINARY; PRT; 10 AA.
 ID Q9QOW1
 AC Q9QOW1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CSFB;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119354; AAF24114.1; -.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 1 1
 1 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 7 PPP 9

RESULT 17

Q8JUV68 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV68
 AC Q8JUV68;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

```

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 18
Q9QOV9
ID Q9QOV9 PRELIMINARY; PRT; 10 AA.
AC Q9QOV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 19
Q9QOW7
ID Q9QOW7 PRELIMINARY; PRT; 10 AA.
AC Q9QOW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;

```

```

RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 20
Q8JUV66
ID Q8JUV66 PRELIMINARY; PRT; 10 AA.
AC Q8JUV66;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
7 PPP 9

RESULT 21
Q9QOV7
ID Q9QOV7 PRELIMINARY; PRT; 10 AA.
AC Q9QOV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119356; AAF24118.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

```

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||

Db 7 PPP 9
 |||

RESULT 22

Q8JV82 ID Q8JV82 PRELIMINARY; PRT; 10 AA.
 AC Q8JV82
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303944; AAM97792.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||

Db 7 PPP 9
 |||

RESULT 23

Q8JV76 ID Q8JV76 PRELIMINARY; PRT; 10 AA.
 AC Q8JV76;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA2;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303947; AAM97798.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||

Db 7 PPP 9

RESULT 24

P90391 ID P90391 PRELIMINARY; PRT; 10 AA.
 AC P90391;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE C2 protein (Fragment).
 OS Tomato yellow leaf curl virus (TYLCV).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10832;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TYLCV-Is;
 RA Wernecke M.E., Roye M.E., McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
 RT "Identification of tomato yellow leaf curl geminivirus (TYLCV-Is) in
 RT tomatoes and peppers in Jamaica.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U84397; AAB47965.1; -.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
 |||

Db 1 MQP 3
 |||

RESULT 25

Q8JV74 ID Q8JV74 PRELIMINARY; PRT; 10 AA.
 AC Q8JV74;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA3;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303948; AAM97800.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 |||

Db 7 PPP 9
 |||

RESULT 26

Q9Q0W5 ID Q9Q0W5 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0W5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119352; AAF24110.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 27
Q9Q0X3
ID Q9Q0X3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN8;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119348; AAF24102.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 28
Q9Q0X5
ID Q9Q0X5 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RX MEDLINE=20087544; PubMed=10618230;

RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119347; AAF24100.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 29
Q9Q0W3
ID Q9Q0W3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA1;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 7 PPP 9

RESULT 30
Q8JV80
ID Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAN97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 31

Q9Q0X1 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN15;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119349; AAF24104.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03; - Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 32

Q9Q0X9 PRELIMINARY; PRT; 10 AA.
 AC Q9Q0X9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCNU;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119345; AAF24096.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 33

Q8JV72 PRELIMINARY; PRT; 10 AA.
 AC Q8JV72;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA 4;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304386; AAM97802.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
 DB 7 PPP 9

RESULT 34

Q8IVG8 PRELIMINARY; PRT; 11 AA.
 AC Q8IVG8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Low density lipoprotein receptor related protein 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Schulz S., Schagdarsurengin U., Greiser P., Birkenmeier G.,
 RA Muller-Werdan U., Hagemann M., Riemann D., Werdan K., Glaser C.;
 RT "The LDL receptor-related protein (LRP1/A2MR) and coronary
 RT atherosclerosis - novel genomic variants and functional
 RT consequences.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18524; CAD57169.1; -.
 KW Receptor; Lipoprotein.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
 DB 4 PPL 6

RESULT 35

P82436 PRELIMINARY; PRT; 11 AA.
 ID P82436
 AC P82436;

DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 65 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A.; Bonham V.A.; Mitchell G.P.; Robertson D.; Slabas A.R.;
 RA Wojtaszek P.; Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture."
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -4- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

 Query Match 42.9%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 PPP 5
 Db |||
 2 PPP 4

 RESULT 36
 Q8UUP1 PRELIMINARY; PRT; 11 AA.
 AC Q8UUP1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Beta-TrCP protein (Fragment).
 GN BETA-TRCP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carnevali F.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ballarino M.;
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus
 RT laevis."
 RL Thesis (2001), Department of Genetica e Biologia Molecolare,
 RL University of Rome La Sapienza, Rome, Italy.
 DR EMBL; AJ428930; CAD21927.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

 Query Match 42.9%; Score 3; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 QPP 4
 Db |||
 9 QPP 11

 RESULT 37
 Q8KZ86 PRELIMINARY; PRT; 12 AA.
 ID Q8KZ86

Q8KZ86;
 AC 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Class I integron DNA integrase (Fragment).
 GN INT1.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=204A;
 RA Dolzani L.; Gombac F.; Lagatolla C.; Riccio M.L.; Rossolini G.M.;
 RA Tonin E.; Monti-Bragadin C.;
 RT "Carriage of class I and II integrons in Italian clinical isolates of
 RT Acinetobacter baumannii."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ313334; CAC85941.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

 Query Match 42.9%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PLP 7
 Db |||
 7 PLP 9

 RESULT 38
 Q9BZ49 PRELIMINARY; PRT; 12 AA.
 ID Q9BZ49;
 AC Q9BZ49;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Glycophorin C (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patel S.S.; Mehlotra R.K.; Kastens W.; Mgone C.S.; Kazura J.W.;
 RA Zimmerman P.A.;
 RT "The association of the glycophorin C exon 3 deletion with
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
 RT Guinea."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF342984; AAK01459.1; -.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

 Query Match 42.9%; Score 3; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 PPP 5
 Db |||
 9 PPP 11

 RESULT 39
 Q9NTQ2 PRELIMINARY; PRT; 12 AA.
 ID Q9NTQ2;
 AC Q9NTQ2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE DJ402L9.1 (Mu opiate receptor (MOR1)) (Fragment).

```
GN DJ402L9.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI32774; CAB76846.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1296 MW; 68479422BDAB1DD8 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 10 PPL 12

RESULT 40
Q93X21 PRELIMINARY; PRT; 12 AA.
ID Q93X21;
AC Q93X21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyubiquitin homolog (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. INRA 258; TISSUE=Leaf;
RC MEDLINE=96236829; PubMed=8680303;
RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
RT "Heavy-metal-responsive genes in maize: identification and comparison
of their expression upon various forms of abiotic stress.";
RL Planta 199;1:8(1996).
DR EMBL; S82313; AAB47175.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db 2 PPP 4

RESULT 41
P82328 PRELIMINARY; PRT; 12 AA.
ID P82328;
AC P82328;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
CX NCBI_TaxID=3888;
[1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
```

```
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1264 MW; 96691C8C663B1B01 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db 9 PPL 11

RESULT 42
Q14182 PRELIMINARY; PRT; 13 AA.
ID Q14182;
AC Q14182;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=87213162; PubMed=3579900;
RA Koizumi O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA
RT expressible in mammalian cells.";
RL Biochem. Biophys. Res. Commun. 144:185-190(1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transferase.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 9 PPL 11

RESULT 43
Q9T569 PRELIMINARY; PRT; 13 AA.
ID Q9T569;
AC Q9T569;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial plasmid S-2 DNA, 5' end (Fragment).
OS Zea mays (Maize).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
[1]
RN SEQUENCE FROM N.A.
```



```

RC TISSUE=Seed;
RA Traynor P.L., Levings C.S. III.;
RT "Transcription of the S-2 maize mitochondrial plasmid.";
RL Plant Mol. Biol. 7:255-263(1986).
DR EMBL; M16992; AAA70281.1; -.
KW Mitochondrion.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1626 MW; 7B5E03673918A1F4 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQP 3
Db 1 MQP 3

RESULT 44
O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawaguchi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncaml.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7
Db 3 PLP 5

RESULT 45
Q67604 PRELIMINARY; PRT; 13 AA.
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BC1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
del Fuerte, Sinaloa, Mexico.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 7 QPP 9

RESULT 46
Q8X4F5 PRELIMINARY; PRT; 13 AA.
AC Q8X4F5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein z5883.
GN Z5883.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005659; AAGS9469.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 13 AA; 1520 MW; 414592273904D877 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQP 3
Db 1 MQP 3

RESULT 47
P82326 PRELIMINARY; PRT; 14 AA.
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";

```

```

RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db |||
6 PPL 8

RESULT 48
Q9TR14 PRELIMINARY; PRT; 15 AA.
AC Q9TR14;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE.
RX MEDLINE=96187584; PubMed=8611748;
RA Nakai Y., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C.";
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C9A5B4A7984777 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
Db |||
2 PPP 4

RESULT 49
Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]_
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;

```

```

Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db |||
4 QPP 6

RESULT 50
Q40562 PRELIMINARY; PRT; 15 AA.
AC Q40562;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein.";
RL Plant J. 6:555-565(1994).
DR EMBL; L16786; AAA73564.1; -.
KW GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1707 MW; 8AB89F924EA30CAF CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PLP 7
Db |||
4 PLP 6

RESULT 51
Q40563 PRELIMINARY; PRT; 15 AA.
AC Q40563;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Small ras-related protein (Fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein.";
RL Plant J. 6:555-565(1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

```

Query Match 42.9%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPL 7
 |||
 Db 5 PPL 7

RESULT 52
 P82439 ID P82439 PRELIMINARY; PRT; 15 AA.
 AC P82439;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE 200 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 FT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture";
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall; Hydroxylation.
 FT MOD RES 6 6 HYDROXYLATION.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1870 MW; 3B1E05A20A3C5681 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
 |||
 Db 6 PPP 8

RESULT 53
 Q9NNZ2 ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.
 AC Q9NNZ2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Integrin alpha-2 subunit (Fragment).
 GN ITGA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98421383; PubMed=9746778;
 RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
 RA Kunicki T.J.;
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
 RT that are associated with differences in platelet alpha2 beta1
 RT density";
 RL Blood 92:2382-2388(1998).
 DR EMBL; AF062039; AAF77577.1; -.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPL 7
 |||
 Db 10 PPL 12

RESULT 54
 Q9TWN7 ID Q9TWN7 PRELIMINARY; PRT; 16 AA.
 AC Q9TWN7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Antigen P30=MAJOR surface immunodominant antigen (Fragment).
 OS Toxoplasma gondii.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94294203; PubMed=7517518;
 RA Bonhomme A., Thirion C., Boulanger F., Charton F., Bulet H.,
 RA Pinon J.M., Alix A.J.;
 RT "Toxoplasma gondii-structure variations of the antigen P30";
 RL Parasitology 108:281-287(1994).
 FT NON_TER 1 1
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1678 MW; FE4CFOA743A796CD CRC64;

Query Match 42.9%; Score 3; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 |||
 Db 3 PPL 5

RESULT 55
 Q9BGG8 ID Q9BGG8 PRELIMINARY; PRT; 16 AA.
 AC Q9BGG8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Thyroid hormone receptor alpha (Fragment).
 GN THRA1.
 OS Sorex araneus (Eurasian common shrew) (European shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
 OX NCBI_TaxID=42254;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Larkin D., Serov O., Zhdanova N.;
 RT "Mapping of five genes from human chromosome 17 to chromosome 16 of
 RT the common shrew (Sorex araneus).";
 RL Acta Theriol. (Warsz) 45:143-146(2000).
 DR EMBL; AF314827; AAK13419.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1951 MW; 775186E3F5F52E2 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
 |||
 Db 4 PPL 6

```

RESULT 56
Q9TQZ7 PRELIMINARY; PRT; 16 AA.
ID Q9TQZ7;
AC Q9TQZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Eubovae; Bos.
CX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "Prediction from sequence comparisons of residues of factor H involved
RT in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531(1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 6 PPP 8

RESULT 57
Q8RVF4 PRELIMINARY; PRT; 16 AA.
ID Q8RVF4;
AC Q8RVF4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Proline rich protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CX NCB1_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. H98, and cv. CI23;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094252; AAM15707.1; -.
DR EMBL; AY094253; AAM15708.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 16 AA; 1720 MW; 02F6CD77295B5610 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 12 PPL 14

RESULT 58
Q83967 PRELIMINARY; PRT; 16 AA.
ID Q83967;
AC Q83967;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Influenza A/netherlands/84/68 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.

```

```

DE Influenza A/cameron/46 (H1n1), non-structural protein (Seg 8), cooh
DE terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
CX NCB1_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1993).
DR EMBL; K00961; AAA43519.1; -.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 16 AA; 1711 MW; 23F43C17AEF9B1E3 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 59
Q83960 PRELIMINARY; PRT; 16 AA.
ID Q83960;
AC Q83960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/ann arbor/6/60 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
CX NCB1_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1993).
DR EMBL; K00962; AAA43516.1; -.
DR InterPro; IPR000256; Flu_NSI.
DR Pfam; PF00600; Flu_NSI; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 16 AA; 1811 MW; 23F434B5AEFAD93 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 60
Q84055 PRELIMINARY; PRT; 16 AA.
ID Q84055;
AC Q84055;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/netherlands/84/68 (H2n2), non-structural protein (Seg 8),
DE cooh terminus of ns1 (Fragment).
OS Influenzavirus A.

```

```

* OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OX Influenza A viruses.
NX NCBI_TaxID=197911;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=8303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1993).
DR EMBL; K00963; AAA43527.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; I.
FT NON TER
SQ SEQUENCE 16 AA; 1810 MW; 23F43C17ABEFAD93 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6
Db 11 PPL 13

RESULT 61
Q96P96 PRELIMINARY; PRT; 17 AA.
AC Q96P96;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NH22-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401217; AAL02173.1; -.
FT NON TER
SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEFCRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPL 7
Db 14 PPL 16

RESULT 62
Q14001 PRELIMINARY; PRT; 17 AA.
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;

```

```

RT "Molecular cloning and chromosomal assignment of the human homologue
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
RT in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; -.
FT NON TER
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 15 QPP 17

RESULT 63
Q9TR22 PRELIMINARY; PRT; 17 AA.
AC Q9TR22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE NONAMELOGENIN glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96126798; PubMed=8564801;
RA Punzi J.S., DenBesten P.K.;
RT "Purification of nonamelogenin proteins from bovine secretory
RT enamel.";
RL Calcif. Tissue Int. 57:379-384(1995).
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
Db 8 PPP 10

RESULT 64
Q9TR78 PRELIMINARY; PRT; 17 AA.
AC Q9TR78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-BOTHRPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE.
RX MEDLINE=95149299; PubMed=7846694;
RA Perales J., Moussatche H., Marangoni S., Oliveira B., Domont G.B.;
RT "Isolation and partial characterization of an anti-bothropic complex
RT from the serum of South American Didelphidae.";
RL Toxicon 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 PPL 6
|||
Db 8 PPL 10

RESULT 65

Q9TRUB PRELIMINARY; PRT; 17 AA.
AC Q9TRUB;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Winer J., Hensel W.J.;
RT "Follicular cells secrete an inhibitor of aortic endothelial cell growth: identification as leukemia inhibitory factor."
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
RT NON_TER 1 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
|||
Db 2 PPL 4

RESULT 66

O49225 PRELIMINARY; PRT; 17 AA.
AC O49225;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (fragment).
GN HRGP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Essex; TISSUE=Root;
RX MEDLINE=94211912; PubMed=8159793;
RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs."
RN Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Essex; TISSUE=Root;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047052; AAC03558.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 11 PPP 13

RESULT 67

Q41400 PRELIMINARY; PRT; 17 AA.
AC Q41400;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sesbania rostrata;
RX TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Goernachtig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M., Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes enhanced by Azorhizobium caulinodans infection."
RL Mol. Plant Microbes Interact. 8:816-824(1995).
DR EMBL; Z48673; CAA88592.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 10 PPP 12

RESULT 68

Q9PS39 PRELIMINARY; PRT; 17 AA.
AC Q9PS39;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EXOGLYCOPROTEIN (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE
RX MEDLINE=93011782; PubMed=1397162;
RA Thordarson F.R., Antonian E., Grafstein B.;
RT "Intracellular proteins of goldfish optic tectum labeled by intracellular injection of 3H-proline."
RN Exp. Neurol. 117:260-268(1992).
SQ SEQUENCE 17 AA; 1946 MW; F227A01978AD0445 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
|||
Db 8 PPL 10

RESULT 69

```

Q16244
ID Q16244 PRELIMINARY; PRT; 18 AA.
AC Q16244;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE STS protein (Fragment).
GN STS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
RT steroid sulfatase deficiency.";
RL Hum. Mutat. 4:76-78(1994).
DR EMBL; S74383; AAD14153.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 2 PPL 4

RESULT 70
Q9UCT9
ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
AC Q9UCT9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE PRG-PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
FT NON_TER 1
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPL 5
Db 4 PPL 6

RESULT 71
Q8NFB4
ID Q8NFB4 PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Mutant.enamelin (Fragment).

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kida M., Ariga T.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelin gene mutation at exon-intron boundary.";
RL J. Dent. Res. 0:0-0(2002).
DR EMBL; AF530444; AAM97323.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3E8BE512 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPL 5
Db 3 PPL 5

RESULT 72
Q9HLI3
ID Q9HLI3 PRELIMINARY; PRT; 18 AA.
AC Q9HLI3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Retinoic acid receptor gamma (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu H., Clifford J.L.;
RT "Genomic organization of the human retinoic acid receptor gamma
RT gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV013704; AAG41595.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1964 MW; A284A1EFB361A22 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db 16 PPL 18

RESULT 73
Q9TOR9
ID Q9TOR9 PRELIMINARY; PRT; 18 AA.
AC Q9TOR9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE VON WILLEBRAND factor (Fragment).
GN VWF.
OS Mammuthus primigenius (Siberian woolly mammoth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Mammuthus.
OX NCBI_TaxID=37349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022977; PubMed=10555277;

```

```
RA Greenwood A.D., Capelli C., Possnert G., Paabo S.;
RT "Nuclear DNA sequences from late Pleistocene megafauna.";
RL Mol. Biol. Evol. 16:1466-1473(1999).
DR EMBL; AF154874; AAF12750.1; -.
DR EMBL; AF154873; AAF12749.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1914 MW; DFCB484B41F69236 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPL 6
Db 16 PPL 18

RESULT 74
Q9S915 PRELIMINARY; PRT; 18 AA.
AC Q9S915;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TETRAMERIC alpha-amylase inhibitor 16 kDa subunit, CM16*
DE (Fragment).
OS Triticum turgidum (Poulard wheat) (Rivet wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]_TaxID=4571;
RP SEQUENCE.
RX MEDLINE=92143804; PubMed=1736890;
RA Sanchez-Monge R., Gomez L., Barber D., Lopez-Otin C., Armentia A.,
RA Salcedo G.;
RT "Wheat and barley allergens associated with baker's asthma.
RT Glycosylated subunits of the alpha-amylase-inhibitor family have
RT enhanced IGE-binding capacity.";
RL Biochem. J. 281:401-405(1992).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1988 MW; 681835D1F68C30F8 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPL 7
Db 16 PPL 18

RESULT 75
Q9JIE9 PRELIMINARY; PRT; 18 AA.
AC Q9JIE9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein arginine N-methyltransferase 1 (Fragment).
GN MMT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=20307889; PubMed=10848611;
RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;
RT "Arginine N-methyltransferase 1 is required for early postimplantation
RT mouse development, but cells deficient in the enzyme are viable.";
```

```
RL Mol. Cell. Biol. 20:4859-4869(2000).
DR EMBL; AF232718; AAF37294.1; -.
KW Methyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db 13 QPP 15

Search completed: November 25, 2003, 18:25:08
Job time : 19.917 secs
```


GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 22.6755 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched. 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 7 | 100.0 | 7 | 22 | Colostrin derive |
| 2 | 7 | 100.0 | 7 | 22 | Colostrin peptid |
| 3 | 7 | 100.0 | 7 | 22 | Colostrin peptid |
| 4 | 7 | 100.0 | 7 | 22 | Ewe colostrin |
| 5 | 7 | 100.0 | 7 | 23 | Colostrin consti |
| 6 | 7 | 100.0 | 7 | 23 | Colostrin consti |
| 7 | 7 | 100.0 | 7 | 23 | Neural cell regula |
| 8 | 7 | 100.0 | 8 | 22 | Ewe colostrin pe |
| 9 | 5 | 71.4 | 6 | 17 | Prolyl endopeptida |

83 SH3 antagonist pep
84 SH3 antagonist pep
85 SH3 antagonist pep
86 Src SH3 region bin
87 Amino acid sequenc
88 Amino acid sequenc
89 Amino acid sequenc
90 Human CAMP-specifi
91 Yeast 2C TCR CDR3a
92 Yeast 2C TCR CDR3a
93 Yeast 2C TCR CDR3a
94 Src homology3 (SH3
95 Src homology3 (SH3
96 Src homology3 (SH3
97 Src homology3 (SH3
98 Src homology3 (SH3
99 Src homology3 (SH3
100 Src homology3 (SH3

XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 2
AAB72500
ID AAB72500 standard; Peptide; 7 AA.

XX AAB72500;
AC
XX 09-MAY-2001 (first entry)
XX Colostrinin peptide #1.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GU, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations -

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), or a derivative thereof, to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.

XX Sequence 7 AA;

XX Query Match 100.0%; Score 7; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
Db 1 MQPPPLP 7

RESULT 3
AAB72532
ID AAB72532 standard; Peptide; 7 AA.

XX AAB72532;

XX 09-MAY-2001 (first entry)

XX

ALIGNMENTS

RESULT 1
AAB72246
ID AAB72246 standard; peptide; 7 AA.

XX AAB72246;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 1.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
XX central nervous system disorder; neurological disorder; mental disorder;
XX dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
XX treating central nervous system diseases and bacterial and viral
XX infections, comprises administering colostrinin as an immunological
XX regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
XX a proline rich polypeptide aggregate contained in colostrum. The
XX peptides have immune response modulatory activity, and are capable of
XX inducing cytokines. Colostrinin and its derived peptides are useful for
XX inducing cytokine production, for modulating an immunological response
XX and for inducing blood cell proliferation. The peptides are useful in the
XX treatment of disorders of the central nervous system, neurological
XX disorders, mental disorders, dementia, neurodegenerative diseases,
XX Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX disorders of the immune system, bacterial and viral infections and
XX acquired immunological deficiencies.

DE Colostrinin peptide #1.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 PI
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
 Db 1 MQPPPLP 7

RESULT 4
 AAB59324
 ID AAB59324 standard; Peptide; 7 AA.
 XX
 AC AAB59324;
 XX
 XX 21-MAR-2001 (first entry)
 DT
 XX Ewe colostrinin peptide fragment B-9.
 DE
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 KW
 XX Ovis sp.
 OS
 XX WO200075173-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from
 PT

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
 Db 1 MQPPPLP 7

RESULT 5
 AAE20228
 ID AAE20228 standard; peptide; 7 AA.
 XX
 AC AAE20228;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #1.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 25; 51pp; English.
 PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/
 CC

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 Db 1 MQPPPLP 7

RESULT 6
 AAMS1036
 ID AAMS1036 standard; Peptide; 7 AA.
 AC AAMS1036;

DT 30-MAY-2002 (first entry)
 DE Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; beta-casein; human.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "optional C-terminal amidation"

XX WO200213849-A1.
 XX 21-FEB-2002.
 XX 17-AUG-2000; 2000WO-US22775.
 XX 17-AUG-2000; 2000WO-US22775.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.
 DR Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.
 XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. It is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
 CC interleukin-12. It was one of the best overall inducers in almost
 CC all cytokine and blood cell proliferation experiments conducted.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7
 Db 1 MQPPPLP 7

RESULT 7
 AAO14577
 ID AAO14577 standard; peptide; 7 AA.
 XX AAO14577;

DT 27-MAY-2002 (first entry)
 DE Neural cell regulatory colostrinin peptide 1.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

OS Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 7
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.
 XX 21-FEB-2002.
 XX 17-AUG-2000; 2000WO-US22777.
 XX 17-AUG-2000; 2000WO-US22777.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.
 DR Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.
 XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQPPPLP 7
Db 1 MQPPPLP 7
RESULT 8
AAB59354
ID AAB59354 standard; Peptide; 8 AA.
XX
AC AAB59354;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment derived sequence #14.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REGS-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
PS Claim 8; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 7; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQPPPLP 7
Db 2 MQPPPLP 8

RESULT 9
AAR91753
ID AAR91753 standard; peptide; 6 AA.
XX
AC AAR91753;
XX
DT 14-AUG-1996 (first entry)
XX
DE Prolyl endopeptidase inhibitor peptide #8.
XX
KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
KW prevention; dementia; human.
XX
OS Synthetic.
XX
PN JP08059697-A.
XX
PD 05-MAR-1996.
XX
PF 09-MAR-1995; 95JP-0079661.
XX
PR 15-JUN-1994; 94JP-0158031.
XX
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (NIHA-) NIPPON HAM KK.
XX
WPI; 1996-184809/19.
XX
PT Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives
PT for food and animal feed and to treat and prevent dementia
XX
PS Claim 1; Page 11; 11pp; Japanese.
XX
CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
CC peptides. These peptides are useful as PEP inhibitors in functional foods
CC and in animal feeds. They are used to prepare oral and parenteral
CC pharmaceutical preparations for the treatment and prevention of dementia
CC of animals, including humans. The advantage with using these peptides,
CC is that they are safe and easily absorbed.
XX
SQ Sequence 6 AA;
Query Match 71.4%; Score 5; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 2 PPPLP 6
RESULT 10
AAR60997
ID AAR60997 standard; peptide; 7 AA.
XX
AC AAR60997;
XX
DT 25-MAR-2003 (updated)
DT 14-APR-1995 (first entry)
XX
DE Fragment of the 3BP1 protein that binds to SH3 of Ab1 kinase.
XX
KW CD4; T cell; surface antigen; receptor; MHC class II antigen;
KW protein-tyrosine kinase; p56lck; tcr/cd3 complex; PI 3-kinase;
KW PI 4-kinase; lipid kinase; T cell receptor complex; 3BP1; SH3;
KW Ab1 kinase.
XX
OS Synthetic.
XX
PN WO9418832-A1.
XX
PD 01-SEP-1994.
XX

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides CC which are used in the exemplification of the present invention.

SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 13

AAM46851
ID AAM46851 standard; Peptide; 7 AA.

XX AC AAM46851;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #3122.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

PS Example 4; Page 112; 154pp; English.

XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides CC which are used in the exemplification of the present invention.

SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 14

AAM46856
ID AAM46856 standard; Peptide; 7 AA.

XX AC AAM46856;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #3127.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

PS Example 4; Page 112; 154pp; English.

XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides CC which are used in the exemplification of the present invention.

```

SQ Sequence 7 AA;
Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 15
AAM46861
ID AAM46861 standard; Peptide; 7 AA.
XX AC
XX DT 25-OCT-2001 (first entry)
XX DE H11 binding site consensus conforming peptide (CCP) #3132.
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-2290722.
XX PR 08-DEC-1999; 99CA-2290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX PS Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX Example 4; Page 112; 154pp; English.
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

RESULT 16
AAM46866
ID AAM46866 standard; Peptide; 7 AA.
XX AC
XX DT 25-OCT-2001 (first entry)
XX DE H11 binding site consensus conforming peptide (CCP) #3137.
XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN CA2290722-A1.
XX PD 08-JUN-2001.
XX PF 08-DEC-1999; 99CA-2290722.
XX PR 08-DEC-1999; 99CA-2290722.
XX PA (NOVO-) NOVOPHARM BIOTECH INC.
XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX PS Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX Example 4; Page 112; 154pp; English.
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 3 PPPLP 7

```



```

Db      3 PPPLP 7

RESULT 17
AAM46871
ID AAM46871 standard; Peptide; 7 AA.
XX
XX AAM46871;
AC
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #3142.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
PD
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 112; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPpC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPpCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPpCs
CC or a population of different SPpCs consisting of immunogenic cancer cell
CC surface-associated SPpC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|
|
|
|
Db 3 PPPLP 7

RESULT 18
AAM46973
ID AAM46973 standard; Peptide; 7 AA.
XX
XX AAM46973;
AC
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #3147.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
PD
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 112; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPpC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPpCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPpCs
CC or a population of different SPpCs consisting of immunogenic cancer cell
CC surface-associated SPpC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
SQ Sequence 7 AA;

Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|
|
|
|
Db 3 PPPLP 7

RESULT 19
AAM46973
ID AAM46973 standard; Peptide; 7 AA.
XX
XX AAM46973;
AC

```

```

XX 25-OCT-2001 (first entry)
XX
XX
XX H11 binding site consensus conforming peptide (CCP) #3244.
DE
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
SQ
Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
DB 3 PPPLP 7
RESULT 20
AAM47027
ID AAM47027 standard; Peptide; 7 AA.
XX
XX AAM47027;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #3298.
DE

```

```

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 112; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
SQ
Query Match 71.4%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
DB 3 PPPLP 7
RESULT 21
AAR71945
ID AAR71945 standard; Peptide; 8 AA.
XX
XX AAR71945;
XX
XX 25-MAR-2003 (updated)
DT 17-OCT-1995 (first entry)
XX
XX Human 3BP1 peptide.
XX
XX Grb3-3; cancer; apoptosis; AIDS; gene therapy; 3BP1; SH3 domain.
XX

```

```

OS Synthetic.
XX WO9507981-A1.
XX 23-MAR-1995.
XX 09-MAY-1994; 94WO-FR00542.
XX 15-SEP-1993; 93FR-0010971.
XX (RHON ) RHONE POULENC RORER SA.
XX Schweighoffer F, Toccoe B;
XX WPI; 1995-131349/17.
XX New human Grb3-3 gene and vectors contg. it - useful in control
XX of cell death etc. partic. for treating cancer and AIDS
XX Example 2; Page 11; 31pp; French.
XX The hSOS1 and 3BP1 peptides given in AAR71944-45 were used to
XX demonstrate that the newly isolated human Grb3-3 protein was
XX able to bind hSOS1, but not to the 3BP1 peptide, which
XX corresponds to the SH3 domain of Abl and Src. A Grb3-3G162R
XX mutant was unable to bind the hSOS1 peptide.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 8 AA;
SQ Query Match 71.4%; Score 5; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 1 PPPLP 5

RESULT 22
AAR77371
ID AAR77371 standard; Peptide; 10 AA.
XX AC AAR77371;
XX DT 17-JAN-1996 (first entry)
XX DE SH3 binding domain 3BP-1.
XX KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer;
XX gene therapy; Src homology 3; SH3 binding domain; 3BP-1.
XX OS Homo sapiens.
XX PN WO9525125-A1.
XX PD 21-SEP-1995.
XX PF 14-MAR-1995; 95WO-US03610.
XX PR 14-MAR-1994; 94US-0212190.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kim YS, Kohn EC, Liotta LA;
XX DR WPI; 1995-336944/43.
XX DNA encoding CAI resistance proteins - used in gene therapy, and for
XX detecting CAI resistance in biological samples
XX Example 4; Page 40; 56pp; English.
XX

CC CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058
CC human melanoma cells, contains a unique proline-rich sequence
CC which fulfills the consensus definition for Src homology 3 (SH3)
CC binding proteins (AAR77366). 4 Unique versions (AAR77367-70) are
CC present that show homology to the known SH3 binding domains: 3BP-1,
CC and the p85-alpha-1 and -2 subunits of phosphatidylinositol 3',
CC kinase (AAR77371-73).
XX SQ Sequence 10 AA;
Query Match 71.4%; Score 5; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 23
AAW06853
ID AAW06853 standard; peptide; 10 AA.
XX AC AAW06853;
XX DT 16-FEB-1997 (first entry)
XX DE Peptide binding the Crk-SH3 domain, used to treat cancer.
XX KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
XX treatment; diagnosis; antibody; signal transduction; disease;
XX disorder; intracellular signalling protein.
XX OS Synthetic.
XX PN WO9621011-A2.
XX PD 11-JUL-1996.
XX PF 28-DEC-1995; 95WO-US16979.
XX PR 30-DEC-1994; 94US-0367070.
XX PA (UYEQ ) UNIV ROCKEFELLER.
XX PI Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
XX Wu X, Zheng J;
XX DR WPI; 1996-333986/33.
XX PT New peptide(s) which bind the Crk-SH3 domain - used to develop
XX prods. for the diagnosis and treatment of defects in intracellular
XX signal transduction, partic. in cancer
XX PS Claim 3; Page 92; 120pp; English.
XX CC New peptides or proteins which comprise these peptides, bind
XX to the Crk-SH3 domain and competitively inhibit the binding of
XX intracellular signalling proteins. They can be used in the
XX treatment of a disease or disorder associated with a defect in
XX intracellular signal transduction, particularly cancer. They can
XX also be used to diagnose such diseases and disorders. Antibodies
XX raised against these proteins can be used for the same purposes. The
XX peptides are derived from the Crk-SH3 binding domains of
XX intracellular signalling proteins. Peptides related to the invention
XX are described in AAW03149-63 and AAW06842-W06866.
XX SQ Sequence 10 AA;
Query Match 71.4%; Score 5; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

XX OS Synthetic.
XX PN WC9737223-A1.
XX XX
XX PD 09-OCT-1997.
XX XX
XX PF 03-APR-1997; 97WO-US05547.
XX PR 03-APR-1996; 96US-0630916.
XX XX
XX PA (CYTO-) CYTOGEN CORP.
XX PU (UUNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Kay BK, Pirozzi G;
XX DR WPI; 1997-503234/46.
XX XX
XX PT Identifying cell signalling and growth regulatory polypeptides by
XX PT reaction with multivalent recognition complex - polypeptides are
XX PT useful in targetted drug selection
XX XX
XX PS Disclosure; Fig 15B; 220pp; English.
XX XX
XX CC Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is
XX CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
XX CC containing this residue have been shown to bind the YAP WW domain, but
XX CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
XX CC AAW38068-92 were biotinylated and complexed with alkaline streptavidin,
XX CC and used in a cross affinity mapping experiment. They were tested for
XX CC their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were
XX CC expressed as glutathione-S-transferase expression proteins. The present
XX CC peptide, derived from formin, does not bind to the WW domains of the
XX CC novel protein. The WW domain is a small functional domain. Its name
XX CC is derived from the observation that two tryptophan residues, one in the
XX CC amino terminal portion of the WW domain and one in the carboxyl terminal
XX CC portion, are conserved. Most proteins containing WW domains have a
XX CC function involving cell signalling and growth regulation or the
XX CC organisation of the cytoskeleton. Polypeptides containing a WW domain
XX CC are identified by treating a multivalent recognition unit complex that
XX CC has selective binding affinity for a WW domain, with many polypeptides
XX CC and identifying those with selective affinity for the complex. Proteins
XX CC containing WW domains are used for targeted drug screening, i.e. to
XX CC identify potential modulators of specific WW domain interactions.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 71.4%; Score 5; DB 18; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 40;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 3 PPPLP 7
XX Db |||||
XX 5 PPPLP 9
XX XX
XX RESULT 27
XX AAB70933
XX ID AAB70933 standard; Protein; 10 AA.
XX AC
XX XX
XX AC AAB70933;
XX XX
XX DT 30-JUL-2001 (first entry)
XX XX
XX DE Polyoma virus VP1 variant PyVP1-WW150 proline-rich fragment.
XX XX
XX KW VP1; coat protein; WW domain; proline-rich; immobilization; biosensor;
XX KW bioreactor; protein packaging; PyVP1-WW150.
XX XX
XX OS Polyoma virus.
XX XX
XX PN WO200132684-A2.
XX XX

```

```

PD 10-MAY-2001.
XX XX
XX PF 03-NOV-2000; 2000WO-BP10873.
XX PR 03-NOV-1999; 99DE-1052956.
XX XX
XX PA (ACGT-) ACGT PROGENOMICS AG.
XX XX
XX PI Boehm G, Schmidt U, Parthier C, Guenther C;
XX DR WPI; 2001-343471/36.
XX XX
XX PT Linking two or more molecules through adapter sequences, useful e.g.
XX PT for purifying recombinant proteins, by exploiting interaction between
XX PT WW domain and proline-rich sequence -
XX XX
XX PS Example 5; Page 26; 100pp; German.
XX XX
XX CC This invention describes a novel method (M1) for linking two or more
XX CC molecular substances (A) together via adapter sequences (AS). One (A) is
XX CC modified so that it contains, as AS, a WW domain or derived structure in
XX CC at least one region, and a second (A) is modified so that it contains,
XX CC as AS, a proline-rich sequence (PRS) able to bind to WW domain or its
XX CC derivative in at least one region and the modified components are
XX CC allowed to interact together through WW and PRS. The method is used to
XX CC provide permanent or temporary association between (A), e.g. temporary
XX CC immobilization, and matrix-assisted refolding of recombinant proteins
XX CC from crude cell extracts or permanent immobilization in biosensors or
XX CC bioreactors, for directing packaging of proteins inside a virus-like
XX CC shell, or production of chimeric proteins (e.g. bispecific antibodies),
XX CC for medical, therapeutic, diagnostic or biotechnological use. Interaction
XX CC between WW and PRS is very strong (dissociation constant 20-100 nM) but
XX CC only temporary, and can be stabilized (e.g. against extremes of salt
XX CC concentration or temperature) by formation of disulfide bridges. Compared
XX CC with other systems with comparable properties, the WW/PRS system is
XX CC exceptionally small and compact and for many applications, e.g.
XX CC antibody-antigen interaction, is clearly superior to other ligand binding
XX CC domains. The system can only produce heterodimers. This sequence
XX CC represents a proline-rich fragment of the Polyoma virus coat protein VP1
XX CC variant PyVP1-WW150 construct which is used to illustrate the method of
XX CC the invention.
XX XX
XX SQ Sequence 10 AA;
XX XX
XX Query Match 71.4%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 40;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 3 PPPLP 7
XX Db |||||
XX 6 PPPLP 10
XX XX
XX RESULT 28
XX AAB86131
XX ID AAB86131 standard; Protein; 10 AA.
XX AC
XX XX
XX AC AAB86131;
XX XX
XX DT 30-JUL-2001 (first entry)
XX XX
XX DE Proline-rich peptide.
XX XX
XX KW Transport system; gene therapy; infection; tumor LLO;
XX KW human immune deficiency virus; hemophilia; muscular dystrophy; capsid;
XX KW cystic fibrosis; virus-like particle; cell targeting; listeriolysin O.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200132851-A2.
XX XX
XX PD 10-MAY-2001.
XX XX

```

PF 03-NOV-2000; 2000WO-EP10876.
 XX
 PR 03-NOV-1999; 99DE-1052957.
 XX
 PA (ACGT-) ACGT PROGENOMICS AG.
 XX
 PI Boehm G, Rudolph R, Schmidt U, Esser D;
 XX
 DR WPI; 2001-316433/33.
 XX
 XX Transport system for compounds, useful e.g. in gene therapy, comprises
 PT mosaic-like assembly of different protein subunits able to encapsulate
 PT compounds -
 XX
 PS Example 11; Page 35; 106pp; German.
 XX
 CC This invention describes a novel transport system (A) for molecular
 CC substances (I) containing recombinantly prepared subunits (SU) based
 CC on amino acids (aa) comprising: (i) at least two modified SU with one
 CC difference; and/or (ii) one or more modified SU with at least two
 CC differences; and (iii) (optionally) unmodified SU. The various SU are
 CC combined in a mosaic fashion to form (A) in which (I) can be
 CC encapsulated. (A) Are used to deliver (I) specifically to cells,
 CC particularly DNA to eukaryotic cells for gene therapy, e.g. of infections
 CC by human immune deficiency virus, tumors and a wide range of inherited
 CC diseases such as hemophilia, muscular dystrophy or cystic fibrosis.
 CC Capsids or other virus-like particles can be assembled, simply and in
 CC modular fashion, in vitro, allowing control over stoichiometric
 CC composition. SU can be modified to impart a wide variety of selected
 CC properties, e.g. cell targeting, improved cellular uptake and reduced
 CC immunogenicity. (A) do not require extensive testing to ensure that they
 CC are safe (contrast replication-deficient viruses), also SU can be
 CC prepared in very pure form and are easily labeled fluorescently (for
 CC quality control or localization). This sequence represents a proline-rich
 CC peptide used in the construction of a *Listeria monocytogenes*
 CC listeriolysin LLO variant which is used to illustrate the method of the
 CC invention.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 71.4%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PPPLP 7
 Db 6 PPPLP 10
 |||||

RESULT 29
 AAB86149
 ID AAB86149 standard; Peptide; 10 AA.
 XX
 AC AAB86149;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Proline-rich peptide fragment.
 XX
 KW Packaging; protein shell; transport system; gene therapy; GFP-PPLP;
 KW icosahedral virus capsid; enhanced green fluorescent protein; eGFP;
 KW fusion construct; proline-rich.
 XX
 OS Unidentified.
 XX
 PN WO200132852-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-BF10878.
 XX
 PR 03-NOV-1999; 99DE-1052982.
 XX

PA (ACGT-) ACGT PROGENOMICS AG.
 XX
 PI Boehm G, Esser D, Schmidt U;
 XX
 DR WPI; 2001-316434/33.
 XX
 XX Packaging compounds in protein shells, useful e.g. in gene therapy, by
 PT binding a compound to immobilized shell fragment, then releasing it
 PT from the matrix and assembly into shells -
 XX
 XX Example 6; Page 26; 62pp; German.
 PS
 PS This invention describes a novel method for packaging molecular
 CC substances (I) in protein shells which comprises binding a shell
 CC fragment (II), via a first region, to a matrix (M), then treating bound
 CC (II) with (I) so that this binds through a second region of (II). The
 CC (I)-(II) product, or part of it, is separated from M and assembled, with
 CC other (II), to form the shells. The separation and assembly steps may be
 CC performed in either sequence. Packaging of (I) is used to prepare
 CC transport systems for genes or active agents, particularly in gene
 CC therapy. The process provides very efficient packaging of (I), including
 CC compounds that aggregate in solution or have other unfavorable
 CC properties. Even very long DNA can be packaged, when combined with a
 CC condensing agent, and the method is applicable to any sort of protein
 CC shell, not just icosahedral virus capsids. The integrated (II) can be
 CC screened for optimization of its packaging properties. e.g. maximum size
 CC of (I) that can be accommodated. This sequence represents a
 CC proline-rich peptide fragment used in the production of the fusion
 CC construct comprising the Aequorea victoria enhanced green fluorescent
 CC protein (eGFP) and a proline rich region which is used to illustrate the
 CC method of the invention.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 71.4%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PPPLP 7
 Db 6 PPPLP 10
 |||||

RESULT 30
 AAE16670
 ID AAE16670 standard; peptide; 10 AA.
 XX
 AC AAE16670;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human YAP65 protein SH3 domain binding motif.
 XX
 KW Human; congestive heart failure; dilative cardiomyopathy; sudden death;
 KW hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder;
 KW heart muscle disease; conduction disorder; coronary heart disease;
 KW systemic arterial hypertension; pulmonary hypertension; endocarditis;
 KW pulmonary heart disease; valvular heart disease; pericardial disease;
 KW congenital heart disease; gene therapy; syncope; transgenic animal;
 KW YAP65 protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200192567-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-EP06165.
 XX
 PR 30-MAY-2000; 2000US-207400P.
 XX
 PA (MEDI-) MEDIGENE AG.
 XX

```
PI Bunk D, Reuner B, Beck J, Henkel T;
XX WPI; 2002-122073/16.
XX
XX
XX Identifying a subject at risk for a heart disease e.g. congestive heart
PT failure, dilative cardiomyopathy, heart muscle disease, by quantifying
PT the polypeptide expressed by genes abnormally expressed in heart tissue
PT
XX
XX Example 7; Page 71; 154pp; English.
XX
XX The patent discloses novel target genes abnormally expressed in heart
CC tissues and their corresponding proteins. The invention also relates to
CC methods for assessing the expression level of these genes. The method
CC is used for testing the predisposition of mammals and preferably humans
CC for a heart disease or for an acute state of such a disease. It is also
CC useful to treat diseases of the heart such as congestive heart failure,
CC dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardio-
CC myopathy, specific heart muscle disease, rhythm and conduction disorders,
CC syncope and sudden death, coronary heart disease, systemic arterial
CC hypertension, pulmonary hypertension, pulmonary heart disease, valvular
CC heart disease, congenital heart disease, pericardial disease and
CC endocarditis. Sequences of the invention are also used in gene therapy.
CC A transgenic non-human mammal comprising the sequences of the invention
CC are useful for the development for medicaments for the treatments of
CC heart diseases. The present sequence is the SH3 domain binding motif
CC of human YAP65 protein.
XX
XX Sequence 10 AA;
SQ
Query Match 71.4%; Score 5; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QPPPL 6
DB 4 QPPPL 8
RESULT 31
AAB21126
ID AAB21126 standard; peptide; 11 AA.
XX
XX AAB21126;
XX
XX 19-JAN-2001 (first entry)
XX
XX Src homology 3 domain binding peptide #3.
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
XX Synthetic.
XX
XX WO2000047607-A1.
XX
XX 17-AUG-2000.
XX
XX 12-FEB-2000; 2000WO-KR00107.
XX
XX 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
XX (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
XX Synthetic.
XX
XX WO2000047607-A1.
XX
XX 17-AUG-2000.
XX
XX 12-FEB-2000; 2000WO-KR00107.
XX
XX 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
XX (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
XX
XX WPI; 2000-533010/48.
XX
XX Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (src homology) 2 and SH3
PT motifs of Src family kinase proteins -
XX
XX Claim 3; Page 71; 154pp; English.
XX
XX The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC suppression-associated diseases.
XX
XX Sequence 11 AA;
SQ
Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
DB 4 PPPLP 8
RESULT 32
AAB21127
ID AAB21127 standard; peptide; 11 AA.
XX
XX AAB21127;
XX
XX 19-JAN-2001 (first entry)
XX
XX Src homology 3 domain binding peptide #4.
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
XX Synthetic.
XX
XX WO2000047607-A1.
XX
XX 17-AUG-2000.
XX
XX 12-FEB-2000; 2000WO-KR00107.
XX
XX 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
XX (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
XX
XX Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (src homology) 2 and SH3
PT motifs of Src family kinase proteins -
XX
XX Claim 3; Page 33; 40pp; English.
XX
XX The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC suppression-associated diseases.
XX
XX Sequence 11 AA;
SQ
Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
DB 4 PPPLP 8
RESULT 32
AAB21127
ID AAB21127 standard; peptide; 11 AA.
XX
XX AAB21127;
XX
XX 19-JAN-2001 (first entry)
XX
XX Src homology 3 domain binding peptide #4.
XX
XX Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.
XX
XX Synthetic.
XX
XX WO2000047607-A1.
XX
XX 17-AUG-2000.
XX
XX 12-FEB-2000; 2000WO-KR00107.
XX
XX 12-FEB-1999; 99AU-0008643.
PR 02-JUN-1999; 99KR-0020282.
XX
XX (YOON/) YOON J H.
PA (HANY/) HAN Y T.
XX
XX Yoon JH, Han YT, Lee KY;
XX
XX Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (src homology) 2 and SH3
PT motifs of Src family kinase proteins -
XX
XX Claim 3; Page 33; 40pp; English.
XX
XX The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC suppression-associated diseases.
XX
XX Sequence 11 AA;
SQ
Query Match 71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 33
AAB21129
ID  AAB21129 standard; peptide; 11 AA.
XX
AC  AAB21129;
XX
DT  19-JAN-2001 (first entry)
XX
DE  Src homology 3 domain binding peptide #6.
XX
KW  Src homology domain 3; SH3; protein-protein interaction; cancer;
KW  signal transduction inhibition; immune suppression-associated disease.
XX
OS  Synthetic.
XX
PN  WO200047607-A1.
XX
PD  17-AUG-2000.
XX
PF  12-FEB-2000; 2000WO-KR00107.
XX
PR  12-FEB-1999; 99AU-0008643.
XX
PR  02-JUN-1999; 99KR-0020282.
XX
PA  (YOON/) YOON J H.
PA  (HANY/) HAN Y T.
XX
PI  Yoon JH, Han YT, Lee KY;
XX
DR  WPI; 2000-533010/48.
XX
PT  Synthetic peptides useful for treating cancers and immunosuppressive
PT  disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT  motifs of Src family kinase proteins -
XX
PS  Claim 3; Page 34; 40pp; English.
XX
CC  The present sequence is a synthetic peptide which has a high affinity for
CC  the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC  involved in signal transduction pathways, and this peptide can be used to
CC  inhibit these, by disrupting protein-protein interactions, in the
CC  treatment of cancer, particularly hepatocellular carcinoma, cervical
CC  cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC  suppression-associated diseases.
XX
SQ  Sequence 11 AA;

Query Match      71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 34
AAB21132
ID  AAB21132 standard; peptide; 11 AA.
XX
AC  AAB21132;
XX
DT  19-JAN-2001 (first entry)
XX
DE  Src homology 3 domain binding peptide #9.
XX
KW  Src homology domain 3; SH3; protein-protein interaction; cancer;
KW  signal transduction inhibition; immune suppression-associated disease.

```

```

XX      Synthetic.
OS
XX      WO200047607-A1.
XX
XX      17-AUG-2000.
XX
XX      12-FEB-2000; 2000WO-KR00107.
XX
XX      12-FEB-1999; 99AU-0008643.
XX
XX      02-JUN-1999; 99KR-0020282.
XX
XX      (YOON/) YOON J H.
XX
XX      (HANY/) HAN Y T.
XX
XX      Yoon JH, Han YT, Lee KY;
XX
XX      WPI; 2000-533010/48.
XX
XX      Synthetic peptides useful for treating cancers and immunosuppressive
XX      disorders by disrupting interactions of the SH (Src homology) 2 and SH3
XX      motifs of Src family kinase proteins -
XX
XX      Claim 3; Page 35; 40pp; English.
XX
XX      The present sequence is a synthetic peptide which has a high affinity for
XX      the src homology 3 (SH3) domain of protein kinases. Protein kinases are
XX      involved in signal transduction pathways, and this peptide can be used to
XX      inhibit these, by disrupting protein-protein interactions, in the
XX      treatment of cancer, particularly hepatocellular carcinoma, cervical
XX      cancer, colon adenocarcinoma and fibrosarcoma, and immune
XX      suppression-associated diseases.
XX
XX      Sequence 11 AA;

Query Match      71.4%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPLP 7
Db      4 PPPLP 8

RESULT 35
AAB21165
ID  AAB21165 standard; peptide; 11 AA.
XX
AC  AAB21165;
XX
XX      22-NOV-2002 (first entry)
XX
XX      Formin-2 FH1 domain repeated proline motif.
XX
XX      Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;
XX      spontaneous abortion; miscarriage; FH1; proline motif.
XX
XX      Unidentified.
XX
XX      Key      Location/Qualifiers
XX      Misc-difference 1
XX      /label= Met, Val

US2002098489-A1.
XX
XX      25-JUL-2002.
XX
XX      12-APR-2001; 2001US-0835232.
XX
XX      13-APR-2000; 2000US-196811P.
XX
XX      {LEDE/} LEDE P.
XX
XX      {LEAD/} LEADER B.

```


XX Leder P, Leader B;
 XX WPI; 2002-690474/74.
 XX
 XX Determining whether patient has increased risk for recurrent pregnancy
 PT loss by determining whether formin-2 (Fmn-2) gene of patient has
 PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression
 PT in patient -
 XX
 XX Example 1; Page 7; 137pp; English.
 XX
 CC The invention relates to a novel method for determining whether a patient
 CC has an increased risk for recurrent pregnancy loss, involving determining
 CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The
 CC method of the invention is useful for determining whether a patient has a
 CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous
 CC abortion/miscarriage). The sequence represents a proline motif which is
 CC repeated 11 times in tandem in the Fhl domain of formin-2.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 71.4%; Score 5; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 6 PPPLP 10
 XX
 XX
 XX RESULT 36
 XX ABB99166
 ID ABB99166 standard; peptide; 11 AA.
 XX
 AC ABB99166;
 XX
 XX 22-NOV-2002 (first entry)
 DT
 XX
 DE Formin-2 Fhl domain repeated proline motif #2.
 XX
 KW Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;
 KW spontaneous abortion; miscarriage; Fhl; proline motif.
 XX
 OS Unidentified.
 XX
 PN US2002098489-A1.
 XX
 XX 25-JUL-2002.
 PD
 XX
 XX 12-APR-2001; 2001US-0835232.
 PF
 XX
 XX 13-APR-2000; 2000US-196811P.
 PR
 XX (LEDE/) LEDER P.
 PA (LEAD/) LEADER B.
 XX
 PI Leder P, Leader B;
 XX
 XX WPI; 2002-690474/74.
 DR
 XX Determining whether patient has increased risk for recurrent pregnancy
 PT loss by determining whether formin-2 (Fmn-2) gene of patient has
 PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression
 PT in patient -
 XX
 XX Example 1; Page 7; 137pp; English.
 PS
 XX
 XX The invention relates to a novel method for determining whether a patient
 CC has an increased risk for recurrent pregnancy loss, involving determining
 CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The
 CC method of the invention is useful for determining whether a patient has a
 CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous

CC abortion/miscarriage). The sequence represents a proline motif which is
 CC repeated in the Fhl domain of formin-2 in the brain clones of the
 CC invention.
 XX
 XX SQ Sequence 11 AA;
 Query Match 71.4%; Score 5; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 7 PPPLP 11
 XX
 XX
 XX RESULT 37
 XX AAW06845
 ID AAW06845 standard; peptide; 12 AA.
 XX
 AC AAW06845;
 XX
 XX 16-FEB-1997 (first entry)
 DT
 XX
 XX Peptide binding the Crk-SH3 domain, used to treat cancer.
 DE
 XX
 KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
 KW treatment; diagnosis; antibody; signal transduction; disease;
 KW disorder; intracellular signalling protein.
 XX
 OS Synthetic.
 XX
 XX WO9621011-A2.
 PN
 XX 11-JUL-1996.
 PD
 XX 28-DEC-1995; 95WO-US16979.
 PF
 XX 30-DEC-1994; 94US-0367070.
 PR
 XX (UVRQ) UNIV ROCKEFELLER.
 PA
 XX Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
 PI Wu X, Zheng J;
 XX
 XX WPI; 1996-333986/33.
 DR
 XX
 XX New peptide(s) which bind the Crk-SH3 domain - used to develop
 PT prods. for the diagnosis and treatment of defects in intracellular
 PT signal transduction, partic. in cancer
 XX
 XX Claim 3; Page 92; 120pp; English.
 PS
 XX New peptides or proteins which comprise these peptides, bind
 CC to the Crk-SH3 domain and competitively inhibit the binding of
 CC intracellular signalling proteins. They can be used in the
 CC treatment of a disease or disorder associated with a defect in
 CC intracellular signal transduction, particularly cancer. They can
 CC also be used to diagnose such diseases and disorders. Antibodies
 CC raised against these proteins can be used for the same purposes. The
 CC peptides are derived from the Crk-SH3 binding domains of
 CC intracellular signalling proteins. Peptides related to the invention
 CC are described in AAW03149-63 and AAW06842-W06866.
 XX
 XX SQ Sequence 12 AA;
 Query Match 71.4%; Score 5; DB 17; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 3 PPPLP 7

```
RESULT 38
AAW03154
ID AAW03154 standard; peptide; 12 AA.
XX
XX AAW03154;
AC AAW03154;
XX
XX 16-FEB-1997 (first entry)
DT
XX
XX Potential Crk-SH3 binding sequence of protein mSos2/p1.
DE
XX
XX Peptide; binding; inhibition; binding domain; Crk-SH3; cancer;
KW treatment; diagnosis; antibody; signal transduction; disease;
KW disorder; intracellular signalling protein.
XX
XX Synthetic.
OS
XX
XX WO9621011-A2.
FN
XX
XX 11-JUL-1996.
PD
XX
XX 28-DEC-1995; 95WO-US16979.
PF
XX
XX 30-DEC-1994; 94US-0367070.
PR
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX
XX Cowburn D, Feller SM, Hanafusa H, Knudsen BS, Kuriyan J;
PI Wu X, Zheng J;
PL
XX
XX WPI; 1996-333986/33.
DR
XX
XX New peptide(s) which bind the Crk-SH3 domain - used to develop
PT prods for the diagnosis and treatment of defects in intracellular
PT signal transduction, partic. in cancer
XX
XX Disclosure; Page 53; 120pp; English.
FS
XX
XX New peptides or proteins which comprise these peptides, bind
CC to the Crk-SH3 domain and competitively inhibit the binding of
CC intracellular signalling proteins. They can be used in the
CC treatment of a disease or disorder associated with a defect in
CC intracellular signal transduction, particularly cancer. They can
CC also be used to diagnose such diseases and disorders. Antibodies
CC raised against these proteins can be used for the same purposes. The
CC peptides are derived from the Crk-SH3 binding domains of
CC intracellular signalling proteins. Peptides related to the invention
CC are described in AAW03149-63 and AAW06842-W06866.
XX
XX
SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 3 PPPLP 7
RESULT 39
AAW05101
ID AAW05101 standard; peptide; 12 AA.
XX
XX AAW05101;
AC AAW05101;
XX
XX 25-MAR-2003 (updated)
DT 17-DEC-1996 (first entry)
DT
XX
XX Proline-rich SH3 binding peptide pL35.
DE
XX
XX Src homology domain; SH3 domain; oncogene; consensus; lambda 35;
KW random display library.
```

```
XX Synthetic.
XX
XX US5541109-A.
XX
XX 30-JUL-1996.
PD
XX
XX 19-APR-1994; 94US-0230047.
PF
XX
XX 19-APR-1994; 94US-0230047.
PR
XX
XX (RHON ) RHONE POULENC RORER PHARM INC.
PA
XX
XX Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC, French SM;
PI Searfoss GH;
XX
XX WPI; 1996-361965/36.
DR
XX
XX New DNA encoding proteins that bind to Src-homology domain 3 - used
PT to inhibit signal transduction, e.g. in cases of T cell activation
PT
XX
XX Example 1; Column 16; 39pp; English.
XX
XX A fusion protein of glutathione-S-transferase, protein kinase A and
CC Src SH3 domain was used to screen a mouse embryonal cDNA library in
CC lambda Exlox. Three positive clones were identified and were
CC designated L17, L14 and L35. The insert from clone L35 encodes a
CC protein which contains a proline-rich, putative SH3-binding
CC sequence. The present peptide sequence is derived from the putative
CC SH3-binding site (i.e. residues 13-24 of L35) and was used in an assay
CC to determine binding to the SH3 domains of c-src and other proteins.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 4 PPPLP 8
RESULT 40
AAW25457
ID AAW25457 standard; peptide; 12 AA.
XX
XX AAW25457;
AC AAW25457;
XX
XX 27-MAR-1998 (first entry)
DT
XX
XX SH3 domain binding responsible peptide SEQ ID NO:251.
DE
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
OS
XX Unidentified.
XX
XX WO9730074-A1.
FN
XX
XX 21-AUG-1997.
PD
XX
XX 14-FEB-1997; 97WO-US02298.
PF
XX
XX 16-FEB-1996; 96US-0602999.
PR
XX
XX (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI
```

PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 21; Page 85; 131pp; English.
 XX
 CC The present sequence represents a peptide responsible for Src homology
 CC region 3 (SH3) binding. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p33bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 6 PPPLP 10
 RESULT 41
 AAW25468
 ID AAW25468 standard; peptide; 12 AA.
 XX
 AC AAW25468;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE SH3 domain binding responsible peptide SEQ ID NO:266.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 PN W09730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US02298.
 XX
 PR 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX

PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 21; Page 85; 131pp; English.
 XX
 CC The present sequence represents a peptide responsible for Src homology
 CC region 3 (SH3) binding. SH3 binding peptides are selected from: (a)
 CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind
 CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
 CC of p33bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QPPPL 6
 DB 4 QPPPL 8
 RESULT 42
 AAB18002
 ID AAB18002 standard; Peptide; 12 AA.
 XX
 AC AAB18002;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Fc-TNF alpha peptide sequence SEQ ID NO:1116.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 OS
 PN W0200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and

PT autoimmune diseases -
XX Disclosure; Page 604; 608pp; English.
XX

CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, P3-(L4)f-P4
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX

SQ Sequence 12 AA;
Query Match 71.4%; Score 5; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 8 PPPLP 12
|||||

RESULT 43
AAR84641
ID AAR84641 standard; Peptide; 13 AA.
AC AAR84641;
XX
XX 26-MAR-1996 (first entry)
XX
DE Grb2-SOS binding blocking peptide.
XX
XX SOS; Grb2; BCR-ABL; tyrosine kinase; transformation; Ras;
KW oncoprotein; leukaemia; Ras guanine nucleotide releasing protein.
XX
OS Synthetic.
XX
PN CA2113494-A.
XX
PD 15-JUL-1995.
XX
PF 14-JAN-1994; 94CA-2113494.
XX
PR 14-JAN-1994; 94CA-2113494.
XX
PR (MOUN) MOUNT SINAI HOSPITAL CORP.
PA (TEXA) UNIV TEXAS.
XX
XX Arllinghaus R, Gish G, Liu J, Pawson A, Puil L;
PI
XX WPI; 1995-302931/40.
DR
XX Detection of agents that modify BCR-ABL mediated transformation -
PT useful in treatment of leukaemia and other malignancies
XX
XX Disclosure; Page 15; 106pp; English.
XX

CC Peptides (AAR84640-48) that block the binding of Grb2 (AAR84636) to
CC SOS Ras guanine nucleotide releasing protein are modelled on the
CC proline-rich motifs in the C-terminal region of mouse SOS1
CC (AAR84638) and SOS2 (AAR84639). The peptides can be used to screen
CC

CC for compounds that affect BCL-ABL mediated transformation. Such
CC compounds have value in the treatment of chronic, acute myelogenous
CC or acute lymphocytic leukaemia.
XX

SQ Sequence 13 AA;
Query Match 71.4%; Score 5; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9
|||||

RESULT 44
AAB70928
ID AAB70928 standard; Protein; 13 AA.
XX
AC AAB70928;
XX
DT 30-JUL-2001 (first entry)
XX
DE Polyoma virus VPI variant proline-rich peptide fragment.
XX
XX VPI; Coat protein; WW domain; proline-rich; immobilization; biosensor;
KW bioreactor; protein packaging; PyVPI-WM150-D8C.
XX
XX Polyoma virus.
OS
XX WO200132684-A2.
PN
XX 10-MAY-2001.
PD
XX 03-NOV-2000; 2000WO-EP10873.
PF
XX 03-NOV-1999; 99DE-1052956.
PR
XX (ACGT-) ACGT PROGENOMICS AG.
PA
XX Boelm G, Schmidt U, Parthier C, Guenther C;
PI WPI; 2001-343471/36.
XX
XX Linking two or more molecules through adapter sequences, useful e.g.
PT for purifying recombinant proteins, by exploiting interaction between
PT WW domain and proline-rich sequence -
XX
XX Example 5; Page 88; 100pp; German.
XX

CC This invention describes a novel method (M1) for linking two or more
CC molecular substances (A) together via adapter sequences (AS). One (A) is
CC modified so that it contains, as AS, a WW domain or derived structure in
CC at least one region, and a second (A) is modified so that it contains,
CC as AS, a proline-rich sequence (PRS) able to bind to WW domain or its
CC derivative in at least one region and the modified components are
CC allowed to interact together through WW and PRS. The method is used to
CC provide permanent or temporary association between (A), e.g. temporary
CC immobilization, and matrix-assisted refolding, of recombinant proteins
CC from crude cell extracts or permanent immobilization in biosensors or
CC bioreactors, for directing packaging of proteins inside a virus-like
CC shell, or production of chimeric proteins (e.g. bispecific antibodies),
CC for medical, therapeutic, diagnostic or biotechnological use. Interaction
CC between WW and PRS is very strong (dissociation constant 20-100 nM) but
CC only temporary, and can be stabilized (e.g. against extremes of salt
CC concentration or temperature) by formation of disulfide bridges. Compared
CC with other systems with comparable properties, the WW/PRS system is
CC exceptionally small and compact and for many applications, e.g.
CC antibody-antigen interaction, is clearly superior to other ligand binding
CC domains. The system can only produce heterodimers. This sequence
CC represents a proline-rich peptide fragment from Polyoma virus coat
CC protein VPI which is used to illustrate the method of the invention.
XX

SQ Sequence 13 AA;
 Query Match 71.4%; Score 5; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 Db 9 PPPLP 13
 |||||

RESULT 45
 AAW05490
 ID AAW05490 standard; Peptide; 14 AA.
 AC AAW05490;
 XX
 DT 24-FEB-1998 (first entry)
 DE SH3-binding peptide CRK.CON.
 KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
 KW cellular signalling element; cellular structural element; malignancy;
 KW protein identification; functional domain; protein screening;
 KW cellular signal transduction process; binding peptide.
 XX
 OS Synthetic.
 XX
 PN WO9631625-A1.
 PD 10-OCT-1996.
 XX
 XX 04-APR-1996; 96WO-US04454.
 XX
 PR 03-APR-1996; 96US-0630915.
 PR 07-APR-1995; 95US-0417872.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
 XX
 DR WPI; 1996-465045/46.
 XX
 XX Identifying polypeptide(s) having specific functional domain (esp.
 PT SH3 domain) - comprises detecting selective binding to recognition
 PT unit, regardless of sequence homology
 XX
 PS Example; Fig 13; 174pp; English.

XX
 CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
 CC peptides. These sequences were used as parts of multivalent recognition
 CC unit complexes used in the method of the invention. The method of the
 CC invention is for identifying polypeptides containing functional domains
 CC of interest (especially SH3 domains). It comprises contacting a
 CC multivalent recognition unit (RU) complex with a number of peptides and
 CC identifying polypeptides having a selective binding affinity for the RU
 CC complex. The method is based on functional similarities and does not
 CC rely on sequence similarities. Prior methods only gave limited success
 CC for identifying proteins containing an SH3 domain due to the minimal
 CC sequence homology among known SH3 proteins. Multivalent RU complexes are
 CC particularly suited to screening for polypeptides containing functional
 CC domains that are similar to, but not identical in sequence to, the
 CC original target functional domain. The new method enables proteins
 CC having a common function to be identified. Identification of novel SH3
 CC proteins will be useful for a better understanding of cell growth,
 CC malignancy, signal transduction processes, etc. New candidate drugs can
 CC be identified, and their specificities (e.g. pharmacological activities)
 CC can be assessed using the method of the invention.

XX
 SQ Sequence 14 AA;
 Query Match 71.4%; Score 5; DB 17; Length 14;

Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 Db 5 PPPLP 9
 |||||

RESULT 46
 AAW38067
 ID AAW38067 standard; Peptide; 14 AA.
 XX
 AC AAW38067;
 XX
 DT 23-APR-1998 (first entry)
 DE PPPY motif containing peptide used to bind WW domains.
 XX
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
 KW cytoskeleton organisation; targeted drug screening; modulator;
 KW WW domain interaction; YAP protein; dystrophin.
 XX
 OS Synthetic.
 XX
 PN WO9737223-A1.
 PD 09-OCT-1997.
 XX
 XX 03-APR-1997; 97WO-US05547.
 XX
 PR 03-APR-1996; 96US-0630916.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Fowlkes DM, Kay BK, Pirozzi G;
 XX
 DR WPI; 1997-503234/46.
 XX
 XX Identifying cell signalling and growth regulatory polypeptides by
 PT reaction with multivalent recognition complex - polypeptides are
 PT useful in targeted drug selection
 XX
 PS Disclosure; Fig 15A; 220pp; English.

XX
 CC Peptides AAW38057-67 contain PPPY-like motifs. The PPPY motif is
 CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
 CC containing this residue have been shown to bind the YAP WW domain, but
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
 CC AAW38057-67 were biotinylated and complexed with alkaline streptavidin,
 CC and used in a cross affinity mapping experiment. They were tested for
 CC their ability to bind to the 12 individual novel WW domains of WWPI
 CC (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which
 CC were expressed as glutathione-S-transferase expression proteins. The
 CC present peptide, derived from Crk protein, does not bind the WW domains
 CC of the novel proteins. The WW domain is a small functional domain. Its
 CC name is derived from the observation that two tryptophan residues, one in
 CC the amino terminal portion of the WW domain and one in the carboxyl
 CC terminal portion, are conserved. Most proteins containing WW domains have
 CC a function involving cell signalling and growth regulation or the
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain
 CC are identified by treating a multivalent recognition unit complex that
 CC has selective binding affinity for a WW domain, with many polypeptides
 CC and identifying those with selective affinity for the complex. Proteins
 CC containing WW domains are used for targeted drug screening, i.e. to
 CC identify potential modulators of specific WW domain interactions.

XX
 SQ Sequence 14 AA;
 Query Match 71.4%; Score 5; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 5 PPPLP 9

RESULT 47

AAW38959
 ID AAW38959 standard; peptide; 15 AA.

XX AAW38959;

XX 27-MAR-1998 (first entry)

XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:356.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 22; Page 91; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 49

AAW39034
 ID AAW39034 standard; peptide; 15 AA.

XX AAW39034;

RESULT 48

AAW39050
 ID AAW39050 standard; peptide; 15 AA.

XX AAW39050;

XX 27-MAR-1998 (first entry)

XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:452.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 22; Page 94; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.

SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

XX 27-MAR-1998 (first entry)
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:435.
 XX
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 PI
 XX WPI; 1997-424972/39.
 DR
 XX Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 PT
 XX Claim 22; Page 94; 131pp; English.
 PS
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 4 PPPLP 8
 RESULT 50
 AAW39040
 ID AAW39040 standard; peptide; 15 AA.
 XX
 XX AAW39040;
 AC
 XX 27-MAR-1998 (first entry)
 DT
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:441.
 XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 XX WO9730074-A1.
 PN
 XX 21-AUG-1997.
 PD
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 PI
 XX WPI; 1997-424972/39.
 DR
 XX Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 PT
 XX Claim 22; Page 94; 131pp; English.
 PS
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 5 PPPLP 9
 RESULT 51
 AAW39005
 ID AAW39005 standard; peptide; 15 AA.
 XX
 XX AAW39005;
 AC
 XX 27-MAR-1998 (first entry)
 DT
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:404.
 DE
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 XX Synthetic.
 XX

```

XX PN WO9730074-A1.
XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 52
AAW39015
ID AAW39015 standard; peptide; 15 AA.
XX
XX AAW39015;
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:414.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 53
AAW38988
ID AAW38988 standard; peptide; 15 AA.
XX
XX AAW38988;
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:385.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.

```

```

PF 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 53
AAW38988
ID AAW38988 standard; peptide; 15 AA.
XX
XX AAW38988;
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:385.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX PN 21-AUG-1997.
XX PD 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.

```



```

PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 92; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
XX Sequence 15 AA;
SQ
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPPLP 7
Db 7 PPPLP 11
RESULT 54
AAW27070
ID AAW27070 standard; peptide; 15 AA.
XX
XX AAW27070;
AC
DT 19-MAR-1998 (first entry)
XX
DE Proline rich peptide.
XX
KW Proline rich; treatment; inflammation; septic shock;
KW rheumatoid arthritis; asthma; adult respiratory distress syndrome;
KW ischaemic heart disease; reperfusion injury;
XX inflammatory bowel disease.
OS Homo sapiens.
XX
XX GB2311067-A.
XX
XX 17-SEP-1997.
XX
XX 08-JAN-1996; 96GB-0000307.
XX
XX 08-JAN-1996; 96GB-0000307.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (YAMA ) YAMANOUCHI UK LTD.
XX
XX Finan P, Kellie S;
XX
XX WPI; 1997-427905/40.
XX
XX Proline rich peptides derived from a protein extracted from Namalwa
XX cells - for treating e.g. inflammatory diseases, rheumatoid and
XX other arthritides, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease and inflammatory bowel disease
XX
XX Claim 2; Page 17; 28pp; English.
XX
XX The present proline rich peptide can be used to treat chronic and
XX acute inflammatory diseases and conditions, e.g. septic shock,
XX rheumatoid arthritis, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease, reperfusion injury and inflammatory bowel
XX disease.
XX
XX Sequence 15 AA;
SQ
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QPPPL 6
Db 6 QPPPL 10
RESULT 55
AAW27073
ID AAW27073 standard; peptide; 15 AA.
XX
XX AAW27073;
AC
DT 19-MAR-1998 (first entry)
XX
DE Proline rich peptide.
XX
KW Proline rich; treatment; inflammation; septic shock;
KW rheumatoid arthritis; asthma; adult respiratory distress syndrome;
KW ischaemic heart disease; reperfusion injury;
XX inflammatory bowel disease.
OS Homo sapiens.
XX
XX GB2311067-A.
XX
XX 17-SEP-1997.
XX
XX 08-JAN-1996; 96GB-0000307.
XX
XX 08-JAN-1996; 96GB-0000307.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (YAMA ) YAMANOUCHI UK LTD.
XX
XX Finan P, Kellie S;
XX
XX WPI; 1997-427905/40.
XX
XX Proline rich peptides derived from a protein extracted from Namalwa
XX cells - for treating e.g. inflammatory diseases, rheumatoid and
XX other arthritides, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease and inflammatory bowel disease
XX
XX Claim 2; Page 17; 28pp; English.
XX
XX The present proline rich peptide can be used to treat chronic and
XX acute inflammatory diseases and conditions, e.g. septic shock,
XX rheumatoid arthritis, asthma, adult respiratory distress syndrome,
XX ischaemic heart disease, reperfusion injury and inflammatory bowel
XX disease.
XX
XX Sequence 15 AA;
SQ

```

Query Match 71.4%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPL 6
 DB 6 QPPPL 10
 |||||

RESULT 56
 AAY41635
 ID AAY41635 standard; peptide; 15 AA.
 XX AC AAY41635;
 XX 02-DEC-1999 (first entry)
 XX Mammalian ion channel proline rich motif containing peptide #29.
 DE SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
 KW proline rich.
 KW Homo sapiens.
 OS US9595259-A.
 PN 21-SEP-1999.
 XX 19-DEC-1996; 96US-0769745.
 XX 19-DEC-1996; 96US-0769745.
 XX (UYBR-) UNIV BRANDEIS.
 XX Holmes TC, Levitan IB;
 PI WPI; 1999-560490/47.
 XX Identification of compounds that modulate potassium ion channel binding
 PT with protein tyrosine kinase SH3 domains -
 PT Disclosure; Column 8; 18pp; English.
 XX A method has been developed for determining if a compound modulates the
 CC binding of a potassium ion channel to the SH3 domain of a protein
 CC tyrosine kinase by contacting the channel with a polypeptide comprising
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3
 CC binding. The method is useful for assessing the ability of a compound to
 CC modulate the formation of channel-SH3 domain complexes to improve the
 CC understanding of mechanisms of potassium channel blockage and assess the
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to
 CC AAY41644 represent mammalian ion channel peptides with proline-rich
 CC motifs.
 XX Sequence 15 AA;
 SQ Query Match 71.4%; Score 5; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLPL 7
 DB 4 PPLPL 8
 |||||

RESULT 57
 AAW25411
 ID AAW25411 standard; peptide; 16 AA.
 XX AC AAW25411;
 XX 27-MAR-1998 (first entry)
 DT Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 XX

DE Crk N-terminal SH3 domain binding peptide SEQ ID NO:197.
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 OS Unidentified.
 XX WO9730074-A1.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 PS Claim 18; Page 100; 131pp; English.
 XX The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding
 CC peptides can be used in the method to identify inhibitors of their
 CC binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX Sequence 16 AA;
 SQ Query Match 71.4%; Score 5; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLPL 7
 DB 9 PPLPL 13
 |||||

RESULT 58
 AAW38963
 ID AAW38963 standard; peptide; 17 AA.
 XX AAW38963;
 XX 27-MAR-1998 (first entry)
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:360.
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 XX

KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.
 PN 21-AUG-1997.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 PF 16-FEB-1996; 96US-0602999.
 PR (CYTO-) CYTOGEN CORP.
 XX (UYN-) UNIV NORTH CAROLINA.
 PA Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 91; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX Sequence 17 AA;
 SQ Query Match 71.4%; Score 5; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 9 PPPLP 13
 RESULT 59
 AAW38977
 ID AAW38977 standard; peptide; 17 AA.
 AC AAW38977;
 XX 27-MAR-1998 (first entry)
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:374.
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.
 PN 21-AUG-1997.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 PF 16-FEB-1996; 96US-0602999.
 PR (CYTO-) CYTOGEN CORP.
 XX (UYN-) UNIV NORTH CAROLINA.
 PA Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 91; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX Sequence 17 AA;
 SQ Query Match 71.4%; Score 5; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 9 PPPLP 13
 RESULT 60
 AAW38977
 ID AAW38977 standard; peptide; 18 AA.
 AC AAW38977;
 XX 14-AUG-1996 (first entry)
 DT Prolyl endopeptidase inhibitor peptide #1.
 DE Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX Synthetic.
 XX JP08059697-A.
 PN 05-MAR-1996.
 PD 09-MAR-1995; 95JP-0079661.
 XX 15-JUN-1994; 94JP-0158031.
 PR

XX 21-AUG-1997.
 PD 14-FEB-1997; 97WO-US02298.
 PF 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 PA (UYN-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 PI Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 92; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX Sequence 17 AA;
 SQ Query Match 71.4%; Score 5; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 DB 9 PPPLP 13
 RESULT 60
 AAW38977
 ID AAW38977 standard; peptide; 18 AA.
 AC AAW38977;
 XX 14-AUG-1996 (first entry)
 DT Prolyl endopeptidase inhibitor peptide #1.
 DE Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX Synthetic.
 XX JP08059697-A.
 PN 05-MAR-1996.
 PD 09-MAR-1995; 95JP-0079661.
 XX 15-JUN-1994; 94JP-0158031.
 PR

XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX
 PT Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives
 for food and animal feed and to treat and prevent dementia
 XX
 PS Claim 1; Page 10; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
 peptides. These peptides are useful as PEP inhibitors in functional foods
 CC and in animal feeds. They are used to prepare oral and parenteral
 CC pharmaceutical preparations for the treatment and prevention of dementia
 CC of animals, including humans. The advantage with using these peptides,
 CC is that they are safe and easily absorbed.
 XX
 SQ Sequence 18 AA;
 Query Match 71.4%; Score 5; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 2 PPPLP 6
 RESULT 61
 AAR91750
 ID AAR91750 standard; peptide; 18 AA.
 AC
 XX AAR91750;
 XX
 DT 14-AUG-1996 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor peptide #5.
 XX
 CC Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;
 KW prevention; dementia; human.
 XX
 OS Synthetic.
 XX
 FN JP08059697-A.
 XX
 PD 05-MAR-1996.
 XX
 PF 09-MAR-1995; 95JP-0079661.
 XX
 PR 15-JUN-1994; 94JP-0158031.
 XX
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (NIHA-) NIPPON HAM KK.
 XX
 DR WPI; 1996-184809/19.
 XX
 PT Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives
 for food and animal feed and to treat and prevent dementia
 XX
 PS Claim 1; Page 10; 11pp; Japanese.
 XX
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory
 CC peptides. These peptides are useful as PEP inhibitors in functional foods
 CC and in animal feeds. They are used to prepare oral and parenteral
 CC pharmaceutical preparations for the treatment and prevention of dementia
 CC of animals, including humans. The advantage with using these peptides,
 CC is that they are safe and easily absorbed.
 XX
 SQ Sequence 18 AA;
 Query Match 71.4%; Score 5; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 2 PPPLP 6
 RESULT 62
 AAW39010
 ID AAW39010 standard; peptide; 18 AA.
 XX
 AC AAW39010;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:409.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 FN WO9730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US02298.
 XX
 PR 16-FEB-1996; 96US-0602999.
 XX
 PA (CVTO-) CYTOGEN CORP.
 PA (UVNC-) UNIV NORTH CAROLINA.
 XX
 FI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 FI Sparks AB, Thorn JN;
 XX
 DR WPI; 1997-424972/39.
 XX
 PT Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 PS Claim 22; Page 93; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC the SH3 domain of p53bp2; (g) peptides which bind the SH3 domain of
 CC the SH3 domain of p53bp2; (g) peptides which bind the SH3 domain of
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 SQ Sequence 18 AA;
 Query Match 71.4%; Score 5; DB 18; Length 18;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 11 PPPLP 15

```

XX AC AAW05473;
XX DT 24-FEB-1998 (first entry)
XX DE SH3-binding peptide bSH3024.
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
XX KW cellular signalling element; cellular structural element; malignancy;
XX KW protein identification; functional domain; protein screening;
XX KW cellular signal transduction process; binding peptide.
XX OS Synthetic.
XX PN W09G31625-A1.
XX PD 10-OCT-1996.
XX PF 04-APR-1996; 96WO-US04454.
XX PR 03-APR-1996; 96US-0630915.
XX PR 07-APR-1995; 95US-0417872.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
XX DR WPI; 1996-465045/46.
XX PT Identifying polypeptide(s) having specific functional domain (esp.
XX PT SH3 domain) - comprises detecting selective binding to recognition
XX PT unit, regardless of sequence homology
XX PS Example; Fig 13; 174pp; English.
XX CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
XX CC peptides. These sequences were used as parts of multivalent recognition
XX CC unit complexes used in the method of the invention. The method of the
XX CC invention is for identifying polypeptides containing functional domains
XX CC of interest (especially SH3 domains). It comprises contacting a
XX CC multivalent recognition unit (RU) complex with a number of peptides and
XX CC identifying polypeptides having a selective binding affinity for the RU
XX CC complex. The method is based on functional similarities and does not
XX CC rely on sequence similarities. Prior methods only gave limited success
XX CC for identifying proteins containing an SH3 domain due to the minimal
XX CC sequence homology among known SH3 proteins. Multivalent RU complexes are
XX CC particularly suited to screening for polypeptides containing functional
XX CC domains that are similar to, but not identical in sequence to, the
XX CC original target functional domain. The new method enables proteins
XX CC having a common function to be identified. Identification of novel SH3
XX CC proteins will be useful for a better understanding of cell growth,
XX CC malignancy, signal transduction processes, etc. New candidate drugs can
XX CC be identified, and their specificities (e.g. pharmacological activities)
XX CC can be assessed using the method of the invention.
XX SQ Sequence 19 AA;

Query Match 71.4%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 2 PPPLP 6

RESULT 65
AAW38961
ID AAW38961 standard; peptide; 20 AA.
XX AC AAW38961;
XX
```

```

XX AC AAW05473;
XX DT 24-FEB-1998 (first entry)
XX DE SH3-binding peptide bSH3024.
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
XX KW cellular signalling element; cellular structural element; malignancy;
XX KW protein identification; functional domain; protein screening;
XX KW cellular signal transduction process; binding peptide.
XX OS Synthetic.
XX PN W09G31625-A1.
XX PD 10-OCT-1996.
XX PF 04-APR-1996; 96WO-US04454.
XX PR 03-APR-1996; 96US-0630915.
XX PR 07-APR-1995; 95US-0417872.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
XX DR WPI; 1996-465045/46.
XX PT Identifying polypeptide(s) having specific functional domain (esp.
XX PT SH3 domain) - comprises detecting selective binding to recognition
XX PT unit, regardless of sequence homology
XX PS Example; Fig 13; 174pp; English.
XX CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
XX CC peptides. These sequences were used as parts of multivalent recognition
XX CC unit complexes used in the method of the invention. The method of the
XX CC invention is for identifying polypeptides containing functional domains
XX CC of interest (especially SH3 domains). It comprises contacting a
XX CC multivalent recognition unit (RU) complex with a number of peptides and
XX CC identifying polypeptides having a selective binding affinity for the RU
XX CC complex. The method is based on functional similarities and does not
XX CC rely on sequence similarities. Prior methods only gave limited success
XX CC for identifying proteins containing an SH3 domain due to the minimal
XX CC sequence homology among known SH3 proteins. Multivalent RU complexes are
XX CC particularly suited to screening for polypeptides containing functional
XX CC domains that are similar to, but not identical in sequence to, the
XX CC original target functional domain. The new method enables proteins
XX CC having a common function to be identified. Identification of novel SH3
XX CC proteins will be useful for a better understanding of cell growth,
XX CC malignancy, signal transduction processes, etc. New candidate drugs can
XX CC be identified, and their specificities (e.g. pharmacological activities)
XX CC can be assessed using the method of the invention.
XX SQ Sequence 19 AA;

Query Match 71.4%; Score 5; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 2 PPPLP 6

RESULT 65
AAW38961
ID AAW38961 standard; peptide; 20 AA.
XX AC AAW38961;
XX
```

DT 27-MAR-1998 (first entry)
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:358.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 XX WO9730074-A1.
 XX
 XX 21-AUG-1997.
 XX
 XX 14-FEB-1997; 97WO-US02298.
 XX
 XX 16-FEB-1996; 96US-0602999.
 XX
 XX (CYTO-) CYTOGEN CORP.
 XX (UNNC-) UNIV NORTH CAROLINA.
 PA
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 XX Sparks AB, Thorn JM;
 XX
 XX WPI; 1997-424972/39.
 XX
 XX Src homology region 3 binding peptide - used to activate Src
 PT tyrosine kinase(s) and to stimulate immune response by increasing
 PT production of certain lymphokine(s), e.g. interleukin-1
 XX
 XX Claim 22; Page 91; 131pp; English.
 XX
 CC The present sequence represents a peptide which resembles a Src homology
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
 CC binding peptides can be used in the method to identify inhibitors of
 CC their binding to their respective SH3 domains, which could be used to
 CC modulate the pharmacological activity of proteins or polypeptide
 CC containing the SH3 domain. The peptides can also be used to activate
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune
 CC response by increasing the production of certain lymphokines, e.g.
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
 CC conjugated molecule to certain cellular compartments containing Src or
 CC Src related proteins.
 XX
 XX SQ Sequence 20 AA;
 Query Match 71.4%; Score 5; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 12 PPPLP 16
 RESULT 66
 AAB39138
 ID AAB39138 standard; Protein; 20 AA.
 XX
 AC AAB39138;
 XX
 XX 02-FEB-2001 (first entry)
 DT
 XX Human secreted protein #46.
 DE
 XX Cytosolic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200058513-A1.
 XX
 XX 05-OCT-2000.
 XX
 XX 22-MAR-2000; 2000WO-US07506.
 XX
 XX 26-MAR-1999; 99US-0126505.
 XX
 XX 17-DEC-1999; 99US-0172412.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.
 XX
 XX Rosen CA, Ruben SM, Komatsoulis G;
 XX
 XX WPI; 2000-594649/56.
 XX N-Psdb; AAC73910.
 XX
 XX Forty-nine polynucleotide sequences, and their encoded secreted
 PT polypeptides, used in the treatment and diagnosis of cancers,
 PT autoimmune disorders, and skin disorders -
 XX
 XX Claim 11; Page 385; 413pp; English.
 XX
 CC Sequences AAB39093-B39141 represent the amino acid sequences of 49
 CC human secreted proteins encoded by the genes AAC73865-C73913. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and antagonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 XX
 XX SQ Sequence 20 AA;
 Query Match 71.4%; Score 5; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPLP 7
 Db 13 PPPLP 17
 RESULT 67
 AAW65841
 ID AAW65841 standard; peptide; 5 AA.
 XX
 AC AAW65841;
 XX
 XX 19-OCT-1998 (first entry)
 DT
 XX Peptide #66 from pentapeptide combinatorial library #3.
 DE
 XX polypoly1; cyclophilin; inhibitor; neurotrophic compound; ppi;
 KW piptidy-prolyl isomerase; rotamase; immunophilin protein; degeneration;
 KW neuronal damage; combinatorial library.
 XX
 OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Misc-difference 5 /note= "equimolar mixtures of 18 amino acids (all
FT naturally occurring amino acids except tryptophan and
FT cysteine), C-terminal amide"
XX WO9825950-A1.
XX 18-JUN-1998.
XX 08-DEC-1997; 97WO-US23102.
XX 09-DEC-1996; 96US-0761902.
XX (GUIL-) GUILFORD PHARM INC.
XX Hamilton GS, Steiner JP, Wei L;
XX WPI; 1998-348444/30.
XX Effecting neuronal activity in mammals - by administering tetra-
XX and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
XX useful in treatment of neuronal damage or degeneration disorders
XX Example 2; Page 31; 70pp; English.
XX The invention relates to neurotrophic low molecular weight, small
XX molecule peptidic cyclophilin inhibitor compounds having an affinity for
XX cyclophilin-type immunophilins, and their use as inhibitors of the
XX enzyme activity associated with immunophilin proteins, particularly
XX peptidyl-prolyl isomerase, or rotamase, enzyme activity. Tetrapeptide
XX and pentapeptide combinatorial libraries were used to map the substrate
XX specificity of the enzyme cyclophilin. Pools of tetrapeptide and
XX pentapeptide substrates were generated and their potencies in binding to
XX cyclophilin A were evaluated by examining the inhibition of peptidyl-
XX prolyl isomerase activity. Positional scanning technique was used to
XX determine the optimal amino acid(s) for each position of the tetra- or
XX penta-peptide. The present sequence represents one of the peptide pools
XX used.
SQ Sequence 5 AA;
Query Match 57.1%; Score 4; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PPLP 7
Db 1 PPLP 4
RESULT 68
AAG63123
ID AAG63123 standard; Protein; 5 AA.
XX AAG63123;
AC AAG63123;
XX 01-OCT-2001 (first entry)
DE Amino acid sequence of a human adenovirus 5 Elb 8.3 kDa protein.
XX
XX Adenovirus protein; Ad; complementing cell line; Ad vector;
XX replication-incompetent Ad vector; E1-deleted virus;
XX transgene expression; Ads.
XX Human adenovirus type 5.
OS
XX WO200144280-A2.
PN 21-JUN-2001.
PD

XX 07-DEC-2000; 2000WO-US33123.
XX 14-DEC-1999; 99US-0170550.
PR 11-APR-2000; 2000US-0196266.
XX (GENO-) GENOVO INC.
XX Himes VB, Rasty S, Peluso RW;
XX WPI; 2001-475764/51.
DR N-PSDB; AAH42482.
XX New nucleic acids for creating complementing cell lines that enable
XX production of high titer adenovirus vectors, comprises a sequence of a
XX polynucleotide which is not a naturally-occurring adenoviral nucleotide
XX sequence -
XX Example 1; Page 96; 104pp; English.
PS The specification describes a nucleic acid molecule, comprising a
XX polynucleotide encoding 5 contiguous amino acids of a naturally-occurring
XX adenovirus (Ad) polypeptide, where the polynucleotide is not a
XX naturally-occurring adenoviral nucleotide sequence and is useful for
XX creating complementing cell lines that enable the efficient production
XX of high titer Ad vectors. The nucleic acid molecule is useful for
XX creating Ad-complementary cell lines which are useful for high yield
XX production of recombinant replication-incompetent Ad vectors, in the
XX absence of detectable replication competent Ad. The adenoviruses
XX free of contamination with RCA are suitable for preclinical and
XX clinical use. E1-deleted viruses are suitable for applications in which
XX transient transgene expression is therapeutic (e.g. p53 gene transfer
XX in cancer, beta-interferon gene transfer in cancer, platelet derived
XX growth factor (PDGF) gene transfer in wound healing, and vascular
XX endothelial growth factor (VEGF) gene transfer in vascular diseases of
XX the heart and limbs). The present sequence encodes a human Ads Elb 8.3
XX kDa protein. It is used to construct an E1 complementation element, for
XX use in the course of the invention.
SQ Sequence 5 AA;
Query Match 57.1%; Score 4; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QPPP 5
Db 1 QPPP 4
RESULT 69
AAY67449
ID AAY67449 standard; peptide; 6 AA.
XX AAY67449;
AC AAY67449;
XX 12-MAY-2000 (first entry)
DT
XX SH3 domain binding proline-rich np70 peptide fragment #7.
DE SH3; np70; src homology 3; nuclear localisation; anticancer;
XX anti-proliferative; anti-inflammatory.
KW Homo sapiens.
XX GB2341182-A.
PN 08-MAR-2000.
PD 01-SEP-1998; 98GB-0019038.
PF 01-SEP-1998; 98GB-0019038.
XX 01-SEP-1998; 98GB-0019038.
PR
XX

PA (YAMA) YAMANOUCHI UK LTD.
 XX Kellie S, Finan P;
 XX WPI; 2000-163495/15.
 XX Src homology 3 protein or fragment for preventing or treating
 PT proliferative disease, such as cancer or chronic inflammatory disease,
 PT comprises src homology 3 domain binding activity and nuclear
 PT localization activity -
 XX
 XX Claim 1; Page 34; 52pp; English.
 PS
 XX The invention provides a novel protein (np70) that has src homology 3
 CC (SH3) domain binding activity and nuclear localization activity. The
 CC proline-rich SH3 binding protein np70 or its fragments are useful for
 CC the prevention or treatment of proliferative disease, such as cancer and
 CC chronic inflammatory disease. Sequences AAY67443-464 represent peptide
 CC fragments of np70 that have SH3 domain binding activity.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 57.1%; Score 4; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PPPL 6
 DB ||||
 1 PPPL 4

RESULT 70
 AAR53972
 ID AAR53972 standard; peptide; 7 AA.
 XX
 AC AAR53972;
 XX
 DT 11-JAN-1995 (first entry)
 XX
 DE Neuropeptide (1).
 XX
 XX Neuropeptide; neurotransmitter; muscle; mussel; Mytilus edulis;
 KW constriction; anterior byssus retractor muscle; ABRM.
 XX
 XX Helix pomatia.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "pyroglutamic acid"
 FT Modified-site 7 /note= "C-terminal is amidated"
 FT
 XX JP06107683-A.
 PN
 XX 19-APR-1994.
 PD
 XX 30-SEP-1992; 92JP-0300245.
 PP
 XX 30-SEP-1992; 92JP-0300245.
 PR
 XX (SUNR) SUNTORY LTD.
 PA
 XX WPI; 1994-163936/20.
 DR
 XX Neuro-peptide(s) isolated from Helix pomatia - useful in studying
 PT neuro-transmitting systems
 XX
 PS Claim 1; Page 2; 10pp; Japanese.
 XX The peptide inhibits strong constriction of the anterior byssus
 CC retractor muscle (ABRM) of Mytilus edulis induced by electrical
 CC irritation and is useful as biochemical reagent in the study of

CC the neurotransmitting system.
 XX Sequence 7 AA;
 SQ
 Query Match 57.1%; Score 4; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPLP 7
 DB ||||
 2 PPLP 5

RESULT 71
 AAW11128
 ID AAW11128 standard; peptide; 7 AA.
 XX
 AC AAW11128;
 XX
 DT 27-JUN-1997 (first entry)
 XX
 XX Src SH3 domain-binding peptide preferred core sequence.
 DE
 XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.
 XX
 OS Synthetic.
 XX WO9603649-A1.
 PN
 XX 08-FEB-1996.
 PD
 XX 24-JUL-1995; 95WO-US09382.
 PF
 XX 07-JUN-1995; 95US-0483555.
 PR
 XX 22-JUL-1994; 94US-0278865.
 PR
 XX (UYNC-) UNIV NORTH CAROLINA.
 PA
 XX Der CU, Kay BK, Quilliam LA, Sparks AB, Thorn JM;
 PT WPI; 1996-117151/12.
 DR
 XX Peptide with binding affinity for Src homology region 3 (SH3)
 PT domains of proteins - useful for e.g. modulating signal transduction
 PT pathways at the cellular level, esp. protein tyrosine
 PT kinase-mediated
 XX
 PS Disclosure; Page 62; 116pp; English.
 XX
 CC AAW11128 represents a preferred core sequence of a set of peptides
 CC that bind to the Src SH3 domain. The SH3 binding peptides are useful in
 CC modulating signal transduction pathways at the cellular level
 CC (especially protein tyrosine kinase-mediated), modulating oncogenic
 CC protein activity, or providing compounds for the development of drugs
 CC with the ability to modulate broad classes, as well as specific classes,
 CC of proteins involved in signal transduction and also for regulating the
 CC processing, trafficking or translation of RNA. Conjugates of the peptides
 CC with detectable labels or imaging agents are useful for imaging cells,
 CC tissues and organs in which Src or Src-related proteins are expressed.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 57.1%; Score 4; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PPLP 7
 DB ||||
 4 PPLP 7


```
XX 13-AUG-1998.
XX
XX PF 06-FEB-1998; 98WO-US02440.
XX
XX PR 16-SEP-1997; 97US-0059049.
XX PR 06-FEB-1997; 97US-0036919.
XX
XX (NOVA-) NOVALON PHARM CORP.
XX PA (UNYC-) UNIV NORTH CAROLINA.
XX
XX Fowlkes DM, Thorp HH;
XX
XX WPI; 1998-467163/40.
XX
XX Apparatus for electrochemically detecting binding - for use in
XX PT biochemical analyses, drug development and protein purification
XX PT assays
XX
XX Example 6; Page 55; 104pp; English.
XX
XX The invention relates to a method and apparatus for performing an
XX CC electrochemical assay for detecting specific binding between members
XX CC of a biological binding pair. The apparatus detects specific binding
XX CC between a first member immobilised on an electrode and a second member
XX CC which is biologically labelled, in the presence of an electrochemical
XX CC mediator. The method may be used for performing binding and competitive
XX CC binding assays. It may be used in performing high throughput screening
XX CC assays for detecting inhibition of specific binding between the members
XX CC of the binding pair for use in drug development, biochemical analyses
XX CC and protein purification assays.
XX CC The present sequence is an example of a peptide which is used in labelled
XX CC form as a second binding member in the above assay. The peptide acts as a
XX CC surrogate ligand for the the first member. Specifically, the peptide
XX CC is a proline-rich peptide which binds with Src SH3 domain.
XX
XX Sequence 7 AA;
SQ
Query Match 57.1%; Score 4; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PPLP 7
Db ||||
4 PPLP 7
RESULT 75
AA0422
ID AAY04422 standard; peptide; 7 AA.
XX
XX AC AAY04422;
XX
XX DT 25-JUN-1999 (first entry)
XX
XX DE Interleukin 6 binding peptide #17.
XX
XX KW Interleukin 6; IL-6; medicine; inhibition; interleukin 6 receptor;
XX KW IL-6R; gp130 protein; stimulation; phase.
XX
XX OS Synthetic.
XX
XX FN JP11092498-A.
XX
XX PD 06-APR-1999.
XX
XX PF 22-SEP-1997; 97JP-0256604.
XX
XX PR 22-SEP-1997; 97JP-0256604.
XX
XX PA (TOYJ ) TOSOH CORP.
XX
XX WP; 1999-283566/24.
```

```
XX Peptides specifically bind with IL-6 - useful for development of
XX PT medicines with IL-6 inhibitory activity
XX
XX Example 3; Page 4; 5pp; Japanese.
XX
XX The present sequence represents a peptide which specifically binds and
XX CC stimulates interleukin 6 (IL-6). The peptide was isolated with a phage
XX CC display method. The peptide can be useful for development of medicines
XX CC with IL-6 inhibitory activity and elucidation of binding form of IL-6,
XX CC IL-6R and gp130 protein.
XX
XX Sequence 7 AA;
SQ
Query Match 57.1%; Score 4; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PPLP 7
Db ||||
3 PPLP 6
Search completed: November 25, 2003, 18:15:37
Job time : 24.6755 secs
```

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 13.9255 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MPPPLP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*

17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 7 | 100.0 | 7 | 15 | US-10-281-652-1 |
| 2 | 5 | 71.4 | 9 | 9 | US-09-835-232-11 |
| 3 | 5 | 71.4 | 9 | 12 | US-10-308-485-11 |
| 4 | 5 | 71.4 | 10 | 12 | US-10-161-791-278 |
| 5 | 5 | 71.4 | 10 | 15 | US-10-185-050-141 |
| 6 | 5 | 71.4 | 10 | 15 | US-10-185-050-178 |
| 7 | 5 | 71.4 | 11 | 9 | US-09-835-232-8 |
| 8 | 5 | 71.4 | 11 | 9 | US-09-835-232-9 |
| 9 | 5 | 71.4 | 11 | 12 | US-10-308-485-8 |
| 10 | 5 | 71.4 | 11 | 12 | US-10-308-485-9 |
| 11 | 5 | 71.4 | 12 | 11 | US-09-845-612B-9 |
| 12 | 5 | 71.4 | 12 | 12 | US-10-161-791-251 |
| 13 | 5 | 71.4 | 12 | 12 | US-10-161-791-266 |
| 14 | 5 | 71.4 | 12 | 12 | US-10-161-791-267 |
| 15 | 5 | 71.4 | 13 | 11 | US-09-945-917-13 |

| | | | | | | |
|----|---|------|----|----|---------------------|--------------------|
| 16 | 5 | 71.4 | 13 | 11 | US-09-945-917-19 | Sequence 19, Appl |
| 17 | 5 | 71.4 | 13 | 11 | US-09-945-917-21 | Sequence 21, Appl |
| 18 | 5 | 71.4 | 13 | 12 | US-09-845-917A-13 | Sequence 13, Appl |
| 19 | 5 | 71.4 | 13 | 12 | US-09-845-917A-19 | Sequence 19, Appl |
| 20 | 5 | 71.4 | 13 | 12 | US-09-845-917A-21 | Sequence 21, Appl |
| 21 | 5 | 71.4 | 13 | 15 | US-10-067-668-11 | Sequence 11, Appl |
| 22 | 5 | 71.4 | 13 | 15 | US-10-175-696-11 | Sequence 11, Appl |
| 23 | 5 | 71.4 | 14 | 9 | US-09-879-957-186 | Sequence 186, App |
| 24 | 5 | 71.4 | 14 | 15 | US-10-185-050-63 | Sequence 63, Appl |
| 25 | 5 | 71.4 | 14 | 15 | US-10-148-936-3 | Sequence 3, Appl |
| 26 | 5 | 71.4 | 15 | 12 | US-10-161-791-356 | Sequence 356, App |
| 27 | 5 | 71.4 | 15 | 12 | US-10-161-791-385 | Sequence 385, App |
| 28 | 5 | 71.4 | 15 | 12 | US-10-161-791-404 | Sequence 404, App |
| 29 | 5 | 71.4 | 15 | 12 | US-10-161-791-414 | Sequence 414, App |
| 30 | 5 | 71.4 | 15 | 12 | US-10-161-791-435 | Sequence 435, App |
| 31 | 5 | 71.4 | 15 | 12 | US-10-161-791-441 | Sequence 441, App |
| 32 | 5 | 71.4 | 15 | 12 | US-10-161-791-452 | Sequence 452, App |
| 33 | 5 | 71.4 | 16 | 12 | US-10-161-791-197 | Sequence 197, App |
| 34 | 5 | 71.4 | 17 | 12 | US-10-161-791-360 | Sequence 360, App |
| 35 | 5 | 71.4 | 17 | 12 | US-10-161-791-374 | Sequence 374, App |
| 36 | 5 | 71.4 | 18 | 12 | US-10-161-791-320 | Sequence 320, App |
| 37 | 5 | 71.4 | 18 | 12 | US-10-161-791-409 | Sequence 409, App |
| 38 | 5 | 71.4 | 19 | 9 | US-09-879-957-169 | Sequence 169, App |
| 39 | 5 | 71.4 | 20 | 12 | US-10-161-791-358 | Sequence 358, App |
| 40 | 4 | 57.1 | 4 | 12 | US-10-181-804A-15 | Sequence 15, Appl |
| 41 | 4 | 57.1 | 4 | 15 | US-10-192-985-3 | Sequence 3, Appl |
| 42 | 4 | 57.1 | 4 | 15 | US-10-028-075B-81 | Sequence 81, Appl |
| 43 | 4 | 57.1 | 4 | 15 | US-10-029-206A-81 | Sequence 81, Appl |
| 44 | 4 | 57.1 | 6 | 14 | US-10-092-219-11 | Sequence 11, Appl |
| 45 | 4 | 57.1 | 6 | 15 | US-10-029-115-14 | Sequence 14, Appl |
| 46 | 4 | 57.1 | 6 | 15 | US-10-028-075B-135 | Sequence 135, Appl |
| 47 | 4 | 57.1 | 6 | 15 | US-10-029-206A-135 | Sequence 135, App |
| 48 | 4 | 57.1 | 7 | 9 | US-09-019-679-4 | Sequence 4, Appl |
| 49 | 4 | 57.1 | 7 | 9 | US-09-879-957-45 | Sequence 45, Appl |
| 50 | 4 | 57.1 | 7 | 9 | US-09-731-242A-17 | Sequence 17, Appl |
| 51 | 4 | 57.1 | 7 | 9 | US-09-731-242A-19 | Sequence 19, Appl |
| 52 | 4 | 57.1 | 7 | 9 | US-09-731-242A-20 | Sequence 20, Appl |
| 53 | 4 | 57.1 | 7 | 9 | US-09-938-315-9 | Sequence 9, Appl |
| 54 | 4 | 57.1 | 7 | 12 | US-10-161-791-9 | Sequence 9, Appl |
| 55 | 4 | 57.1 | 7 | 15 | US-10-028-075B-136 | Sequence 136, App |
| 56 | 4 | 57.1 | 7 | 15 | US-10-028-075B-137 | Sequence 137, App |
| 57 | 4 | 57.1 | 7 | 15 | US-10-029-206A-136 | Sequence 136, App |
| 58 | 4 | 57.1 | 7 | 15 | US-10-029-206A-137 | Sequence 137, App |
| 59 | 4 | 57.1 | 8 | 7 | US-08-344-824-113 | Sequence 113, App |
| 60 | 4 | 57.1 | 8 | 7 | US-08-344-824-329 | Sequence 329, App |
| 61 | 4 | 57.1 | 8 | 12 | US-10-224-999A-2749 | Sequence 2749, Ap |
| 62 | 4 | 57.1 | 8 | 12 | US-10-224-999A-2750 | Sequence 2750, Ap |
| 63 | 4 | 57.1 | 8 | 15 | US-10-028-075B-138 | Sequence 138, App |
| 64 | 4 | 57.1 | 8 | 15 | US-10-029-206A-138 | Sequence 138, App |
| 65 | 4 | 57.1 | 9 | 7 | US-08-344-824-212 | Sequence 212, App |
| 66 | 4 | 57.1 | 9 | 9 | US-09-938-315-8 | Sequence 8, Appl |
| 67 | 4 | 57.1 | 9 | 9 | US-09-938-315-11 | Sequence 11, Appl |
| 68 | 4 | 57.1 | 9 | 11 | US-09-945-917-34 | Sequence 34, Appl |
| 69 | 4 | 57.1 | 9 | 12 | US-09-932-165-51 | Sequence 51, Appl |
| 70 | 4 | 57.1 | 9 | 12 | US-09-932-165-66 | Sequence 66, Appl |
| 71 | 4 | 57.1 | 9 | 12 | US-09-932-165-669 | Sequence 669, App |
| 72 | 4 | 57.1 | 9 | 12 | US-09-932-165-1013 | Sequence 1013, Ap |
| 73 | 4 | 57.1 | 9 | 12 | US-09-932-165-1032 | Sequence 1032, Ap |
| 74 | 4 | 57.1 | 9 | 12 | US-09-932-165-1050 | Sequence 1050, Ap |
| 75 | 4 | 57.1 | 9 | 12 | US-09-932-165-1212 | Sequence 1212, Ap |
| 76 | 4 | 57.1 | 9 | 12 | US-09-932-165-1222 | Sequence 1222, Ap |
| 77 | 4 | 57.1 | 9 | 12 | US-09-845-917A-34 | Sequence 34, Appl |
| 78 | 4 | 57.1 | 9 | 12 | US-10-210-148-36 | Sequence 36, Appl |
| 79 | 4 | 57.1 | 9 | 12 | US-10-224-999A-2754 | Sequence 2754, Ap |
| 80 | 4 | 57.1 | 9 | 12 | US-10-224-999A-2755 | Sequence 2755, Ap |
| 81 | 4 | 57.1 | 9 | 12 | US-10-224-999A-2756 | Sequence 2756, Ap |
| 82 | 4 | 57.1 | 9 | 12 | US-10-161-791-8 | Sequence 8, Appl |
| 83 | 4 | 57.1 | 9 | 12 | US-10-161-791-11 | Sequence 11, Appl |
| 84 | 4 | 57.1 | 10 | 12 | US-09-932-165-152 | Sequence 152, App |
| 85 | 4 | 57.1 | 10 | 12 | US-09-932-165-568 | Sequence 568, App |
| 86 | 4 | 57.1 | 10 | 12 | US-09-932-165-1101 | Sequence 1101, Ap |
| 87 | 4 | 57.1 | 10 | 12 | US-09-932-165-1107 | Sequence 1107, Ap |
| 88 | 4 | 57.1 | 10 | 12 | US-09-932-165-1121 | Sequence 1121, Ap |

89 4 57.1 10 12 US-09-932-165-1309
90 4 57.1 10 12 US-09-932-165-1313
91 4 57.1 10 12 US-09-932-165-1343
92 4 57.1 10 12 US-09-932-165-1398
93 4 57.1 10 12 US-10-192-381-60
94 4 57.1 10 12 US-10-192-381-61
95 4 57.1 10 12 US-10-224-999A-2760
96 4 57.1 10 12 US-10-224-999A-2761
97 4 57.1 10 12 US-10-224-999A-2762
98 4 57.1 10 12 US-10-224-999A-2763
99 4 57.1 10 12 US-10-200-708-126
100 4 57.1 10 12 US-10-200-708-232

ALIGNMENTS

RESULT 1
US-10-281-652-1
; Sequence 1, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-1

Query Match 100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 |||||
DB 1 MQPPPLP 7

RESULT 2
US-09-835-232-11
; Sequence 11, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-835-232-11
Query Match 71.4%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
DB 4 PPPLP 8

RESULT 3
US-10-308-485-11
; Sequence 11, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-308-485-11

Query Match 71.4%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
DB 4 PPPLP 8

RESULT 4
US-10-161-791-278
; Sequence 278, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-278
```

```
Query Match 71.4%; Score 5; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 PPPLP 7
Db 2 PPPLP 6
```

```
RESULT 5
US-10-185-050-141
; Sequence 141, Application US/10185050
; Publication No. US2003007577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-185-050-141
Query Match 71.4%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 5 PPPLP 9
RESULT 6
US-10-185-050-178
; Sequence 178, Application US/10185050
; Publication No. US2003007577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-185-050-178
Query Match 71.4%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 PPPLP 7
Db 5 PPPLP 9
RESULT 7
```

US-09-835-232-8
 ; Sequence 8, Application US/09835232
 ; Patent No. US20020098489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 00383/052002 AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/09/835,232
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa=Met or Val
 US-09-835-232-8

Query Match 71.4%; Score 5; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 8
 US-09-835-232-9
 ; Sequence 9, Application US/09835232
 ; Patent No. US20020098489A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 00383/052002 AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/09/835,232
 ; CURRENT FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-835-232-9

Query Match 71.4%; Score 5; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 9
 US-10-308-485-8
 ; Sequence 8, Application US/10308485
 ; Publication No. US20030170683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 00383/052002
 ; CURRENT APPLICATION NUMBER: US/10/308,485
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/835,232
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa=Met or Val
 US-10-308-485-8

Query Match 71.4%; Score 5; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 10
 US-10-308-485-9
 ; Sequence 9, Application US/10308485
 ; Publication No. US20030170683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leder, Philip
 ; APPLICANT: Leder, Benjamin
 ; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 00383/052002 AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/308,485
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/835,232
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: US 60/196,811
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-308-485-9

Query Match 71.4%; Score 5; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 |||||
 Db 7 PPPLP 11

RESULT 11
 US-09-845-612B-9
 ; Sequence 9, Application US/09845612B
 ; Publication No. US20030083261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, HONGTAO
 ; APPLICANT: TANG, ZHANYUN
 ; APPLICANT: LUO, XUELIAN
 ; APPLICANT: RIZO-REV, JOSE
 ; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MI
 ; TITLE OF INVENTION: POINT PROTEIN MAD2

FILE REFERENCE: UTSD:795
CURRENT APPLICATION NUMBER: US/09/845,612B
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1)..(12)
OTHER INFORMATION: synthetic peptide
US-09-845-612B-9

Query Match 71.4%; Score 5; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 6 QPPPL 10

RESULT 12

US-10-161-791-251
; Sequence 251, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-251

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 6 PPPLP 10

RESULT 13

US-10-161-791-266
; Sequence 266, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 266:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-266

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 4 QPPPL 8

RESULT 14

US-10-161-791-267
; Sequence 267, Application US/10161791
; Publication No. US20030186863A1

GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-267

Query Match 71.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 15
US-09-945-917-13
; Sequence 13, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-21

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-13

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9

RESULT 16
US-09-945-917-19
; Sequence 19, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-19

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 6 PPPLP 10

RESULT 17
US-09-945-917-21
; Sequence 21, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-21

Query Match 71.4%; Score 5; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 5 PPPLP 9


```

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-21

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 21
US-10-067-668-11
; Sequence 11, Application US/10067668
; Publication No. US2003002334A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-136001
; CURRENT APPLICATION NUMBER: US/10/067,668
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-10-067-668-11

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 22
US-10-175-696-11
; Sequence 11, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720

```

```

; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-13

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 19
US-09-845-917A-19
; Sequence 19, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-19

Query Match          71.4%; Score 5; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 20
US-09-845-917A-21
; Sequence 21, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND

```

; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-03-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-175-696-11

Query Match 71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 23

US-09-879-957-186
; Sequence 186, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-879-957-186

Query Match 71.4%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 24

US-10-185-050-63
; Sequence 63, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-185-050-63

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 25
US-10-148-936-3
; Sequence 3, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: GB 9928674.2
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligomer
US-10-148-936-3

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 26
US-10-161-791-356
; Sequence 356, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-356

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 27
US-10-161-791-385
; Sequence 385, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
```

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-385

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 28

US-10-161-791-404
; Sequence 404, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-404

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 29

US-10-161-791-414
; Sequence 414, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-414

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 4 PPPLP 8

RESULT 30

US-10-161-791-435
; Sequence 435, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 435:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-435

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 31
US-10-161-791-441
Sequence 441, Application US/10161791
Publication No. US2003018683A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-441

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

RESULT 32
US-10-161-791-452
Sequence 452, Application US/10161791
Publication No. US2003018683A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 452:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-452

Query Match 71.4%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||

Db 7 PPPLP 11
|||||

RESULT 33

US-10-161-791-197
; Sequence 197, Application US/10161791
; Publication No. US20030186863A1

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-197

Query Match 71.4%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||

Db 9 PPPLP 13
|||||

RESULT 34

US-10-161-791-360
; Sequence 360, Application US/10161791
; Publication No. US20030186863A1

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-360

Query Match 71.4%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||

Db 9 PPPLP 13
|||||

RESULT 35

US-10-161-791-374
; Sequence 374, Application US/10161791
; Publication No. US20030186863A1

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-374

Query Match 71.4% Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
Db 9 PPLP 13

RESULT 36
US-10-161-791-320
; Sequence 320, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-374
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-320

Query Match 71.4% Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLP 7
Db 10 PPLP 14

RESULT 37
US-10-161-791-409
; Sequence 409, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-409

Query Match 71.4%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 11 PPPLP 15

RESULT 38
US-09-879-957-169
; Sequence 169, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-09-879-957-169

Query Match 71.4%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
```

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 2 PPPLP 6

RESULT 39
US-10-161-791-358
; Sequence 358, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-358

Query Match 71.4%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
DB 12 PPPLP 16

RESULT 40
US-10-181-804A-15
; Sequence 15, Application US/10181804A
; Publication No. US20030162220A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, HARUO
; APPLICANT: KIM, EUI HO
```



```

; TITLE OF INVENTION: WT1 INTERACTING PROTEIN WTIP
; FILE REFERENCE: 053466/0335
; CURRENT APPLICATION NUMBER: US/10/181,804A
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: PCT/JP01/00461
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: JP 2000-14949
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: motif
US-10-181-804A-15

Query Match          57.1%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 41
US-10-192-985-3
; Sequence 3, Application US/10192985
; Publication No. US20030084483A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Gordon G
; APPLICANT: Dean, Caroline
; APPLICANT: Dijkwel, Paul
; TITLE OF INVENTION: Methods and Means for Modification of Plant
; TITLE OF INVENTION: Characteristics
; FILE REFERENCE: 0380-P02932US0
; CURRENT APPLICATION NUMBER: US/10/192,985
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: GB 0117054.7
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-10-192-985-3

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 42
US-10-028-075B-81
; Sequence 81, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5233US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21

```

```

; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1RLQ/1RLQ-R; swissnew/P01229/LSHB HUMAN
US-10-028-075B-81

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 43
US-10-029-206A-81
; Sequence 81, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5232US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1RLQ/1RLQ-R; swissnew/P01229/LSHB HUMAN
US-10-029-206A-81

Query Match          57.1%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 44
US-10-092-219-11
; Sequence 11, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

```



```

RESULT 49
US-09-879-957-45
; Sequence 45, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-879-957-45

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
   ||||
Db 4 PPLP 7

RESULT 50
US-09-731-242A-17
; Sequence 17, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
   ||||
Db 4 PPLP 7

RESULT 51
US-09-731-242A-19
; Sequence 19, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-19

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
   ||||
Db 3 PPPL 6

RESULT 52
US-09-731-242A-20
; Sequence 20, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06

```

;; CURRENT FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: US 60/169,179
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: US 09/009,388
;; PRIOR FILING DATE: 1998-01-20
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 20
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: ARTIFICIAL SEQUENCE
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1..7)
;; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-20

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Mismatches 0; Indels 0;
Matches 4; Conservative 0; Gaps 0;

QY 3 PPLP 6
|||
DB 3 PPLP 6

RESULT 53
US-09-938-315-9
;; Sequence 9, Application US/09938315
;; Patent No. US20020091089A1
;; GENERAL INFORMATION:
;; APPLICANT: KAY, BRIAN K.
;; SPARKS, ANDREW B.
;; THORN, JUDITH M.
;; QUILLIAM, LAWRENCE A.
;; DER, CHANNING J.
;; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
;; ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; P.C.
;; STREET: 1755 S. Jefferson Davis Highway, Suite 400
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/938,315
;; FILING DATE: 23-Aug-2001
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Villacorta, Gilberto M.
;; REGISTRATION NUMBER: 34,038
;; REFERENCE/DOCKET NUMBER: 4980-007-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 413-3000
;; TELEFAX: (703) 413-2220
;; TELEX: 248855 OPAT UR
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-938-315-9

Query Match 57.1%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Mismatches 0; Indels 0;
Matches 4; Conservative 0; Gaps 0;

QY 4 PPLP 7
|||
DB 4 PPLP 7

RESULT 54
US-10-161-791-9
;; Sequence 9, Application US/10161791
;; Publication No. US2003018663A1
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/161,791
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-10-161-791-9

Query Match 57.1%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Mismatches 0; Indels 0;
Matches 4; Conservative 0; Gaps 0;

QY 4 PPLP 7
|||
DB 4 PPLP 7

RESULT 55
US-10-028-075B-136
;; Sequence 136, Application US/10028075B
;; Publication No. US20030113733A1
;; GENERAL INFORMATION:

```
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Gene regulator
/ FILE REFERENCE: 2183-5223US
/ CURRENT APPLICATION NUMBER: US/10/028,075B
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: EP 01203748.7
/ PRIOR FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 136
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-136

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 3 PPLP 6

RESULT 56
US-10-028-075B-137
/ Sequence 137, Application US/10028075B
/ Publication No. US20030113733A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Gene regulator
/ FILE REFERENCE: 2183-5223US
/ CURRENT APPLICATION NUMBER: US/10/028,075B
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: EP 01203748.7
/ PRIOR FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-137

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 57
US-10-029-206A-136
/ Sequence 136, Application US/10029206A
/ Publication No. US20030119720A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Oligopeptide treatment of anthrax
/ FILE REFERENCE: 2183-5222US
/ CURRENT APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-136

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 58
US-10-029-206A-137
/ Sequence 137, Application US/10029206A
/ Publication No. US20030119720A1
/ GENERAL INFORMATION:
/ APPLICANT: Khan, Nisar A.
/ APPLICANT: Benner, Robert
/ TITLE OF INVENTION: Oligopeptide treatment of anthrax
/ FILE REFERENCE: 2183-5222US
/ CURRENT APPLICATION NUMBER: US/10/029,206A
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/821,380
/ PRIOR FILING DATE: 2001-03-29
/ NUMBER OF SEQ ID NOS: 175
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 137
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-137

Query Match          57.1%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 4 PPLP 7

RESULT 59
US-08-344-824-113
/ Sequence 113, Application US/08344824
/ Publication No. US20030152580A1
/ GENERAL INFORMATION:
/ APPLICANT: SETTE, Alessandro
/ APPLICANT: SIDNEY, John
/ TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
/ NUMBER OF SEQUENCES: 399
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Steuart Street Tower, 20th
/ STREET: Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-113

Query Match          57.1%; Score 4; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 1 PPLP 4

RESULT 60
US-08-344-824-329
; Sequence 329, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 329:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-329

Query Match          57.1%; Score 4; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 2 PPLP 5

RESULT 61
US-10-224-999A-2749
; Sequence 2749, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2749
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis E virus
US-10-224-999A-2749

Query Match          57.1%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 5 PPLP 8

RESULT 62
US-10-224-999A-2750
; Sequence 2750, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2750
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis E virus
US-10-224-999A-2750

Query Match          57.1%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||||
Db 4 PPLP 7

RESULT 63
US-10-028-075B-138
; Sequence 138, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-138

Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||||
Db 4 PPLP 7

RESULT 64
US-10-029-206A-138
; Sequence 138, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-138

Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||||
Db 4 PPLP 7

RESULT 65
US-08-344-824-212
; Sequence 212, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-212

Query Match 57.1%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||||
Db 2 PPLP 5

RESULT 66
US-09-938-315-8
; Sequence 8, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia

```

; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "hydrophobic residue"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-938-315-8

Query Match          57.1%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPLP 7
Db      4 PPLP 7

RESULT 67
US-09-945-917-34
; Sequence 34, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-34

Query Match          57.1%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PPLP 7
Db      3 PPLP 6

RESULT 69
US-09-932-165-51
; Sequence 51, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83p2H3 and Cat-P2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00

```


; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-51

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPL 6
| | | |
Db 4 PPPL 7

RESULT 70
US-09-932-165-66
; Sequence 66, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-66

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 3 QPPP 6

RESULT 71
US-09-932-165-669
; Sequence 669, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-669

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 3 QPPP 6

RESULT 72
US-09-932-165-1013
; Sequence 1013, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1013
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1013

Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPP 5
| | | |
Db 5 QPPP 8

```
RESULT 73
US-09-932-165-1032
; Sequence 1032, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1032
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1032

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      1 PPPL 4

RESULT 74
US-09-932-165-1050
; Sequence 1050, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1050
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1050

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      1 PPPL 4
```

```
Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPPL 6
Db      6 PPPL 9

RESULT 75
US-09-932-165-1212
; Sequence 1212, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1212

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QPPP 5
Db      1 QPPP 4

Search completed: November 25, 2003, 20:25:24
Job time : 14.9255 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 : Search time 7.63298 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-1

Perfect score: 7

Sequence: 1 MQPPPLP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCFUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 7 | 100.0 | 7 | 4 | US-09-641-801-1 |
| 2 | 5 | 71.4 | 7 | 1 | US-08-230-047-40 |
| 3 | 5 | 71.4 | 7 | 5 | PCT-US94-01840-11 |
| 4 | 5 | 71.4 | 8 | 1 | US-09-641-640-11 |
| 5 | 5 | 71.4 | 8 | 2 | US-08-612-857-8 |
| 6 | 5 | 71.4 | 10 | 1 | US-08-230-047-12 |
| 7 | 5 | 71.4 | 10 | 1 | US-08-230-047-14 |
| 8 | 5 | 71.4 | 10 | 1 | US-08-212-190A-8 |
| 9 | 5 | 71.4 | 10 | 2 | US-08-900-321-8 |
| 10 | 5 | 71.4 | 10 | 3 | US-08-348-518C-26 |
| 11 | 5 | 71.4 | 10 | 3 | US-08-476-509B-26 |
| 12 | 5 | 71.4 | 10 | 3 | US-08-899-595-8 |
| 13 | 5 | 71.4 | 10 | 3 | US-08-602-999A-278 |
| 14 | 5 | 71.4 | 10 | 4 | US-09-500-124-278 |
| 15 | 5 | 71.4 | 10 | 5 | PCT-US95-03610-8 |
| 16 | 5 | 71.4 | 11 | 1 | US-08-336-343A-25 |
| 17 | 5 | 71.4 | 11 | 3 | US-08-652-877-22 |
| 18 | 5 | 71.4 | 11 | 3 | US-08-652-877-32 |
| 19 | 5 | 71.4 | 11 | 3 | US-08-476-515A-22 |
| 20 | 5 | 71.4 | 11 | 3 | US-08-476-515A-32 |
| 21 | 5 | 71.4 | 12 | 1 | US-08-230-047-17 |
| 22 | 5 | 71.4 | 12 | 3 | US-08-602-999A-251 |
| 23 | 5 | 71.4 | 12 | 3 | US-08-602-999A-266 |
| 24 | 5 | 71.4 | 12 | 3 | US-08-602-999A-267 |
| 25 | 5 | 71.4 | 12 | 4 | US-09-500-124-251 |
| 26 | 5 | 71.4 | 12 | 4 | US-09-500-124-266 |
| 27 | 5 | 71.4 | 12 | 4 | US-09-500-124-267 |
| 28 | 5 | 71.4 | 14 | 1 | US-08-185-432-12 |
| 29 | 5 | 71.4 | 14 | 3 | US-08-630-916A-63 |
| 30 | 5 | 71.4 | 14 | 4 | US-08-630-915A-186 |
| 31 | 5 | 71.4 | 15 | 1 | US-08-185-432-10 |
| 32 | 5 | 71.4 | 15 | 2 | US-08-769-745-31 |
| 33 | 5 | 71.4 | 15 | 3 | US-08-602-999A-356 |
| 34 | 5 | 71.4 | 15 | 3 | US-08-602-999A-385 |
| 35 | 5 | 71.4 | 15 | 3 | US-08-602-999A-404 |
| 36 | 5 | 71.4 | 15 | 3 | US-08-602-999A-414 |
| 37 | 5 | 71.4 | 15 | 3 | US-08-602-999A-435 |
| 38 | 5 | 71.4 | 15 | 3 | US-08-602-999A-441 |
| 39 | 5 | 71.4 | 15 | 3 | US-08-602-999A-452 |
| 40 | 5 | 71.4 | 15 | 4 | US-09-500-124-356 |
| 41 | 5 | 71.4 | 15 | 4 | US-09-500-124-385 |
| 42 | 5 | 71.4 | 15 | 4 | US-09-500-124-404 |
| 43 | 5 | 71.4 | 15 | 4 | US-09-500-124-414 |
| 44 | 5 | 71.4 | 15 | 4 | US-09-500-124-435 |
| 45 | 5 | 71.4 | 15 | 4 | US-09-500-124-441 |
| 46 | 5 | 71.4 | 15 | 4 | US-09-500-124-452 |
| 47 | 5 | 71.4 | 16 | 1 | US-08-185-432-9 |
| 48 | 5 | 71.4 | 16 | 1 | US-08-185-432-14 |
| 49 | 5 | 71.4 | 16 | 3 | US-08-602-999A-197 |
| 50 | 5 | 71.4 | 16 | 4 | US-09-500-124-197 |
| 51 | 5 | 71.4 | 17 | 1 | US-08-330-047-10 |
| 52 | 5 | 71.4 | 17 | 3 | US-08-602-999A-360 |
| 53 | 5 | 71.4 | 17 | 3 | US-08-602-999A-374 |
| 54 | 5 | 71.4 | 17 | 4 | US-09-500-124-360 |
| 55 | 5 | 71.4 | 17 | 4 | US-09-500-124-374 |
| 56 | 5 | 71.4 | 18 | 3 | US-08-602-999A-320 |
| 57 | 5 | 71.4 | 18 | 3 | US-08-602-999A-409 |
| 58 | 5 | 71.4 | 18 | 4 | US-09-500-124-320 |
| 59 | 5 | 71.4 | 18 | 4 | US-09-500-124-409 |
| 60 | 5 | 71.4 | 19 | 4 | US-08-630-915A-169 |
| 61 | 5 | 71.4 | 20 | 3 | US-08-602-999A-358 |
| 62 | 5 | 71.4 | 20 | 4 | US-09-500-124-358 |
| 63 | 4 | 57.1 | 4 | 4 | US-09-006-428A-25 |
| 64 | 4 | 57.1 | 6 | 3 | US-09-195-868-19 |
| 65 | 4 | 57.1 | 6 | 3 | US-08-664-962B-18 |
| 66 | 4 | 57.1 | 6 | 3 | US-09-311-743-18 |
| 67 | 4 | 57.1 | 6 | 3 | US-08-743-168B-38 |
| 68 | 4 | 57.1 | 6 | 4 | US-09-355-160D-11 |
| 69 | 4 | 57.1 | 6 | 4 | US-09-119-507B-117 |
| 70 | 4 | 57.1 | 6 | 4 | US-09-645-456A-36 |
| 71 | 4 | 57.1 | 6 | 4 | US-09-425-324A-36 |
| 72 | 4 | 57.1 | 6 | 4 | US-08-081-539-113 |
| 73 | 4 | 57.1 | 7 | 1 | US-08-466-647-113 |
| 74 | 4 | 57.1 | 7 | 3 | US-08-602-999A-9 |
| 75 | 4 | 57.1 | 7 | 4 | US-08-278-865-9 |
| 76 | 4 | 57.1 | 7 | 4 | US-08-630-915A-45 |
| 77 | 4 | 57.1 | 7 | 4 | US-08-185-883-6 |
| 78 | 4 | 57.1 | 8 | 3 | US-09-203-921-6 |
| 79 | 4 | 57.1 | 8 | 3 | US-08-424-414C-8 |
| 80 | 4 | 57.1 | 8 | 3 | US-08-615-181-97 |
| 81 | 4 | 57.1 | 8 | 3 | US-08-586-234-77 |
| 82 | 4 | 57.1 | 9 | 2 | US-08-986-184-77 |
| 83 | 4 | 57.1 | 9 | 3 | US-08-602-999A-8 |
| 84 | 4 | 57.1 | 9 | 3 | US-08-652-877-21 |
| 85 | 4 | 57.1 | 9 | 3 | US-08-185-883-8 |
| 86 | 4 | 57.1 | 9 | 3 | US-08-185-883-11 |
| 87 | 4 | 57.1 | 9 | 3 | US-08-476-515A-21 |
| 88 | 4 | 57.1 | 9 | 3 | US-09-203-921-8 |
| 89 | 4 | 57.1 | 9 | 3 | US-09-203-921-10 |
| 90 | 4 | 57.1 | 9 | 3 | US-09-424-414C-10 |
| 91 | 4 | 57.1 | 9 | 3 | US-09-424-414C-13 |
| 92 | 4 | 57.1 | 9 | 4 | US-08-278-865-8 |
| 93 | 4 | 57.1 | 9 | 4 | US-08-278-865-11 |
| 94 | 4 | 57.1 | 9 | 4 | US-09-500-124-8 |
| 95 | 4 | 57.1 | 9 | 4 | US-09-500-124-11 |
| 96 | 4 | 57.1 | 9 | 4 | US-09-023-905A-19 |
| 97 | 4 | 57.1 | 9 | 4 | US-09-023-905A-20 |
| 98 | 4 | 57.1 | 9 | 4 | US-09-023-905A-38 |
| 99 | 4 | 57.1 | 9 | 4 | US-09-023-905A-38 |
| 100 | 4 | 57.1 | 9 | 4 | US-09-023-905A-38 |

Sequence 12, Appl
Sequence 63, Appl
Sequence 186, Appl
Sequence 10, Appl
Sequence 31, Appl
Sequence 356, Appl
Sequence 385, Appl
Sequence 404, Appl
Sequence 414, Appl
Sequence 435, Appl
Sequence 441, Appl
Sequence 452, Appl
Sequence 452, Appl
Sequence 385, Appl
Sequence 404, Appl
Sequence 414, Appl
Sequence 435, Appl
Sequence 441, Appl
Sequence 452, Appl
Sequence 9, Appl
Sequence 14, Appl
Sequence 137, Appl
Sequence 157, Appl
Sequence 10, Appl
Sequence 360, Appl
Sequence 374, Appl
Sequence 360, Appl
Sequence 374, Appl
Sequence 320, Appl
Sequence 409, Appl
Sequence 320, Appl
Sequence 409, Appl
Sequence 169, Appl
Sequence 358, Appl
Sequence 358, Appl
Sequence 25, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 38, Appl
Sequence 11, Appl
Sequence 117, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 113, Appl
Sequence 113, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 45, Appl
Sequence 9, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 38, Appl

ALIGNMENTS

RESULT 1
 US-09-641-803-1
 ; Sequence 1, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDGOH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; CURRENT FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; PRIOR FILING DATE: 1998-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-1

Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7
 Db 1 MQPPPLP 7

RESULT 2
 US-08-230-047-40
 ; Sequence 40, Application US/08230047
 ; Patent No. 5541109
 ; GENERAL INFORMATION:
 ; APPLICANT: Searfoss III, George H.
 ; APPLICANT: Ivashchenko, Yuri D.
 ; APPLICANT: Jays, Michael C.
 ; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.0 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/230,047
 ; FILING DATE: 19-APR-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: A1465-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3817

; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-230-047-40

Query Match 71.4%; Score 5; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 Db 1 PPPLP 5

RESULT 3
 PCT-US94-01840-11
 ; Sequence 11, Application PC/TUS9401840
 ; GENERAL INFORMATION:
 ; APPLICANT: Christopher E. Rudd
 ; APPLICANT: Prasad Kanteti
 ; APPLICANT: Lewis Cantley
 ; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
 ; TITLE OF INVENTION: LIPID KINASES
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/01840
 ; FILING DATE:
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/023,915
 ; FILING DATE: February 26, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Janis K. Fraser
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 00530/063001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: Linear
 PCT-US94-01840-11

Query Match 71.4%; Score 5; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
 Db 1 PPPLP 5

RESULT 4

US-09-641-640-8
; Sequence 8, Application US/09641640
; Patent No. RE37952
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641.640
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,857
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8
Query Match 71.4%; Score 5; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PpPLP 7
Db 1 PpPLP 5
RESULT 5
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230.047

STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,857
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93-10971
FILING DATE: 15-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00542
FILING DATE: 09-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST93044-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..8
OTHER INFORMATION: /note= "3BP1 peptide"
US-08-612-857-8
Query Match 71.4%; Score 5; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PpPLP 7
Db 1 PpPLP 5
RESULT 6
US-08-230-047-12
; Sequence 12, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230.047

/ FILING DATE: 19-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goodman, Rosanne
/ REGISTRATION NUMBER: 32,534
/ REFERENCE/DOCKET NUMBER: A1465-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (610) 454-3817
/ TELEFAX: (610) 454-3808
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-230-047-12

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 7
US-08-230-047-14
/ Sequence 14, Application US/08230047
/ Patent No. 5541109
/ GENERAL INFORMATION:
/ APPLICANT: Searfoss III, George H.
/ APPLICANT: Ivashchenko, Yuri D.
/ APPLICANT: Jaye, Michael C.
/ TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Rhone-Poulenc Rorer Inc.
/ STREET: 500 Arcoia Road, 3C43
/ CITY: Collegeville
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19426

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: System 7.1
/ SOFTWARE: Word 5.0 (PatentIn)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/230,047
/ FILING DATE: 19-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goodman, Rosanne
/ REGISTRATION NUMBER: 32,534
/ REFERENCE/DOCKET NUMBER: A1465-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (610) 454-3817
/ TELEFAX: (610) 454-3808
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-230-047-14

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

Db 6 PPPLP 10

RESULT 8
US-08-212-190A-8
/ Sequence 8, Application US/08212190A
/ Patent No. 5652223
/ GENERAL INFORMATION:
/ APPLICANT: KOHN, Elise C.
/ APPLICANT: LIOTTA, Lance A.
/ APPLICANT: KIM, Young Sook
/ TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
/ TITLE OF INVENTION: USES THEREOF
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew
/ STREET: Steuart Street Tower, One Market Plaza
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: US
/ ZIP: 94105-1493
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/212,190A
/ FILING DATE: 14-MAR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 15280-204US
/ REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-212-190A-8

Query Match 71.4%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 9
US-08-900-321-8
/ Sequence 8, Application US/08900321
/ Patent No. 5981712
/ GENERAL INFORMATION:
/ APPLICANT: Kohn, Elise C.
/ APPLICANT: Liotta, Lance A.
/ APPLICANT: Kim, Young S.
/ TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
/ TITLE OF INVENTION: Uses Thereof
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; BEST LOCAL SIMILARITY: 71.4%; Score 5; DB 2; Length 10;
; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-900-321-8

Query Match 71.4%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 10
US-08-348-518C-26
; Sequence 26, Application US/08348518C
; Patent No. 6022740
; GENERAL INFORMATION:
; APPLICANT: SUDOL, MARIUS
; APPLICANT: PEER, BORK
; APPLICANT: HENRY, CHEN
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
; TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,518C
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-101
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-348-518C-26

Query Match 71.4%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPL 6
Db 4 QPPPL 8

RESULT 11
US-08-476-509B-26
; Sequence 26, Application US/08476509B
; Patent No. 6034212
; GENERAL INFORMATION:
; APPLICANT: SUDOL, MARIUS
; APPLICANT: PEER, BORK
; APPLICANT: HENRY, CHEN
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
; TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,509B
; FILING DATE: 01-DEC-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-101 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-509B-26

Query Match 71.4%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPL 6
 Db 4 QPPPL 8

RESULT 12

US-08-899-595-8
 ; Sequence 8, Application US/08899595
 ; Patent No. 6111072
 ; GENERAL INFORMATION:
 ; APPLICANT: Narumiya, Shuh
 ; APPLICANT: Takahashi, No. 6111072uaki
 ; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
 ; TITLE OF INVENTION: ENCODING SAME
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/899,595
 ; FILING DATE: 24-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 8-242701
 ; FILING DATE: 26-AUG-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 9-90170
 ; FILING DATE: 25-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stephen A. Bent
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 049441/0112
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "G/S/A/V"
 US-08-899-595-8

Query Match 71.4%; Score 5; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLPL 7
 Db 4 PPLPL 8

RESULT 13

US-08-602-999A-278
 ; Sequence 278, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 278:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-08-602-999A-278

Query Match 71.4%; Score 5; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPLPL 7
 Db 2 PPLPL 6

RESULT 14

US-09-500-124-278
 ; Sequence 278, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 278:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-09-500-124-278

Query Match 71.4%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 2 PPPLP 6

RESULT 15
PCT-US95-03610-8
;; Sequence 8, Application PC/TUS9503610
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
;; NUMBER OF SEQUENCES: 10
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03610
;; FILING DATE: 14-MAR-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,190
;; FILING DATE: 14-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Kenneth A.
;; REGISTRATION NUMBER: 31,677
;; REFERENCE/DOCKET NUMBER: 15280-204000PC
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US95-03610-8

Query Match 71.4%; Score 5; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 5 PPPLP 9

RESULT 16
US-08-336-343A-25
;; Sequence 25, Application US/08336343A
;; Patent No. 5677144
;; GENERAL INFORMATION:
;; APPLICANT: Ullrich, Axel
;; TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/336,343A
;; FILING DATE: 08-NOV-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7693-065
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-336-343A-25

Query Match 71.4%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 17
US-08-652-877-22
;; Sequence 22, Application US/08652877
;; Patent No. 6187548
;; GENERAL INFORMATION:
;; APPLICANT: Akerstrom, Goran
;; APPLICANT: Juhlin, Claes
;; APPLICANT: Rask, Lars
;; APPLICANT: Crumley, Gregg R.
;; APPLICANT: Morse, Clarence C.
;; APPLICANT: Murray, Edward M.
;; APPLICANT: Hjalms, Goran
;; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
;; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Rd., 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.5.1
 ; SOFTWARE: Word 6.0 (Patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,877
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/15203
 ; FILING DATE: 22-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/344,836
 ; FILING DATE: 23-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,314
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Savitzky, Martin
 ; REGISTRATION NUMBER: 29,699
 ; REFERENCE/DOCKET NUMBER: A1355E-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-454-3816
 ; TELEFAX: 610-454-3808
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: internal
 ; US-08-652-877-22

Query Match 71.4%; Score 5; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred.No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 18
 US-08-652-877-32
 ; Sequence 32, Application US/08652877
 ; Patent No. 6187548
 ; GENERAL INFORMATION:
 ; APPLICANT: Akerstrom, Goran
 ; APPLICANT: Juhlin, Claes
 ; APPLICANT: Rask, Lars
 ; APPLICANT: Crumley, Gregg R.
 ; APPLICANT: Morse, Clarence C.
 ; APPLICANT: Murray, Edward M.
 ; APPLICANT: Hjaln, Goran
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
 ; TITLE OF INVENTION: Thereof and DNA Encoding Same
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Rd., 3C43
 ; CITY: Collegeville
 ; STATE: PA

; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.5.1
 ; SOFTWARE: Word 6.0 (Patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,877
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/15203
 ; FILING DATE: 22-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/344,836
 ; FILING DATE: 23-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,314
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Savitzky, Martin
 ; REGISTRATION NUMBER: 29,699
 ; REFERENCE/DOCKET NUMBER: A1355E-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-454-3816
 ; TELEFAX: 610-454-3808
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: internal
 ; US-08-652-877-32

Query Match 71.4%; Score 5; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred.No. 9.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 19
 US-08-476-515A-22
 ; Sequence 22, Application US/08476515A
 ; Patent No. 6239270
 ; GENERAL INFORMATION:
 ; APPLICANT: Akerstrom, Goran
 ; APPLICANT: Juhlin, Claes
 ; APPLICANT: Rask, Lars
 ; APPLICANT: Crumley, Gregg R.
 ; APPLICANT: Morse, Clarence C.
 ; APPLICANT: Murray, Edward M.
 ; APPLICANT: Hjaln, Goran
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
 ; TITLE OF INVENTION: Thereof and DNA Encoding Same
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Martin Savitzky
 ; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
 ; STREET: 3C43,
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Compaq PC

```

; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA: US/08/476,515A
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-22

```

```

Query Match 71.4%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 PPPLP 7
Db 4 PPPLP 8

```

```

RESULT 20
US-08-476-515A-32
; Sequence 32, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akersstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Raek, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43.
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995

```

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-32

```

```

Query Match 71.4%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 PPPLP 7
Db 4 PPPLP 8

```

```

RESULT 21
US-08-230-047-17
; Sequence 17, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashenko, Yuri D.
; APPLICANT: Jaye, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

```

```
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-17

Query Match 71.4%; Score 5; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 22
US-08-602-999A-251
; Sequence 251, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-266

Query Match 71.4%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPL 6
Db 4 QPPPL 8

RESULT 24
US-08-602-999A-267
; Sequence 267, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-267

Query Match 71.4%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 25
US-09-500-124-251
; Sequence 251, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
```

```
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-251

Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 6 PPPLP 10

RESULT 26
US-09-500-124-266
; Sequence 266, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 266:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-266
```

Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPL 6
| | | | |
Db 4 QPPL 8

RESULT 27
US-09-500-124-267
; Sequence 267, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/500,124
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/602,999
; APPLICATION NUMBER: 16-FEB-1996
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-267

Query Match 71.4%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
| | | | |
Db 6 PPPLP 10

RESULT 28
US-08-185-432-12
; Sequence 12, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:

; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/185,432
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-185-432-12

Query Match 71.4%; Score 5; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
| | | | |
Db 4 PPPLP 8

RESULT 29
US-08-630-916A-63
; Sequence 63, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

| Query Match | 71.4% | Score 5 | DB 3 | Length 14 |
|---|-----------|--------------|------|---------------------------------|
| Best Local Similarity | 100.0% | Pred. No. 11 | | |
| Matches | 5 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0; |
| QY | 3 PPPLP 7 | | | |
| Db | 5 PPPLP 9 | | | |
| <p>RESULT 31</p> <p>US-08-185-432-10</p> <p>; Sequence 10, Application US/08185432</p> <p>; Patent No. 5750652</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Artavanis-Tsakonas, Spyridon</p> <p>; APPLICANT: Busseau, Isabelle</p> <p>; APPLICANT: Diederich, Robert J.</p> <p>; APPLICANT: Xu, Tian</p> <p>; APPLICANT: Matsuno, Kenji</p> <p>; TITLE OF INVENTION: DETOX PROTEINS, NUCLEIC ACIDS, AND</p> <p>; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS</p> <p>; NUMBER OF SEQUENCES: 23</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: PENNIE & EDMONDS</p> <p>; STREET: 1155 Avenue of the Americas</p> <p>; CITY: New York</p> <p>; STATE: New York</p> <p>; COUNTRY: U.S.A.</p> <p>; ZIP: 10036-2711</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/185,432</p> <p>; FILING DATE: 21-JAN-1994</p> <p>; CLASSIFICATION: 530</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Misrock, S. Leslie</p> <p>; REGISTRATION NUMBER: 18,872</p> <p>; REFERENCE/DOCKET NUMBER: 7326-006</p> <p>; TELEPHONE: (212) 790-9090</p> <p>; TELEFAX: (212) 869-8864/9741</p> <p>; TELEX: 66141 PENNIE</p> <p>; INFORMATION FOR SEQ ID NO: 10:</p> <p>; SEQUENCE CHARACTERISTICS:</p> <p>; LENGTH: 15 amino acids</p> <p>; TYPE: amino acid</p> <p>; TOPOLOGY: unknown</p> <p>; MOLECULE TYPE: peptide</p> <p>US-08-185-432-10</p> | | | | |
| QY | 3 PPPLP 7 | | | |
| Db | 5 PPPLP 9 | | | |
| <p>RESULT 32</p> <p>US-08-769-745-31</p> <p>; Sequence 31, Application US/08769745</p> <p>; Patent No. 5955259</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Holmes, Todd C.</p> <p>; APPLICANT: Levitan, Irwin B.</p> <p>; APPLICANT: Brandeis University</p> | | | | |

| Query Match | 71.4% | Score 5 | DB 3 | Length 14 |
|--|-----------|--------------|------|---------------------------------|
| Best Local Similarity | 100.0% | Pred. No. 11 | | |
| Matches | 5 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0; |
| QY | 3 PPPLP 7 | | | |
| Db | 5 PPPLP 9 | | | |
| <p>RESULT 31</p> <p>US-08-630-915A-186</p> <p>Sequence 186, Application US/08630915A</p> <p>Patent No. 6309820</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: SPARKS, Andrew B.</p> <p>APPLICANT: HOFFMAN, No. 6309820h</p> <p>APPLICANT: KAY, Brian K.</p> <p>APPLICANT: FOWLES, Dana M.</p> <p>APPLICANT: MCCONNELL, Stephen J.</p> <p>TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL</p> <p>TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND</p> <p>TITLE OF INVENTION: USING SAME</p> <p>NUMBER OF SEQUENCES: 227</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Pennie & Edmonds LLP</p> <p>STREET: 1155 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10036-2711</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/630,915A</p> <p>FILING DATE: 03-APR-1996</p> <p>CLASSIFICATION: 536</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Misrock, S. Leslie</p> <p>REGISTRATION NUMBER: 18,872</p> <p>REFERENCE/DOCKET NUMBER: 1101-174</p> <p>TELEPHONE: (212) 790-9090</p> <p>TELEFAX: (212) 869-8864/9741</p> <p>TELEX: 66141 PENNIE</p> <p>INFORMATION FOR SEQ ID NO: 186:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 14 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: unknown</p> <p>MOLECULE TYPE: peptide</p> | | | | |
| QY | 3 PPPLP 7 | | | |
| Db | 5 PPPLP 9 | | | |
| <p>RESULT 30</p> <p>US-08-630-915A-186</p> <p>Sequence 186, Application US/08630915A</p> <p>Patent No. 6309820</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: SPARKS, Andrew B.</p> <p>APPLICANT: HOFFMAN, No. 6309820h</p> <p>APPLICANT: KAY, Brian K.</p> <p>APPLICANT: FOWLES, Dana M.</p> <p>APPLICANT: MCCONNELL, Stephen J.</p> <p>TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL</p> <p>TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND</p> <p>TITLE OF INVENTION: USING SAME</p> <p>NUMBER OF SEQUENCES: 227</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Pennie & Edmonds LLP</p> <p>STREET: 1155 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10036-2711</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/630,915A</p> <p>FILING DATE: 03-APR-1996</p> <p>CLASSIFICATION: 536</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Misrock, S. Leslie</p> <p>REGISTRATION NUMBER: 18,872</p> <p>REFERENCE/DOCKET NUMBER: 1101-174</p> <p>TELEPHONE: (212) 790-9090</p> <p>TELEFAX: (212) 869-8864/9741</p> <p>TELEX: 66141 PENNIE</p> <p>INFORMATION FOR SEQ ID NO: 186:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 14 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: unknown</p> <p>MOLECULE TYPE: peptide</p> | | | | |

; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-769-745-31

Query Match 71.4%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 33
US-08-602-999A-356
; Sequence 356, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-356

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

US-08-602-999A-356
; Sequence 356, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-356

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 34
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

US-08-602-999A-404
; Sequence 404, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.


```
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-404

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 36
US-08-602-999A-414
; Sequence 414, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435
```

```
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-414

Query Match 71.4%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 4 PPPLP 8

RESULT 37
US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-435
```

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 4 PPPLP 8

RESULT 38

US-08-602-999A-441
 ; Sequence 441, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 441:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-441

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 5 PPPLP 9

RESULT 39

US-08-602-999A-452
 ; Sequence 452, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 452:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-452

Query Match 71.4%; Score 5; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 Db 7 PPPLP 11

RESULT 40

US-09-500-124-356
 ; Sequence 356, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: KAY, Brian K.
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16-FEB-1996
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-356

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 41
US-09-500-124-385
Sequence 385, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 385:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-385

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 7 PPPLP 11

RESULT 42
US-09-500-124-404
Sequence 404, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 404:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-404

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 43

US-09-500-124-414
; Sequence 414, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-414

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 44

US-09-500-124-435
; Sequence 435, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-435

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
|||||
Db 4 PPPLP 8

RESULT 45

US-09-500-124-441
; Sequence 441, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```
;
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/500,124
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-441

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 5 PPPLP 9

RESULT 46
US-09-500-124-452
; Sequence 452, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-452

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 7 PPPLP 11

RESULT 47
US-08-185-432-9
; Sequence 9, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-185-432-9

Query Match 71.4%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 48

US-08-185-432-14
 ; Sequence 14, Application US/08185432
 ; Patent No. 5750652
 ; GENERAL INFORMATION:
 ; APPLICANT: Artavanis-Tsakonas, Spyridon
 ; APPLICANT: Busseau, Isabelle
 ; APPLICANT: Diederich, Robert J.
 ; APPLICANT: Xu, Tian
 ; APPLICANT: Matsuno, Kenji
 ; TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
 ; ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185,432
 ; FILING DATE: 21-JAN-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7326-006
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9690
 ; TELEFAX: (212) 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-185-432-14

Query Match 71.4%; Score 5; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||
 Db 6 PPPLP 10

RESULT 49

US-08-602-999A-197
 ; Sequence 197, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 197:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Peptide
 ; US-08-602-999A-197

Query Match 71.4%; Score 5; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
 |||||
 Db 9 PPPLP 13

RESULT 50

US-09-500-124-197
 ; Sequence 197, Application US/09500124
 ; Patent No. 6432920
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/500,124
 ; FILING DATE:
 ; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 197:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-09-500-124-197

Query Match 71.4%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

;; RESULT 51
;; US-08-230-047-10
;; Sequence 10, Application US/08230047
;; Patent No. 5541109
;; GENERAL INFORMATION:
;; APPLICANT: Seafross III, George H.
;; APPLICANT: Ivashchenko, Yuri D.
;; APPLICANT: Jaye, Michael C.
;; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Road, 3043
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Macintosh
;; OPERATING SYSTEM: System 7.1
;; SOFTWARE: Word 5.0 (patentin)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/230,047
;; FILING DATE: 19-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goodman, Rosanne
;; REGISTRATION NUMBER: 32,534
;; REFERENCE/DOCKET NUMBER: A1465-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610) 454-3817
;; TELEFAX: (610) 454-3808
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-230-047-10

Query Match 71.4%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 5 PPPLP 9

;; RESULT 52
;; US-08-602-999A-360
;; Sequence 360, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.
;; APPLICANT: RIDER, James E.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mirock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 360:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-602-999A-360

Query Match 71.4%; Score 5; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

;; RESULT 53
;; US-08-602-999A-374
;; Sequence 374, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILLIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-374

Query Match 71.4%; Score 5; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 3 PPPLP 7
Db 9 PPPLP 13

RESULT 54
US-09-500-124-360
Sequence 360, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-360

Query Match 71.4%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 9 PPPLP 13

RESULT 55
US-09-500-124-374
Sequence 374, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 374;
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-374

Query Match 71.4%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 9 PPPLP 13

RESULT 56
US-08-602-999A-320
; Sequence 320, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-320

Query Match 71.4%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 10 PPPLP 14

RESULT 57
US-08-602-999A-409
; Sequence 409, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-409

Query Match 71.4%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7
Db 11 PPPLP 15

RESULT 58
US-09-500-124-320
; Sequence 320, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-320
Query Match 71.4%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 3 PPPLP 7
Db 10 PPPLP 14
RESULT 59
US-09-500-124-409
Sequence 409, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 409:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-409
Query Match 71.4%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 3 PPPLP 7
Db 11 PPPLP 15
RESULT 60
US-08-630-915A-169
Sequence 169, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-630-915A-169

Query Match 71.4%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 2 PPPLP 6

RESULT 61

US-08-602-999A-358
; Sequence 358, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602.999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-358

Query Match 71.4%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 12 PPPLP 16

RESULT 62

US-09-500-124-358
; Sequence 358, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-358

Query Match 71.4%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7
Db 12 PPPLP 16

RESULT 63

US-09-006-428A-25
; Sequence 25, Application US/09006428A
; Patent No. 6444439
; GENERAL INFORMATION:
; APPLICANT: Jing Li
; APPLICANT: Kazuhisa Nishizawa
; APPLICANT: Wenqian An
; APPLICANT: Ellis L. Reinherz
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A
; TITLE OF INVENTION: cdc15-LIKE ADAPTOR PROTEIN (CD2BP1)
; FILE REFERENCE: 1062.1020-000
; CURRENT APPLICATION NUMBER: US/09/006,428A
; CURRENT FILING DATE: 1998-01-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens

```
;
; FEATURE:
; OTHER INFORMATION: polypeptide
US-09-006-428A-25

Query Match          57.1%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 64
US-09-195-868-19
; Sequence 19, Application US/09195868
; Patent No. 6090621
; GENERAL INFORMATION:
; APPLICANT: KAVANAUGH MD, MICHAEL
; APPLICANT: POT PH.D., DAVID
; APPLICANT: WILLIAMS MDPHD, LEWIS T.
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
; TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/195,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FIRESTONE, LEIGH H.
; REGISTRATION NUMBER: 36,831
; REFERENCE/DOCKET NUMBER: 1182.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-923-2707
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-195-868-19

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 3 PPLP 6

RESULT 65
US-08-664-962B-18
; Sequence 18, Application US/08664962B
; Patent No. 6218162
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
```

```
;
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MERCHANT & GOULD
; STREET: 3100 NO. 6218162west Center, 90 South Seventh Street
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: U.S.A.
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/664,962B
; APPLICATION NUMBER: US/08/664,962B
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Douglas P.
; REGISTRATION NUMBER: 30,300
; REFERENCE/DOCKET NUMBER: M&G 7933.49-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-664-962B-18

Query Match          57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
Db 1 PPLP 4

RESULT 66
US-09-311-743-18
; Sequence 18, Application US/09311743
; Patent No. 6238903
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,743
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7771-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-364-7311
```

```

, PRIOR APPLICATION NUMBER: PCT/GB98/00244
, PRIOR FILING DATE: 1998-01-27
, PRIOR APPLICATION NUMBER: 9701652.1

```

```

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11

```

```

; ORGANISM: Homo sapiens
US-09-355-160D-11

Query Match
Best Local Similarity 57.1%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 1 PPLP 4

RESULT 69
US-09-119-507B-117
; Sequence 117, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION.

```

```

1  APPLICANT: Kieliszewski, Marcia J.
2  TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
3  FILE REFERENCE: OHU-03417
4  CURRENT APPLICATION NUMBER: US/09/119,507B
5  CURRENT FILING DATE: 1998-07-20
6  NUMBER OF SEQ ID NOS: 118
7  SOFTWARE: PatentIn Ver. 2.0
8  SEQ ID NO 117
9  LENGTH: 6
10 TYPE: PRT
11 ORGANISM: Artificial Sequence
12 FEATURE:
13 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
14
15 FEATURE:
16 NAME/KEY: SITE
17 LOCATION: (2)..(5)
18 OTHER INFORMATION: The Proline at these positions is a
19 OTHER INFORMATION: hydroxyproline.
20 US-09-119-507B-117
21
22 Query Match 57.1%; Score 4; DB 4; Length 6;
23 Best Local Similarity 100.0%; Pred.No. 2.5e+05;
24 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
25
26 Qy 3 PPPL 6
27  ||||
28 3 PPPL 6
29 db

```

RESULT 70
US-09-645-456A-36

Patent No. 6562580
GENERAL INFORMATION:
APPLICANT: Fu, C. Alan

APPLICANT: FU, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS

; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,456A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US/09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-456A-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 1 PPLP 4

RESULT 71
US-09-425-324A-36
; Sequence 36, Application US/09425324A
; Patent No. 6562591
; GENERAL INFORMATION:
; APPLICANT: Fu, C. Alan
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: A-68344/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/425,324A
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-425-324A-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 1 PPLP 4

RESULT 72
US-09-645-791-36
; Sequence 36, Application US/09645791
; Patent No. 6569658
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: A-68344-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/645,791
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 09/425,324
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-645-791-36

Query Match 57.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 1 PPLP 4

RESULT 73
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESS: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-081-539-113

Query Match 57.1%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPLP 7
|||
Db 2 PPLP 5

RESULT 74
US-08-466-647-113
; Sequence 113, Application US/08466647

Patent No. 5543141
GENERAL INFORMATION:
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: ChimERIC Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,647
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,539
FILING DATE: 21-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-647-113

Query Match 57.1%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 2 PPLP 5

RESULT 75

US-08-602-999A-9
Sequence 9, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-9

Query Match 57.1%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7
Db 4 PPLP 7

Search completed: November 25, 2003, 20:15:56
Job time : 9.63298 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 15.6436 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQPLQVMMEPQGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 4 | 23.5 | 10 | 2 PQ0788 | NADH2 dehydrogenas |
| 2 | 4 | 23.5 | 14 | 2 PQ0147 | Omega-gliadine 1 a |
| 3 | 4 | 23.5 | 15 | 2 A61391 | alpha-1-antitrypsi |
| 4 | 4 | 23.5 | 15 | 2 A42413 | IG heavy chain V r |
| 5 | 4 | 23.5 | 20 | 2 D42842 | antifungal 2S stor |
| 6 | 4 | 23.5 | 20 | 2 PS0028 | flagellar motor sw |
| 7 | 4 | 23.5 | 20 | 2 F24417 | interphotoreceptor |
| 8 | 3 | 17.6 | 8 | 2 A35180 | neutral proteinase |
| 9 | 3 | 17.6 | 9 | 2 B33098 | 231K exoantigen - |
| 10 | 3 | 17.6 | 9 | 2 A41978 | calliFWRamide 1 - |
| 11 | 3 | 17.6 | 10 | 2 S33844 | alpha-2-macroglobu |
| 12 | 3 | 17.6 | 10 | 2 JQ0943 | hypothetical 1.3K |
| 13 | 3 | 17.6 | 10 | 2 A61622 | vitellogenin, 190K |
| 14 | 3 | 17.6 | 10 | 2 E86128 | hypothetical prote |
| 15 | 3 | 17.6 | 11 | 2 PC2330 | cycloinulooligosac |
| 16 | 3 | 17.6 | 11 | 2 A34662 | Achatina cardio-ex |
| 17 | 3 | 17.6 | 11 | 2 S68637 | acetylcholinestera |
| 18 | 3 | 17.6 | 12 | 2 S25485 | transcription fact |
| 19 | 3 | 17.6 | 12 | 2 S67528 | napin - rape (frag |
| 20 | 3 | 17.6 | 13 | 2 S15755 | actin 7 - soybean |
| 21 | 3 | 17.6 | 13 | 2 D39690 | neural cell adhesi |
| 22 | 3 | 17.6 | 13 | 2 S09716 | 2S albumin large c |
| 23 | 3 | 17.6 | 13 | 2 I84603 | deoxynucleotidylr |
| 24 | 3 | 17.6 | 14 | 2 A35105 | hypothetical prote |
| 25 | 3 | 17.6 | 14 | 2 S00150 | ovostatin - duck (|
| 26 | 3 | 17.6 | 14 | 2 B20872 | alpha-2-macroglobu |
| 27 | 3 | 17.6 | 14 | 2 PH1566 | cerebrin 30 - huma |
| 28 | 3 | 17.6 | 14 | 2 B61235 | fibroblast-activat |
| 29 | 3 | 17.6 | 14 | 2 PH1327 | Ig heavy chain DJ |

| | | | | | |
|-----|------|----|---|--------|---------------------|
| 30 | 17.6 | 14 | 2 | PN0666 | dystrophin-associa |
| 31 | 17.6 | 14 | 2 | PC7075 | guanylate cyclase |
| 32 | 17.6 | 15 | 2 | PA0021 | protein QA300016 - |
| 33 | 17.6 | 15 | 2 | PN0148 | omega-gliadine 3 - |
| 34 | 17.6 | 15 | 2 | A41436 | alpha-macroglobuli |
| 35 | 17.6 | 15 | 2 | PN0665 | dystrophin-associa |
| 36 | 17.6 | 15 | 2 | PH0789 | T-cell receptor al |
| 37 | 17.6 | 16 | 2 | B42324 | cytochrome P450c27 |
| 38 | 17.6 | 16 | 2 | C49048 | T-cell receptor be |
| 39 | 17.6 | 16 | 2 | PH0763 | T-cell receptor be |
| 40 | 17.6 | 16 | 2 | PH0767 | transforming prote |
| 41 | 17.6 | 16 | 2 | A46236 | hypothetical prote |
| 42 | 17.6 | 16 | 2 | D83794 | actin 6 - soybean |
| 43 | 17.6 | 17 | 2 | S15754 | aleurone protein - |
| 44 | 17.6 | 17 | 2 | S40530 | hypothetical prote |
| 45 | 17.6 | 17 | 2 | C43599 | photosystem II pro |
| 46 | 17.6 | 17 | 2 | S05033 | F420-non-reducing- |
| 47 | 17.6 | 17 | 2 | S41207 | glutathione transf |
| 48 | 17.6 | 17 | 2 | S21289 | glutathione transf |
| 49 | 17.6 | 18 | 2 | B24735 | glutathione transf |
| 50 | 17.6 | 18 | 2 | S52614 | u-plasminogen acti |
| 51 | 17.6 | 18 | 2 | S46418 | NHL protein - cur |
| 52 | 17.6 | 18 | 2 | S55002 | protein 1 - Legion |
| 53 | 17.6 | 18 | 2 | S10452 | hypothetical prote |
| 54 | 17.6 | 18 | 2 | B48408 | 21K high mobility |
| 55 | 17.6 | 18 | 2 | A61392 | brain-associated s |
| 56 | 17.6 | 18 | 2 | D85601 | hypothetical prote |
| 57 | 17.6 | 18 | 4 | S56393 | lacZ/lsl mutant fu |
| 58 | 17.6 | 19 | 2 | C32735 | thyroglobulin - pi |
| 59 | 17.6 | 19 | 2 | B32735 | thyroglobulin - sh |
| 60 | 17.6 | 19 | 2 | P00548 | capsid protein VP2 |
| 61 | 17.6 | 19 | 2 | S29766 | cytochrome c(EDH) |
| 62 | 17.6 | 19 | 2 | S63489 | dissimilatory sulf |
| 63 | 17.6 | 19 | 2 | A48408 | 21K high mobility |
| 64 | 17.6 | 19 | 2 | I39327 | pre-T/NK cell-asso |
| 65 | 17.6 | 19 | 2 | A34467 | 36K microfibril-as |
| 66 | 17.6 | 20 | 2 | A60822 | cytochrome P450 PB |
| 67 | 17.6 | 20 | 2 | A39328 | notochis II-5b non |
| 68 | 17.6 | 20 | 2 | PH0111 | style glycoprotein |
| 69 | 17.6 | 20 | 2 | A05313 | apolipoprotein A-I |
| 70 | 17.6 | 20 | 2 | JN0252 | water-soluble 35K |
| 71 | 17.6 | 20 | 2 | S08605 | hypothetical prote |
| 72 | 17.6 | 20 | 2 | PL0039 | outer membrane pro |
| 73 | 17.6 | 20 | 2 | I64036 | hypothetical prote |
| 74 | 17.6 | 20 | 2 | S63490 | dissimilatory sulf |
| 75 | 17.6 | 20 | 2 | D56046 | urinary tract ston |
| 76 | 17.6 | 20 | 2 | A42865 | Ca2+/calmodulin-de |
| 77 | 17.6 | 20 | 2 | S65884 | translation initia |
| 78 | 17.6 | 20 | 2 | S33291 | lipopolysaccharide |
| 79 | 17.6 | 20 | 2 | A33592 | H+-exporting ATPas |
| 80 | 11.8 | 3 | 3 | A23751 | spinal cord peptid |
| 81 | 11.8 | 3 | 3 | B23751 | spinal cord peptid |
| 82 | 11.8 | 3 | 3 | A33802 | thyrotropin-releas |
| 83 | 11.8 | 4 | 1 | ECXAA | tyrosine-melanocy |
| 84 | 11.8 | 4 | 2 | A32039 | gamma subunit of p |
| 85 | 11.8 | 4 | 2 | A48360 | 22K superhelical D |
| 86 | 11.8 | 4 | 2 | A61300 | D-mannosate hydrol |
| 87 | 11.8 | 4 | 2 | S17745 | ribosomal protein |
| 88 | 11.8 | 4 | 2 | S17255 | autoph-RF amide neu |
| 89 | 11.8 | 4 | 2 | A25844 | synaptosomal-assoc |
| 90 | 11.8 | 4 | 2 | E44823 | T-cell receptor be |
| 91 | 11.8 | 4 | 2 | PT0711 | globulin IV alpha |
| 92 | 11.8 | 4 | 2 | S09478 | hypothetical prote |
| 93 | 11.8 | 5 | 2 | T10954 | photosystem I 10.4 |
| 94 | 11.8 | 5 | 2 | PQ0689 | acid proteinase li |
| 95 | 11.8 | 5 | 2 | B7988 | T-cell receptor be |
| 96 | 11.8 | 5 | 2 | PT0513 | T-cell receptor be |
| 97 | 11.8 | 5 | 2 | PT0625 | T-cell receptor be |
| 98 | 11.8 | 5 | 2 | PT0538 | T-cell receptor be |
| 99 | 11.8 | 5 | 2 | PT0703 | T-cell receptor be |
| 100 | 11.8 | 5 | 2 | PT0690 | T-cell receptor be |

ALIGNMENTS

RESULT 1
 PQ0788
 NADH2 dehydrogenase (EC 1.6.99.3) 20K chain - fava bean mitochondrion (fragment)
 N:Alternate names: complex I 20K chain; NADH-ubiquinone reductase 20K chain
 C:Species: mitochondrion Vicia faba (fava bean)
 C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
 C:Accession: PQ0788
 R:Letierme, S.; Boutry, M.
 Plant Physiol. 102, 435-443, 1993
 A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH-ubiquinone reductase)
 A:Reference number: PQ0775; MUID:94151437; PMID:8108509
 A:Accession: PQ0788
 A:Molecule type: protein
 A:Residues: 1-10 <DET>
 C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the three complexes in the mitochondrial electron transport chain, ranging from 5K to 75K.
 C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by a series of redox reactions.
 C:Genetics:
 A:Genome: mitochondrion
 C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.5%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LLQV 10
 ||||
 Db 7 LLQV 10

RESULT 2
 PN0147
 omega-gliadine 1 and 2 - Aegilops longissima (fragment)
 C:Species: Aegilops longissima
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PN0147; PN0146
 R:Odintsova, T.I.; Egorov, T.A.
 Biokhimiya 55, 509-516, 1990
 A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the omega-gliadin gene
 A:Reference number: PN0146; MUID:90283493; PMID:2354218
 A:Accession: PN0147
 A:Molecule type: protein
 A:Residues: 1-14 <ODI>
 A:Experimental source: strain K-202
 A>Note: omega-gliadine 2 (amino-terminal fragment)
 A:Accession: PN0146
 A:Molecule type: protein
 A:Residues: 1-9 <OD2>
 A:Experimental source: strain K-202
 A>Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 23.5%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTP 4
 ||||
 Db 11 LQTP 14

RESULT 3
 A61391
 alpha-1-antitrypsin homolog - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
 C:Accession: A61391
 R:Tanaka, N.; Sekiya, S.; Takamizawa, H.; Kato, N.; Moriyama, Y.; Fujimura, S.
 Jpn. J. Cancer Res. 82, 693-700, 1991
 A:Title: Characterization of a 54 kDa, alpha-1-antitrypsin-like protein isolated from ascaris suum
 A:Reference number: A61391; MUID:91310496; PMID:1906855

A:Accession: A61391
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <PAN>

Query Match 23.5%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
 ||||
 Db 3 PQGD 6

RESULT 4
 A42413
 Ig heavy chain V region (UBL-copurifying) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 C:Accession: A42413
 R:Bao, Z.; Muschler, J.; Horwitz, A.F.
 J. Biol. Chem. 267, 4974-4980, 1992
 A:Title: LBL, a novel, developmentally regulated, laminin-binding lectin.
 A:Reference number: A42413; MUID:92165867; PMID:1531660
 A:Accession: A42413
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <BAO>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 23.5%; Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
 Db 11 LQTP 14

RESULT 5
 D42842
 antifungal 2S storage albumin large chain - radish (fragment)
 C:Species: Raphanus sativus (radish)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C:Accession: D42842
 R:Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.E.; Vanderleyde, J. Biol. Chem. 267, 15301-15309, 1992
 A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus)
 A:Reference number: A42842; MUID:92348373; PMID:1639777
 A:Accession: D42842
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <TER>
 A:Experimental source: seed
 A>Note: sequence extracted from NCBI backbone (NCBI:109925)
 C:Superfamily: wheat alpha-amylase inhibitor

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
 ||||
 Db 9 PLLQ 12

RESULT 6
 PS0028
 flagellar motor switch protein flbD - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
 C:Accession: PS0028
 R:Malakooti, J.; Kameda, Y.; Matsumura, P.

J. Bacteriol. 171, 2728-2734, 1989
 A>Title: DNA sequence analysis, gene product identification, and localization of flagellin
 A:Reference number: PS0027; MUID:89213963; PMID:2651416
 A:Accession: PS0028
 A:Molecule type: DNA
 A:Residues: 1-20 <NAL>
 C:Genetics:
 A:Gene: flbD

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
 ||||
 Db 17 PLLQ 20

RESULT 7
 F24417
 N:Interphotoreceptor retinoid-binding protein - bush baby (fragment)
 N:Alternate names: interstitial retinol-binding protein
 C:Species: Galago sp. (bush baby)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 18-Jun-1993
 C:Accession: F24417
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A>Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A:Reference number: A91365; MUID:86301171; PMID:3743780
 A:Accession: F24417
 A:Molecule type: protein
 A:Residues: 1-20 <PON>

Query Match 23.5%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
 ||||
 Db 5 QPLL 8

RESULT 8
 A35180
 neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
 C:Accession: A35180
 R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
 J. Biol. Chem. 265, 5809-5815, 1990
 A>Title: Purification of a novel type of calcium-activated neutral protease from rat bra
 A:Reference number: A35180; MUID:90202830; PMID:2318836
 A:Accession: A35180
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <YOS>
 C:Keywords: hydrolase

Query Match 17.6%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 ||||
 Db 1 PLL 3

RESULT 9
 B33098
 231K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: B33098

R:Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: B33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <NIC>

Query Match 17.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
 ||||
 Db 2 LQT 4

RESULT 10
 A41978
 callipermamide 1 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C:Accession: A41978
 R:Dube, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tho;
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
 A>Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (d
 A:Reference number: A41978; MUID:92196111; PMID:1549595
 A:Accession: A41978
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <DUV>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 17.6%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
 ||||
 Db 1 TPQ 3

RESULT 11
 S33844
 alpha-2-macroglobulin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 22-Nov-1993 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: S33844
 R:Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J.
 Eur. J. Biochem. 214, 803-809, 1993
 A>Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mamma
 A:Reference number: S33843; MUID:93307297; PMID:7686489
 A:Accession: S33844
 A:Molecule type: protein
 A:Residues: 1-10 <WAR>
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond

Query Match 17.6%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 ||||
 Db 6 EPQ 8

RESULT 12
 JQ0943
 hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)
 C:Species: infectious bursal disease virus
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Oct-1999

C;Accession: JQ0943
R;Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bourc
J. Gen. Virol. 71, 1303-1312, 1990
A;Title: A comparison of the sequences of segment A of four infectious bursal disease vi
A;Reference number: JQ0941; MUID:90278420; PMID:2161902
A;Accession: JQ0943
A;Status: translation not shown
A;Molecule type: genomic RNA
A;Residues: 1-10 <BAV>
A;Cross-references: GB:D00869; NID:g221038; PIDN:BAA00743.1; PID:di001203; PID:g221039

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQ 9
|||
Db 5 LQ 7

RESULT 13
A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N;Contains: vitellin
C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C;Accession: A61622
R;Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria
A;Reference number: A61622
A;Accession: A61622
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HIR>
C;Keywords: egg yolk; hemolymph

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||
Db 5 EPQ 7

RESULT 14
E86128
hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E86128
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E86128
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <STO>
A;Cross-references: GB:AE005174; NID:gi2519314; PIDN:AA059489.1; GSPDB:GN00145; UNGP:Z59
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5903

Query Match 17.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
|||
Db 5 LQV 7

RESULT 15
PC2330
cycloinulooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-
C;Species: Bacillus circulans
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 07-May-1999
C;Accession: PC2330
R;Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A;Title: Purification and characterization of cycloinulooligosaccharide fructanotrans
A;Reference number: PC2330; MUID:95201377; PMID:7765973
A;Accession: PC2330
A;Molecule type: protein
A;Residues: 1-11 <KUS>
C;Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermol
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 9 PQG 11

RESULT 16
A34662
Achatina cardio-excitatory peptide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
C;Accession: A34662
R;Fujiimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A;Title: A novel cardio-excitatory peptide isolated from the atria of the African gia
A;Reference number: A34662; MUID:90211261; PMID:2322251
A;Accession: A34662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FUU>
C;Keywords: amidated carboxyl end
F,11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 7 PQG 9

RESULT 17
S68637
acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a si
A;Reference number: S68637; MUID:96181683; PMID:8603722
A;Accession: S68637
A;Molecule type: protein
A;Residues: 1-11 <BOS>
A;Experimental source: brain
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 BPQ 15
|||
Db 1 BPQ 3

RESULT 18

S25485
transcription factor NF1 - rat
N/Alternate names: HNF1 protein; LFBI protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Oct-1999
R/Tomei, L.; Piaggio, G.; Toniatti, C.; Lazaro, D.; de Francesco, R.; Pozzi, L.; Gerstner, R.
C/Accession: S25485; S50121
submitted to the EMBL Data Library, August 1992
A/Description: LFBI/HNF1 acts as a repressor of its own transcription.
A/Reference number: S25485
A/Accession: S25485
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-12 <TOM>
A/Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576
R/Piaggio, G.; Tomei, L.; Toniatti, C.; de Francesco, R.; Gerstner, J.; Cortese, R.
Nucleic Acids Res. 22, 4284-4290, 1994
A/Title: LFBI/HNF1 acts as a repressor of its own transcription.
A/Reference number: S50121; MUID:95023202; PMID:7937157
A/Accession: S50121
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-12 <PIA>
A/Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576
C/Suprafamily: transcription factor HNF-1; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 17.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
|||
Db 8 LQT 10

RESULT 19

S67528
napin - rape (fragments)
C/Species: Brassica napus (rape)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S67528
R/Muren, E.; Ek, B.; Rask, L.
Eur. J. Biochem. 227, 316-321, 1995
A/Title: Processing of the 2S storage protein pronapin in Brassica napus and in transfor
A/Reference number: S67528; MUID:95154306; PMID:7851402
A/Accession: S67528
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-6; 7-12 <MUR>

Query Match 17.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 7 PQG 9

RESULT 20

S15755
actin 7 - soybean (fragment)
C/Species: Glycine max (soybean)
C/Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C/Accession: S15755
R/Pearson, L.; Meagher, R.B.

Query Match 17.6%; Score 3; DB 2; Length 13;

Plant Mol. Biol. 14, 513-526, 1990
A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A/Reference number: S15754; MUID:91346640; PMID:2102831
A/Accession: S15755
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-13 <PEA>
A/Cross-references: EMBL:X17120; NID:G18527; PIDN:CAA34980.1; PID:G18528
C/Suprafamily: actin
C/Keywords: cytoskeleton; structural protein

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||
Db 8 QPL 10

RESULT 21

D39690
neural cell adhesion molecule, cardiac splice form +,-,+ - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C/Accession: D39690
R/Keyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule
A/Reference number: A39690; MUID:91141516; PMID:1996115
A/Accession: D39690
A/Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual
A/Molecule type: mRNA
A/Residues: 1-13 <REY>
A/Cross-references: GB:M63970
C/Suprafamily: neural cell adhesion molecule; fibronectin type III repeat homology; ir
C/Keywords: cardiac muscle; cell adhesion; heart

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
Db 8 PQG 10

RESULT 22

S09716
2S albumin large chain (1 and 2) NII - rape (fragments)
N/Alternate names: 2S albumin large chain NIII
C/Species: Brassica napus (rape)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C/Accession: S09716; S09718; S09717
R/Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A/Title: Beta-turns as structural motifs for the proteolytic processing of seed protei
A/Reference number: S09720; MUID:9042974; PMID:2185951
A/Accession: S09716
A/Molecule type: protein
A/Residues: 1-9;10-13 <MON>
A/Experimental source: seed
A/Note: 3-Ser was also found
A/Accession: S09718
A/Molecule type: protein
A/Residues: 1-9;10-13 <MO2>
A/Experimental source: seed
A/Accession: S09717
A/Molecule type: protein
A/Residues: 1-9;10-13 <MO3>
A/Experimental source: seed

Query Match 17.6%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.1e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 14 PQG 16
|||
Db 1 PQG 3

RESULT 23

I84603
deoxynucleotidyltransferase - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
R:Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A:Reference number: 145884; MUID:87213162; PMID:3579900
A:Accession: I84603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:M26144; MID:g951194; PIDN:AAA74588.1; PID:g951195
C:Genetics:
A:Gene: GDB:DNTT
A:Cross-references: GDB:119100; OMTM:187410
A:Map position: 10q23-10q24

Query Match 17.6%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 QPL 7
|||
Db 8 QPL 10

RESULT 24

A35105
hypothetical protein - Neurospora crassa mitochondrion (fragment)
C:Species: mitochondrion Neurospora crassa
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C:Accession: A35105
R:Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A:Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora
A:Reference number: A35105; MUID:90263093; PMID:2160856
A:Accession: A35105
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-14 <SAV>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LLQ 9
|||
Db 7 LLQ 9

RESULT 25

S00150
ovostatin - duck (fragment)
R:Alternate names: ovomacroglobulin
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C:Accession: S00150
R:Nagase, H.; Harris Jr., E.D.; Brew, K.

J. Biol. Chem. 261, 1421-1426, 1986
A:Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).
A:Reference number: S00150; MUID:86111792; PMID:3511043
A:Accession: S00150
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NAG>
A>Note: part of this sequence, including the amino end of the mature chicken and duck

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 13 EPQ 15
|||
Db 4 EPQ 6

RESULT 26

B20872
alpha-2-macroglobulin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: B20872
R:Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.
J. Biol. Chem. 258, 7481-7489, 1983
A:Title: Ovostatin: a novel proteinase inhibitor from chicken egg white. I. Purificat
A:Reference number: A92427; MUID:83238315; PMID:6408074
A:Accession: B20872
A:Molecule type: protein
A:Residues: 1-14 <NAG>

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 13 EPQ 15
|||
Db 5 EPQ 7

RESULT 27

PH1566
cerebrin 30 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: PH1566
R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.
J. Neurochem. 61, 533-540, 1993
A:Title: Micropurification of two human cerebrospinal fluid proteins by high performa
A:Reference number: PH1566; MUID:93329419; PMID:8336140
A:Accession: PH1566
A:Molecule type: protein
A:Residues: 1-14 <LEO>

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 QPL 7
|||
Db 9 QPL 11

RESULT 28

B61235
fibroblast-activating factor 35K precursor - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 12-May-1994
C:Accession: B61235
R:Deneter, J.; Medzhradszky, D.; Kha, H.; Goetzl, E.J.; Turck, C.W.
Immunology 72, 350-354, 1991
A:Title: Isolation and partial characterization of the structures of fibroblast activ

A:Reference number: A61235; MUID:91224664; PMID:2026444
 A:Accession: B61235
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <DEM>

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 |||
 Db 6 LLQ 8

RESULT 29

PHI327
 Ig heavy chain DJ region (clone C113-105) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PHI327
 R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
 A:Reference number: PHI302; MUID:93094761; PMID:1460419
 A:Accession: PHI327
 A:Molecule type: DNA
 A:Residues: 1-14 <NAS>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VMN 12
 |||
 Db 3 VMN 5

RESULT 30

PN0666
 dystrophin-associated glycoprotein A3a-V - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C:Accession: PN0666
 R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in dystrophic muscle
 A:Reference number: PN0662; MUID:94156881; PMID:8113213
 A:Accession: PN0666
 A:Molecule type: protein
 A:Residues: 1-14 <YOS>
 C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C:Keywords: glycoprotein; skeletal muscle

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
 |||
 Db 3 PLL 5

RESULT 31

PC7075
 Guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: PC7075
 R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b

A:Reference number: PC7072
 A:Accession: PC7075
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Experimental source: strain C57BL/6Cr Sic, male; brain, striatum
 C:Keywords: brain; phosphorus-oxygen lyase

Query Match 17.6%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
 |||
 Db 9 PQG 11

RESULT 32

PA0021
 protein QA300016 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0021
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JTPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
 A:Reference number: PA0001
 A:Accession: PA0021
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: leaf

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 9 EPQ 11

RESULT 33

PN0148
 omega-gliadine 3 - Aegilops longissima (fragment)
 C:Species: Aegilops longissima
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PN0148
 R:Odintsova, T.I.; Egorov, T.A.
 Biochimia 55, 509-516, 1990
 A:Title: N-terminal sequences of omega-gliadins of Aegilops longissima: On the origin of the omega-gliadins
 A:Reference number: PN0146; MUID:90283493; PMID:2354218
 A:Accession: PN0148
 A:Molecule type: protein
 A:Residues: 1-15 <ODI>
 A:Experimental source: strain K-202
 A:Note: 11-Gln was also found

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
 |||
 Db 13 TPQ 15

RESULT 34

A41436
 alpha-macroglobulin - green sea turtle (fragment)
 C:Species: Chelonia mydas (green sea turtle)
 C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
 C:Accession: A41436
 R:Osada, T.; Sasaki, T.; Ikai, A.
 J. Biochem. 103, 212-217, 1988

A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin d
 A;Reference number: A41436; MUID:88227890; PMID:2453503
 A;Accession: A41436
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <OSA>

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQ 15
 |||
 Db 3 EPQ 5

RESULT 35

PN0665
 dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0665

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
 A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0665

A;Molecule type: protein

A;Residues: 1-15 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
 |||
 Db 3 PLL 5

RESULT 36

PH0789
 T-cell receptor alpha chain (E22 V-alpha-4.delta-7R) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PH0789

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0789

A;Molecule type: mRNA

A;Residues: 1-15 <CAS>

A;Cross-references: EMBL:X60894

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQT 3
 |||
 Db 10 LQT 12

RESULT 37

B42324
 cytochrome P450c27/25 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Mar-1999

C;Accession: B42324
 R;Shayiq, R.M.; Avadhani, N.G.
 J. Biol. Chem. 267, 2421-2428, 1992
 A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat m1
 ap.

A;Reference number: A42324; MUID:92129322; PMID:1733943

A;Accession: B42324

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <SHA>

A;Note: sequence extracted from NCBI backbone (NCBIN:78408, NCBIP:88990)

C;Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology

C;Keywords: heme; transmembrane protein

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QVM 11
 |||
 Db 3 QVM 5

RESULT 38

C49048
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen
 C;Species: Homo sapiens (man)
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C;Accession: C49048

R;Sloud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2418, 1992

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
 A;Reference number: A49048; MUID:92387250; PMID:1387614

A;Accession: C49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113265)

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
 |||
 Db 6 LLQ 8

RESULT 39

PH0763
 T-cell receptor beta chain (F15) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PH0763

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility comple
 allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0763

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60857; NID:950933; PIDN:CAA43247.1; PID:g50934

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQG 16

A;Cross-references: GB:AP001511; GB:BA000004; NID:gi0173727; PIDN:BA04875.1; GSPDB:GN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1156

Db |||
6 PQG 8

RESULT 40
PH0767
T-cell receptor beta chain (J5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0767
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J.; Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078946; PMID:1836010
A;Accession: PH0767
A;Molecule type: mRNA
A;Residues: 1-16 <AS>
A;Cross-references: EMBL:X60861; NID:g52752; PIDN:CAA43251.1; PID:g52753
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 17.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
|||
6 PQG 8

Db

RESULT 41
A46236
transforming protein myc, form 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: A46236
R;Hann, S.R.; Sloan-Brown, K.; Spotts, G.D.
Genes Dev. 6, 1229-1240, 1992
A;Title: Translational activation of the non-AUG-initiated c-myc 1 protein at high cell
A;Reference number: A46236; MUID:92331929; PMID:1628829
A;Accession: A46236
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <HAN>
A;Cross-references: GB:X01023
C;Genetics:
A;Start codon: CTG
C;Keywords: alternative initiators

Query Match 17.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
|||
9 TPQ 11

Db

RESULT 42
D83794
hypothetical protein BH1156 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83794
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <STO>

Query Match 17.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
|||
3 QGD 5

Db

RESULT 45
C43599
hypothetical protein (cylIIA 3' region) - Actinobacillus pleuropneumoniae (serotype 9)
N;Alternate names: CylII-B (truncated)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C;Accession: C43599; S18854
R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.

A;Cross-references: GB:AP001511; GB:BA000004; NID:gi0173727; PIDN:BA04875.1; GSPDB:GN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1156

Query Match 17.6%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MME 13
|||
10 MME 12

Db

RESULT 43
S15754
actin 6 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
C;Accession: S15754; S08049
R;Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A;Reference number: S15754; MUID:91346640; PMID:2102831
A;Accession: S15754
A;Molecule type: DNA
A;Residues: 1-17 <PEA>
A;Cross-references: EMBL:X17119; NID:gi18525; PIDN:CAA34979.1; PID:gi18526
A;Superfamily: actin
C;Keywords: cytoskeleton

Query Match 17.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||
8 QPL 10

Db

RESULT 44
S40530
aleurone protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
C;Accession: S40530
R;Yupanis, T.; Burgess, S.R.; Jackson, P.J.; Shewry, P.R.
J. Exp. Bot. 41, 385-392, 1990
A;Title: Characterization of the major protein component from aleurone cells of barley
A;Reference number: S40530
A;Accession: S40530
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <YUP>
C;Superfamily: glycinin

Query Match 17.6%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
|||
3 QGD 5

Db

RESULT 45
C43599
hypothetical protein (cylIIA 3' region) - Actinobacillus pleuropneumoniae (serotype 9)
N;Alternate names: CylII-B (truncated)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C;Accession: C43599; S18854
R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.

Infect. Immun. 59, 4497-4504, 1991
 A;Title: Cytolysins of *Actinobacillus pleuropneumoniae* serotype 9.
 A;Reference number: A43599; MUID:92040145; PMID:1937809
 A;Accession: C43599
 A;Molecule type: DNA
 A;Residues: 1-17 <SMI>
 A;Cross-references: GB:X61111; NID:g38939; PIDN:CRA43424.1; PID:g38942

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 1 MEP 3

RESULT 46

S05033
 photosystem II protein psbL - *Synechococcus* sp. (strain Copeland) (fragment)
 N;Alternate names: photosystem II 5K protein
 C;Species: *Synechococcus* sp.
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C;Accession: S05033
 R;Keuchi, M.; Koike, H.; Inoue, Y.
 FEBS Lett. 251, 155-160, 1989

A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
 A;Reference number: S05033
 A;Accession: S05033
 A;Molecule type: protein
 A;Residues: 1-17 <IKE>
 A;Note: the source is designated as *Synechococcus vulcanus*
 C;Genetics:
 A;Gene: psbL
 C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 1 MEP 3

RESULT 47

S41207
 F420-non-reducing-hydrogenase (EC 1.12.99.-) 51K chain - *Methanobacterium thermoautotrophicum*
 C;Species: *Methanobacterium thermoautotrophicum*
 A;Variety: strain Marburg
 C;Date: 06-Feb-1995 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
 C;Accession: S41207
 R;Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.
 Eur. J. Biochem. 220, 139-149, 1994

A;Title: H(2): heterodisulfide oxidoreductase complex from *Methanobacterium thermoautotrophicum*
 A;Reference number: S41204; MUID:94164153; PMID:8119281
 A;Accession: S41207
 A;Molecule type: protein
 A;Residues: 1-17 <SET>
 A;Experimental source: strain Marburg
 C;Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.-) and a F420-non-reducing-hydrogenase (EC 1.12.99.-)

A;Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreonine phosphate heterodisulfide (EC 1.12.99.2)
 C;Keywords: membrane-associated complex; oxidoreductase

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||

Db 5 MEP 7

RESULT 48

S21289
 glutathione transferase (EC 2.5.1.18) - rat
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S21289
 R;Meyer, D.J.; Gilmore, K.S.; Coles, B.; Dalton, K.; Hulbert, P.B.; Ketterer, B.
 Biochem. J. 283, 919, 1992
 A;Title: Corrigendum. Structural distinction of rat GSH transferase subunit 10.
 A;Reference number: S21289; MUID:92272699; PMID:1590780

A;Accession: S21289
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-17 <MEY>
 C;Keywords: transferase

Query Match 17.6%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
 |||
 Db 13 LQT 15

RESULT 49

B24735
 glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
 C;Accession: B24735
 R;Mannervik, B.; Alin, P.; Guthenberg, C.; Jonsson, H.; Tahir, M.K.; Warholm, M.; Jor. Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985

A;Title: Identification of three classes of cytosolic glutathione transferase common
 A;Reference number: A24735; MUID:86042634; PMID:3864155

A;Accession: B24735
 A;Molecule type: protein
 A;Residues: 1-18 <MAN>
 C;Superfamily: glutathione transferase
 C;Keywords: transferase

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 |||
 Db 15 MEP 17

RESULT 50

I52614
 u-plasminogen activator receptor precursor - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C;Accession: I52614
 R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.
 Blood 86, 624-635, 1995
 A;Title: A conserved TATA-less proximal promoter drives basal transcription from the
 A;Reference number: I52614; MUID:95329719; PMID:7605992

A;Accession: I52614
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <RES>

A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989
 C;Genetics:
 A;Gene: uPAR
 C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 17.6%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|||
Db 5 PLL 7

RESULT 51
S46418
NTL1 protein - curled-leaved tobacco
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02-Aug-2002
C:Accession: S46418
R:Daniel-Vedele, F.; Caboche, M.
Mol. Gen. Genet. 240, 365-373, 1993
A:Title: A tobacco cDNA clone encoding a GATA-1 zinc finger protein homologous to regula
A:Reference number: S46418; MUID:94019241; PMID:8413186
A:Accession: S46418
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <DNA>
A:Cross-references: EMBL:S65745
C:Superfamily: Arabidopsis thaliana GATA transcription factor 4

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQ 5
|||
Db 5 TPQ 7

RESULT 52
S55002
protein 1 - Legionella pneumophila (fragment)
C:Species: Legionella pneumophila
C:Date: 23-Aug-1995 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C:Accession: S55002
R:Kaik, Y.A.; Eisenstein, B.I.; Engleberg, N.C.
Infect. Immun. 61, 1320-1329, 1993
A:Title: Phenotypic modulation by Legionella pneumophila upon infection of macrophages.
A:Reference number: S55002; MUID:93202732; PMID:8454334
A:Accession: S55002
A:Molecule type: protein
A:Residues: 1-18 <KWA>

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|||
Db 10 PLL 12

RESULT 53
S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C:Accession: S10452
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452
A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
|||
Db 4 QPL 6

RESULT 54
B48408
21K high mobility group protein, hepatic (isoform 2) - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997
C:Accession: B48408
R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification
A:Reference number: A48408
A:Accession: B48408
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <WAT>
C:Keywords: liver

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||
Db 13 EPQ 15

RESULT 55
A61392
brain-associated small cell lung cancer antigen - human (fragment)
N:Alternate names: BASCA
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
C:Accession: A61392
R:Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A:Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NK)
A:Reference number: A61392; MUID:92046737; PMID:1719260
A:Accession: A61392
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <UME>

Query Match 17.6%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
|||
Db 1 LQV 3

RESULT 56
D85601
hypothetical protein z1127 [imported] - Escherichia coli (strain O157:H7, substrain EI
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: D85601; E85652
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <STO>
A:Cross-references: GB:AE005174; NID:g12513923; PIDN:AA05272.1; GSPDB:GN00145; UWGP:Z

A;Experimental source: strain O157:H7, substrain EDL933
 A;Accession: E85652
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-18 <ST2>
 A;Cross-references: GB:AE005174; NID:g12514440; PIDN:AAG55681.1; GSPDB:GNO0145; UWGP:Z15
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z1127; Z1566

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
 ||||
 Db 3 LLQ 5

RESULT 57

I56393
 lacZ/IS1 mutant fusion protein - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
 C;Accession: I56393
 R;Malamy, M.H.; Rahaim, P.T.; Hoffman, C.S.; Baghdoyan, D.; O'Connor, M.B.; Miller, J.F.
 J. Mol. Biol. 181, 551-555, 1985
 A;Title: A frameshift mutation at the junction of an IS1 insertion within lacZ restores
 A;Reference number: I56393; MUID:85210885; PMID:2987506
 A;Accession: I56393
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <MAL>
 A;Cross-references: GB:K03504; NID:g146583; PIDN:AAA24058.1; PID:g146584
 C;Keywords: fusion protein

Query Match 17.6%; Score 3; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
 ||||
 Db 12 QVM 14

RESULT 58

C32735
 thyroglobulin - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
 C;Accession: C32735
 R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
 Biochem. Biophys. Res. Commun. 118, 423-429, 1984
 A;Title: The isolation of identical thyroxine containing amino acid sequences from bovin
 A;Reference number: A32735; MUID:84153804; PMID:6704086
 A;Accession: C32735
 A;Status: preliminary
 A;Molecule type: protein

A;Residues: 1-19 <RAW>
 C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
 C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
 F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.6%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 ||||
 Db 10 QPL 12

RESULT 59

I56393
 lacZ/IS1 mutant fusion protein - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000
 C;Accession: I56393
 R;Malamy, M.H.; Rahaim, P.T.; Hoffman, C.S.; Baghdoyan, D.; O'Connor, M.B.; Miller, J.F.
 J. Mol. Biol. 181, 551-555, 1985
 A;Title: A frameshift mutation at the junction of an IS1 insertion within lacZ restores
 A;Reference number: I56393; MUID:85210885; PMID:2987506
 A;Accession: I56393
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <MAL>
 A;Cross-references: GB:K03504; NID:g146583; PIDN:AAA24058.1; PID:g146584
 C;Keywords: fusion protein

B32735
 thyroglobulin - sheep (fragment)
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Apr-1997
 C;Accession: B32735
 R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
 Biochem. Biophys. Res. Commun. 118, 423-429, 1984
 A;Title: The isolation of identical thyroxine containing amino acid sequences from bo
 A;Reference number: A32735; MUID:84153804; PMID:6704086
 A;Accession: B32735
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <RAW>
 C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat ho
 C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
 F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 ||||
 Db 10 QPL 12

RESULT 60

PQ0548
 capsid protein VP26 - human herpesvirus 1 (fragment)
 C;Species: human herpesvirus 1
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: PQ0548
 R;Davison, M.D.; Rixon, F.J.; Davison, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp
 A;Reference number: PQ0544; MUID:93019027; PMID:1328483
 A;Accession: PQ0548
 A;Molecule type: protein
 A;Residues: 1-19 <DAV>
 A;Experimental source: strain 17
 C;Genetics:
 A;Gene: UL35
 C;Keywords: capsid protein

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQG 16
 ||||
 Db 15 PQG 17

RESULT 61

S29766
 cytochrome c (EDH) - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S29766
 R;Schrover, J.M.J.; Frank, J.; van Wielink, J.E.; Duine, J.A.
 Biochem. J. 290, 123-127, 1993
 A;Title: Quaternary structure of quinoprotein ethanol dehydrogenase from Pseudomonas
 A;Reference number: S29766; MUID:93176105; PMID:8382472
 A;Accession: S29766
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <SCH>

Query Match 17.6%; Score 3; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFG 5

```

Db          |||
            5 TPQ 7
Query Match 17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 62
S63489
disseminatory sulfite reductase alpha chain, membrane-bound - Desulfovibrio desulfurican
C:Species: Desulfovibrio desulfuricans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63489
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the disseminatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152; PMID:8521853
A:Accession: S63489
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <STE>

Query Match 17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 PLL 8
            |||
            6 PLL 8
Db

RESULT 63
A48408
21K high mobility group protein, hepatic (isoform 1) - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997
C:Accession: A48408
R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification a
A:Reference number: A48408
A:Accession: A48408
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <WAT>
C:Keywords: liver

Query Match 17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          13 EPQ 15
            |||
            14 EPQ 16
Db

RESULT 64
I39327
pre-T/NK cell-associated protein 1D12A2 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I39327
R:Rans-Goldberg, M.G.; Hori, T.; Mohan-Peterson, S.; Spits, H.
J. Immunol. 151, 5810-5821, 1993
A:Title: Identification of human pre-T/NK cell-associated genes.
A:Reference number: I39327; MUID:94044805; PMID:8228263
A:Accession: I39327
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:I17325; NID:g306322; PIDN:AAA16780.1; PID:g306323
C:Genetics:
A:Gene: GDB:PTNKAP1
A:Cross-references: GDB:5507882
A:Map position: 8p21-8p11.2

Db          |||
            5 TPQ 7
Query Match 17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 65
A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Nunata, Y.; Miyauchi, K.; Hayah
J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycop
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match 17.6%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 QPL 7
            |||
            16 QPL 18
Db

RESULT 66
A60822
cytochrome P450 PB-3a - rat (fragment)
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
C:Accession: A60822; 155191
R:Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
Biochem. Pharmacol. 37, 3245-3249, 1988
A:Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
A:Reference number: A60822; MUID:88293549; PMID:3041969
A:Accession: A60822
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <AME>
R:Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.
J. Biochem. 103, 487-492, 1988
A:Title: A mutant rat strain deficient in induction of a phenobarbital-inducible form
A:Reference number: 155191; MUID:88273074; PMID:2839467
A:Accession: 155191
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: GB:D00250; NID:g220727; PIDN:BAA00181.1; PID:g220728
C:Superfamily: human cytochrome P450 CYP2B6; cytochrome P450 homology
C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane prot

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 MEP 14
            |||
            1 MEP 3
Db

RESULT 67
A39328
norechis II-5b nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
```

C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
 C;Accession: A39328
 R;fang, C.C.; Chang, L.S.; Wu, F.S.
 Toxicon 29, 1337-1344, 1991
 A;Title: Venom constituents of Notochis scutatus (Australian tiger snake) from
 A;Reference number: A39328; PMID:92263371; PMID:1814009
 A;Accession: A39328
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <YAN>
 C;Superfamily: phospholipase A2

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 |||
 Db 17 QPL 19

RESULT 68

PH0111
 style glycoprotein S3 - garden petunia (fragment)
 C;Species: Petunia x hybrida (garden petunia)
 C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Apr-2001
 C;Accession: PH0111
 R;Broothaerts, W.J.; van Laere, A.; Witters, R.; Preaux, G.; Decock, B.; van Damme, J.;
 Plant Mol. Biol. 14, 93-102, 1990
 A;Title: Purification and N-terminal sequencing of style glycoproteins associated with s
 A;Reference number: PH0109; PMID:91322492; PMID:2101314
 A;Accession: PH0111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <BRO>
 C;Superfamily: Enterobacter ribonuclease

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQ 9
 |||
 Db 4 LQ 6

RESULT 69

A05313
 apolipoprotein A-I - red guenon (fragment)
 N;Alternate names: apo-A-I
 C;Species: Erythrocebus patas (red guenon, hussar)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-May-2000
 C;Accession: A05313
 R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
 Biochemistry 15, 1928-1933, 1976
 A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus
 A;Reference number: A90395; PMID:76184721; PMID:178359

A;Accession: A05313
 A;Molecule type: protein
 A;Residues: 1-20 <MAH>
 C;Superfamily: apolipoprotein A-I
 C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
 |||
 Db 5 QTP 7

RESULT 70

JN0252
 water-soluble 35K protein - soybean (fragment)
 C;Species: Glycine max (soybean)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 23-Mar-1995
 C;Accession: JN0252
 R;Akhtaruzzaman, M.; Kimura, Y.; Takagi, S.
 Biosci. Biotechnol. Biochem. 56, 873-878, 1992
 A;Title: Glycinin A4A5 subunit digesting protease in soybean seeds.
 A;Reference number: JN0252
 A;Accession: JN0252
 A;Molecule type: protein
 A;Residues: 1-20 <AKH>
 A;Experimental source: seed
 C;Superfamily: glycinin

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 16 EPQ 18

RESULT 71

S08605
 hypothetical protein 1 estrogen receptor 5'-region - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
 C;Accession: S08605
 R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
 EMBO J. 5, 891-897, 1986
 A;Title: The chicken estrogen receptor sequence: homology with v-erbA and the human
 A;Reference number: S07192; PMID:86247578; PMID:3755102
 A;Accession: S08605
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-20 <KRU>
 A;Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27431.1; PID:G63379
 A;Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue
 C;Superfamily: unassigned leader peptides

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
 |||
 Db 11 EPQ 13

RESULT 72

PL0039
 outer membrane protein C class 5 - Neisseria meningitidis (fragment)
 C;Species: Neisseria meningitidis
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
 C;Accession: PL0039
 R;Achtman, M.; Neibert, M.; Crowe, B.A.; Strittmatter, W.; Kusecek, B.; Weyse, E.; Wa
 J. Exp. Med. 168, 507-525, 1988
 A;Title: Purification and characterization of eight class 5 outer membrane protein va
 A;Reference number: PL0038; PMID:88316168; PMID:2457646
 A;Accession: PL0039
 A;Molecule type: protein
 A;Residues: 1-20 <ACH>

A;Note: residues 17-18 are probably Lys-Ser
 C;Comment: The Neisseria meningitidis class 5 proteins are proposed to correspond to
 C;Keywords: membrane protein

Query Match 17.6%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3

Db 4 LQT 6
Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
|||
8 QTP 10

Search completed: November 25, 2003, 18:28:13
Job time : 17.6436 secs

RESULT 73
I64036
Hypothetical protein HI1571 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C/Accession: I64036
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
R/Glitschmann, R.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; Gocayne, J.D.; Scott, J.; Shetty, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: I64036
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-20 <TIGR>
A/Cross-references: GB:U32831; GB:L42023; NID:G1574407; PID:G1574420; TIGR:HI1571
C/Genetics:
A/Start codon: GTG

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
|||
16 EPQ 18

RESULT 74
S63490
dissimilatory sulfite reductase alpha chain, soluble - Desulfovibrio desulfuricans (frag
C/Species: Desulfovibrio desulfuricans
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C/Accession: S63490
R/Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A/Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A/Reference number: S63489; MUID:96085152; PMID:8521853
A/Accession: S63490
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <STE>

Query Match 17.6%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
|||
6 PLL 8

RESULT 75
D56046
urinary tract stone matrix protein 6, 15K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
C/Accession: D56046
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A/Description: Isolation, characterization and sequence of stone proteins.
A/Reference number: A56046
A/Accession: D56046
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <BIN>

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 8.22872 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQLQVMPEQGD 17

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 3 | 17.6 | 9 | 1 | AL10 CARMA |
| 2 | 3 | 17.6 | 9 | 1 | FAR1 CALVO |
| 3 | 3 | 17.6 | 9 | 1 | OXYT_RAJCL |
| 4 | 3 | 17.6 | 9 | 1 | RT33_BOVIN |
| 5 | 3 | 17.6 | 10 | 1 | FAR6_PANRE |
| 6 | 3 | 17.6 | 10 | 1 | RT02_BOVIN |
| 7 | 3 | 17.6 | 11 | 1 | CEPI_ACHFU |
| 8 | 3 | 17.6 | 11 | 1 | RANC_RANPI |
| 9 | 3 | 17.6 | 12 | 1 | FIFI_SARBU |
| 10 | 3 | 17.6 | 13 | 1 | ACT7_SOYBN |
| 11 | 3 | 17.6 | 13 | 1 | CRBL_ICASP |
| 12 | 3 | 17.6 | 13 | 1 | LPAA_PORGI |
| 13 | 3 | 17.6 | 15 | 1 | ARCA_STRP5 |
| 14 | 3 | 17.6 | 15 | 1 | UC30_MAIZE |
| 15 | 3 | 17.6 | 16 | 1 | PA21_TPIST |
| 16 | 3 | 17.6 | 17 | 1 | AC16_SOYBN |
| 17 | 3 | 17.6 | 17 | 1 | B29K_PORGI |
| 18 | 3 | 17.6 | 17 | 1 | PSBL_SYNVU |
| 19 | 3 | 17.6 | 18 | 1 | UC03_MAIZE |
| 20 | 3 | 17.6 | 20 | 1 | ALB6_EQUAS |
| 21 | 3 | 17.6 | 20 | 1 | APAI_ERYPA |
| 22 | 3 | 17.6 | 20 | 1 | OMPW_VIBAL |
| 23 | 3 | 17.6 | 20 | 1 | SCBI_CANFA |
| 24 | 3 | 17.6 | 20 | 1 | OCPI_OCTMI |
| 25 | 2 | 11.8 | 4 | 1 | RM01_YEAST |
| 26 | 2 | 11.8 | 5 | 1 | UXA4_CHLTR |
| 27 | 2 | 11.8 | 6 | 1 | ACPH_RABIT |
| 28 | 2 | 11.8 | 6 | 1 | VP19_HSVIK |
| 29 | 2 | 11.8 | 7 | 1 | ALL3_CARMA |
| 30 | 2 | 11.8 | 7 | 1 | E105_LITRU |
| 31 | 2 | 11.8 | 7 | 1 | FAR1_HELTI |
| 32 | 2 | 11.8 | 7 | 1 | GFRP_MOUSE |
| 33 | 2 | 11.8 | 7 | 1 | LANC_CARUI |

| | | | | | |
|-----|---|------|----|---|------------|
| 34 | 2 | 11.8 | 7 | 1 | MNP1_LEPDE |
| 35 | 2 | 11.8 | 7 | 1 | PPH2_LYCES |
| 36 | 2 | 11.8 | 7 | 1 | UH11_RAT |
| 37 | 2 | 11.8 | 8 | 1 | ACL_THUAL |
| 38 | 2 | 11.8 | 8 | 1 | AKHG_GRYBI |
| 39 | 2 | 11.8 | 8 | 1 | AKH_LIBAU |
| 40 | 2 | 11.8 | 8 | 1 | AKH_TABAT |
| 41 | 2 | 11.8 | 8 | 1 | ALL6_CYDPO |
| 42 | 2 | 11.8 | 8 | 1 | COM2_CONPU |
| 43 | 2 | 11.8 | 8 | 1 | CPD1_ENTFA |
| 44 | 2 | 11.8 | 8 | 1 | FAR1_PENMO |
| 45 | 2 | 11.8 | 8 | 1 | HTF1_PERAM |
| 46 | 2 | 11.8 | 8 | 1 | HTF2_PERAM |
| 47 | 2 | 11.8 | 8 | 1 | LCK3_LEUMA |
| 48 | 2 | 11.8 | 8 | 1 | LMT2_LOCMI |
| 49 | 2 | 11.8 | 8 | 1 | LPK_LEUMA |
| 50 | 2 | 11.8 | 8 | 1 | NPB_BOVIN |
| 51 | 2 | 11.8 | 8 | 1 | UC26_MAIZE |
| 52 | 2 | 11.8 | 8 | 1 | UF06_MOUSE |
| 53 | 2 | 11.8 | 8 | 1 | WP1_PERAT |
| 54 | 2 | 11.8 | 9 | 1 | BUK_CLOPA |
| 55 | 2 | 11.8 | 9 | 1 | CONV_CONVE |
| 56 | 2 | 11.8 | 9 | 1 | COKE_THUOB |
| 57 | 2 | 11.8 | 9 | 1 | DSIP_RABIT |
| 58 | 2 | 11.8 | 9 | 1 | FAR2_CALVO |
| 59 | 2 | 11.8 | 9 | 1 | FAR3_PENMO |
| 60 | 2 | 11.8 | 9 | 1 | FAR4_PENMO |
| 61 | 2 | 11.8 | 9 | 1 | FAR9_ASCSU |
| 62 | 2 | 11.8 | 9 | 1 | FARA_CALVO |
| 63 | 2 | 11.8 | 9 | 1 | FRP1_SARBU |
| 64 | 2 | 11.8 | 9 | 1 | KNL3_BOMVA |
| 65 | 2 | 11.8 | 9 | 1 | LMT3_LOCMI |
| 66 | 2 | 11.8 | 9 | 1 | MGMT_BOVIN |
| 67 | 2 | 11.8 | 9 | 1 | OXYA_SQUAC |
| 68 | 2 | 11.8 | 9 | 1 | OXYT_RABIT |
| 69 | 2 | 11.8 | 9 | 1 | PPH1_LYCES |
| 70 | 2 | 11.8 | 9 | 1 | RE42_LITRU |
| 71 | 2 | 11.8 | 9 | 1 | TAL1_PICUA |
| 72 | 2 | 11.8 | 9 | 1 | TAL3_PICUA |
| 73 | 2 | 11.8 | 9 | 1 | THYF_PIG |
| 74 | 2 | 11.8 | 9 | 1 | UF02_MOUSE |
| 75 | 2 | 11.8 | 9 | 1 | ULAD_HUMAN |
| 76 | 2 | 11.8 | 9 | 1 | UPA3_HUMAN |
| 77 | 2 | 11.8 | 9 | 1 | UPA6_HUMAN |
| 78 | 2 | 11.8 | 10 | 1 | AKHX_LOCMI |
| 79 | 2 | 11.8 | 10 | 1 | BPE2_BOTIN |
| 80 | 2 | 11.8 | 10 | 1 | BPE2_BOTJA |
| 81 | 2 | 11.8 | 10 | 1 | BPP_VIPAS |
| 82 | 2 | 11.8 | 10 | 1 | BRK_ONCMY |
| 83 | 2 | 11.8 | 10 | 1 | COMX_RAT |
| 84 | 2 | 11.8 | 10 | 1 | COXQ_RABIT |
| 85 | 2 | 11.8 | 10 | 1 | COXQ_SHEEP |
| 86 | 2 | 11.8 | 10 | 1 | CU30_LOCMI |
| 87 | 2 | 11.8 | 10 | 1 | FAR5_MACRS |
| 88 | 2 | 11.8 | 10 | 1 | FAR7_MACRS |
| 89 | 2 | 11.8 | 10 | 1 | FARP_MYTED |
| 90 | 2 | 11.8 | 10 | 1 | GONI_ILLMI |
| 91 | 2 | 11.8 | 10 | 1 | HTF1_ROMMI |
| 92 | 2 | 11.8 | 10 | 1 | HTF2_CARMO |
| 93 | 2 | 11.8 | 10 | 1 | HTF_NAUCI |
| 94 | 2 | 11.8 | 10 | 1 | HTF_TABAT |
| 95 | 2 | 11.8 | 10 | 1 | LPK2_LOCMI |
| 96 | 2 | 11.8 | 10 | 1 | NSI_MYCTU |
| 97 | 2 | 11.8 | 10 | 1 | PNEU_HUMAN |
| 98 | 2 | 11.8 | 10 | 1 | PNEU_RAT |
| 99 | 2 | 11.8 | 10 | 1 | TEMK_RANTE |
| 100 | 2 | 11.8 | 10 | 1 | TKL2_LOCMI |

ALIGNMENTS

RESULT 1

```
AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGP 6
DB 2 PGP 4

RESULT 2
FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Callifmrfamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifmrfamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FPMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPG 5

AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGP 6
DB 2 PGP 4

RESULT 2
FARI_CALVO
ID FARI_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Callifmrfamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifmrfamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FPMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPG 5

AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiogaster; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurophyophyseal peptides: isolation of a new hormone,
RT glumitocin (Ser 4-Gln 8-cytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 984 MW; 17E9C76EBE455B04B CRC64;

Query Match 17.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGP 16
DB 7 PGP 9

RESULT 4
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;
```


Query Match 17.6%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
 Db 5 QPL 7

RESULT 5

ID FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P8260;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PF6 (NGAPQFFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRamide-related
 RT peptides (FarPs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 10 10
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1132 NW; CB13E4C9D776C76D CRC64;

Query Match 17.6%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 POP 6
 Db 4 POP 6

RESULT 6

ID RT02 BOVIN STANDARD; PRT; 10 AA.
 AC P82923;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
 GN MRPS2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RT Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present."
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR Pfam: PF00318; Ribosomal_S2; PARTIAL.

DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 17.6%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
 Db 2 MEP 4

RESULT 7

ID CEPI ACHFU STANDARD; PRT; 11 AA.
 AC P22750;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigamurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.

RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica."
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -!- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
 CC MOVEMENT OF ACHATINA.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.

DR PIR; A34662; A34662.
 KW Hormone; Amidation.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 POG 16
 Db 7 POG 9

RESULT 8

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;

```

RL Comp. Biochem. Physiol. 77C:99-108 (1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TPQ 5
Db 2 TPQ 4
RESULT 9
FIF1_SARBU STANDARD; PRT; 12 AA.
ID -FIF1_SARBU
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusert T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368 (2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FAPR (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12
FT SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PQP 6
Db 3 PQP 5
RESULT 10
ACT7_SOYBN STANDARD; PRT; 13 AA.
ID -ACT7_SOYBN
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT7.
OS Glycine max (Soybean).
CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

```

```

OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526 (1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X17120; CAA34980.1; -
CC PIR: S15755; S15755.
CC InterPro: IPR004001; Actin.
CC InterPro: IPR004000; Actin_like.
CC PROSITE: PS00406; ACTINS_1; PARTIAL.
CC PROSITE: PS00432; ACTINS_2; PARTIAL.
CC PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
CC Structural protein; Multigene family.
KW NON_TER 13 13
FT SEQUENCE 13 AA; 1420 MW; 8BEFF3C6D4FD05A CRC64;
SQ
Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPL 7
Db 8 QPL 10
RESULT 11
CRBL_ICASP STANDARD; PRT; 13 AA.
ID -CRBL_ICASP
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotactic peptide (I-CP).
OS Icaria sp. (Rhopalidian wasp).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
CC Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RA (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
CC Mast cell degranulation; Chemotaxis; Amidation.
KW MOD_RES 13 13
FT SEQUENCE.

```

```

SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;
Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db |||
7 PLL 9

RESULT 12
LPAA_PORGI STANDARD; PRT; 13 AA.
AC P81411;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Lipid-A-associated protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]_
RP SEQUENCE.
RC STRAIN=W50;
RX MEDLINE=99061194; PubMed=9846737;
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
RA Curtis M., Henderson B., Tabona P.;
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
RT from the haemagglutinating domain of the RI protease gene family, is
RT a potent stimulator of interleukin 6 synthesis.";
RL Microbiology 144:3019-3026(1998).
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
CC CELL.
FT VARIANT 12 12 G -> F.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
Db |||
2 QGD 4

RESULT 13
ARCA_STRPS STANDARD; PRT; 15 AA.
AC P58827;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)
DE (Streptococcus acid glycoprotein) (Fragment).
GN ARCA OR SAGP.
OS Streptococcus pyogenes (serotype M5).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=160491;
RN [1]_
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=Manfredo / Serotype M5;
RX MEDLINE=98298018; PubMed=9632565;
RA Degnan B.A., Palmer J.M., Robson T., Jones C.B.D., Fischer M.,
RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;
RT "Inhibition of human peripheral blood mononuclear cell proliferation
RT by Streptococcus pyogenes cell extract is associated with arginine
RT deiminase activity";
RL Infect. Immun. 66:3050-3058(1998).

```

```

CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent
CC inhibitory effect on antigen, superantigen, or mitogen-stimulated
CC human peripheral blood mononuclear cell (PBMC) proliferation. It
CC may inhibit cell proliferation by arresting cell cycle and
CC inducing apoptosis.
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
DR HAMAP; MF_00242; -; 1.
KW Hydrolase; Arginine metabolism; Glycoprotein.
FT INIT_MET 0
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EB46 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
Db |||
3 QTP 5

RESULT 14
UC30_MAIZE STANDARD; PRT; 15 AA.
AC P80636;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 662)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 32.3 kDa.
DR Maize-2DPAGE; P80636; COLEOPTILE.
DR MaizeDB; 123961; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1545 MW; 3485190F4EF38018 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db |||
5 PLL 7

RESULT 15
PA21_TRIST STANDARD; PRT; 16 AA.
AC P82892;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-I) (PLA2-I)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).

```

OS Trimeresurus stejnegeri (Chinese green tree viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=39682;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Li S.Y., Wang W.Y., Xiong Y.L.;
 RT "Isolation, sequence and characterization of five variants of
 RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H₂O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
 CC SUBFAMILY.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR PROSITE: PS00119; PA2 ASP; PARTIAL.
 DR PROSITE: PS00118; PA2 HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 2012 MW; 4EF2D4959B981117 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LLQ 9
 Db 2 LLQ 4
 RESULT 16
 ACT6_SOYEN STANDARD; PRT; 17 AA.
 ID ACT6_SOYEN STANDARD; PRT; 17 AA.
 AC P15986;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin 6 (Fragment).
 GN SAG6.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Weagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5'
 RT untranslated leader: structural similarity to vertebrate muscle actin
 RT genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
 CC IN ALL EUKARYOTIC CELLS.
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
 CC -!- SIMILARITY: Belongs to the actin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X17119; CAA34979.1; -.
 DR DR
 DR PIR; S15754; S15754.
 DR InterPro: IPR004001; Actin.
 DR InterPro: IPR004000; Actin_like.
 DR Pfam: PF00022; actin; 1.
 DR PROSITE: PS00406; ACTINS_1; PARTIAL.
 DR PROSITE: PS00432; ACTINS_2; PARTIAL.
 DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 QPL 7
 Db 8 QPL 10
 RESULT 17
 B29K_PORGI STANDARD; PRT; 17 AA.
 ID B29K_PORGI STANDARD; PRT; 17 AA.
 AC P81784;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 29 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VEB 3547;
 RX MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RT "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis.";
 RL Vet. Microbiol. 73:37-49(2000).
 KW Antigen.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1756 MW; 383DE6AA14331AE0 CRC64;
 Query Match 17.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 QGD 17
 Db 14 QGD 16
 RESULT 18
 PSBL_SYNVU STANDARD; PRT; 17 AA.
 ID PSBL_SYNVU STANDARD; PRT; 17 AA.
 AC P12241;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)
 DE (Fragment).
 GN PSBL.
 OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
 OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
 OX NCBI_TaxID=32053;
 RN [1]
 RP SEQUENCE.

RA Ikeuchi M., Koike H., Inoue Y.;
 RT "Identification of psbI and psbL gene products in cyanobacterial
 RL photosystem II reaction center preparation.";
 CC PERS Lett. 231:155-160(1989).
 CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
 CC B559.
 CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
 DR PIR: S05033; S05033.
 DR InterPro: IPR003372; PSII_PsBL.
 DR Pfam: PF02419; PsbL; I.
 KW Photosynthesis; Photosystem II.
 FT NON TER 17
 FT 17
 SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14
 ||||
 Db 1 MEP 3

RESULT 19
 UC03_MAIZE
 ID_UC03_MAIZE STANDARD; PRT; 18 AA.
 AC P80609;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 146)
 DE (Fragments).
 DE Zea mays (Maize).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Coleoptile;
 RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
 RN Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 29.3 kDa.
 CC -!- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.
 DR Maize-2DPAGE; P80609; COLEOPTILE.
 DR MaizeDB; 123924; --
 FT NON_TER 1 1
 FT NON_CONS 9 10
 FT NON_TER 18 18
 FT 18
 SQ SEQUENCE 18 AA; 1938 MW; 6F513BBEC35881C0 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
 ||||
 Db 5 LLQ 7

RESULT 20
 AIBG_EQUAS
 ID_AIBG_EQUAS STANDARD; PRT; 20 AA.
 AC P39030;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-1B-glycoprotein (Alpha-1-B glycoprotein) (Postalbumin)
 DE (Fragment).

GN AIBG.
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Plasma;
 RX MEDLINE=91330579; PubMed=1868686;
 RA Patterson S.D., Bell K., Shaw D.C.;
 RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization
 RT and new alleles";
 RL Comp. Biochem. Physiol. 98B:523-528(1991).
 CC -!- FUNCTION: Unknown.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 KW Immunoglobulin domain; Glycoprotein; Plasma.
 FT NON_TER 20 20
 FT 20
 SQ SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 POP 6
 ||||
 Db 6 POP 8

RESULT 21
 APAL_ERYPA
 ID_APAL_ERYPA STANDARD; PRT; 20 AA.
 AC P18647;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apolipoprotein A-I (Apo-AI) (Fragment).
 DE APOA1
 GN APOA1
 OS Erythrocytus patas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheciniae; Erythrocybus.
 OX NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76184721; PubMed=178359;
 RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
 RT "Characterization of the plasma lipoproteins and apoproteins of the
 RT Erythrocybus patas monkey";
 RL Biochemistry 15:1928-1933(1976).
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 DR PIR; A05313; A05313.
 DR Plasma; Lipid transport; HDL; Cholesterol metabolism.
 KW NON TER 20 20
 FT 20
 SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
 ||||
 Db 5 QTP 7

RESULT 22

```

OMPW VIBAL
ID OMPW VIBAL STANDARD; PRT; 20 AA.
AC P83151;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)
DE (Fragment).
GN OMPW.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
RT alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: BELONGS TO THE OMPW/ALKL FAMILY.
KW Outer membrane.
FT NON TER 20
SQ SEQUENCE 20 AA; 2096 MW; D29EE7FCA16C0D37 CRC64;

Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
DB |||
3 QGD 5

RESULT 23
SCB1 CANFA
ID SCB1 CANFA STANDARD; PRT; 20 AA.
AC P99507;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial
DE (EC 6.2.1.5) (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP-
DE specific succinyl-CoA synthetase beta subunit) (fragment).
GN SUCLA2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA +
CC phosphate.
CC -!- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
CC ACID CYCLE.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
CC subunit family.
DR HSC-2DPAGE; P99507; DOG.
DR InterPro; IPR005809; CoA_lig_beta.
DR PROSITE; PS01217; SUCCINYL-CoA_Lig_3; PARTIAL.
KW Ligase; Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
FT NON TER 20
SQ SEQUENCE 20 AA; 2248 MW; BE9AEFD54BDBAC2E CRC64;

```

```

Query Match 17.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
DB |||
11 LLQ 13

RESULT 24
OCPI OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810C00000 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
DB |||
3 GD 4

RESULT 25
RM01 YEAST
ID RM01 YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR FIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON TER 4 4

```

```

SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
  Query Match 11.8%; Score 2; DB 1; Length 4;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
  ||
Db 3 TP 4

RESULT 26
ID UXA4 CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.,
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Siena-2DPAGE; P38005; -.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 5;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
  ||
Db 3 GD 4

RESULT 27
ACPH RABIT
ID ACPH RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (BC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
RN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase."
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.

```

```

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 ACETYLATION.
FT NON_TER 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 6;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QV 10
  ||
Db 4 QV 5

RESULT 28
VP19 HSV1K
ID VP19 HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly."
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M57646; AAA45830.1; -.
KW Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

  Query Match 11.8%; Score 2; DB 1; Length 6;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
  ||
Db 5 PL 6

RESULT 29
ALL3 CARMA
ID ALL3 CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

```

```

DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCB1_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 796 MW; 672879CDBC476B70 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 1 EP 2

RESULT 30
EI05_LITRU
ID EI05_LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCB1_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RA "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 3 EP 4

RESULT 31
FAR1_HELTI
ID FAR1_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCB1_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RA "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
Db 1 GD 2

RESULT 32
GFRP_MOUSE
ID GFRP_MOUSE STANDARD; PRT; 7 AA.
AC P99025;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN GCHFR OR GFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RA Submitted (AUG-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: MEDIATES TETRAHYDROBIOTRIN INHIBITION OF GTP
CC CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
DR SWISS-2DPAGE; P99025; MOUSE.
FT INIT MET 0
FT NON TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LL 8
Db 3 LL 4

RESULT 33
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;

```


| | | |
|-------------|--|--|
| DT | 01-JUN-1994 | (Rel. 29, Created) |
| DT | 01-JUN-1994 | (Rel. 29, Last sequence update) |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) |
| DE | Lanthibiotic carnocin U149 (Fragment). | |
| OS | Carnobacterium sp. (strain UI49). | |
| OC | Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae; | |
| CC | Carnobacterium. | |
| OK | NCBI_TaxID=35782; | |
| RN | {1} | |
| RP | SEQUENCE. | |
| FX | MEDLINE=92321768; PubMed=1622206; | |
| RA | Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H., | |
| EA | Nes I.P.; | |
| RT | "Purification and characterization of a new bacteriocin isolated from | |
| RT | a Carnobacterium sp."; | |
| RL | Appl. Environ. Microbiol. 58:1417-1422(1992). | |
| CC | -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC). | |
| CC | ACTIVE ON GRAM-POSITIVE BACTERIA. | |
| KW | Antibiotic; Bacteriocin; Lantibiotic. | |
| FT | NON_TER | 7 |
| SQ | SEQUENCE | 7 AA; 786 MW; 741776D05B05B810 CRC64; |
| | Query Match | 11.8%; Score 2; DB 1; Length 7; |
| | Best Local Similarity | 100.0%; Pred.No. 1.3e+05; |
| | Matches | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 5 QP 6 | |
| Dd | | |
| | 5 QP 6 | |
| | | |
| RESULT 34 | | |
| MNP1 LEPEDE | | |
| ID | _MNP1 LEPEDE | STANDARD; PRT; 7 AA. |
| AC | P42984; | |
| DT | 01-NOV-1995 | (Rel. 32, Created) |
| DT | 01-NOV-1995 | (Rel. 32, Last sequence update) |
| DT | 01-NOV-1995 | (Rel. 32, Last annotation update) |
| DE | Myotrophic neuropeptide 1 (led-MNP-I). | |
| OS | Leptinotarsa decemlineata (Colorado potato beetle). | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota; | |
| OC | Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; | |
| OC | Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae; | |
| CC | Chrysomelini; Leptinotarsa. | |
| OK | NCBI_TaxID=7539; | |
| RN | {1} | |
| RP | SEQUENCE, AND SYNTHESIS. | |
| RC | TISSUE=Head; | |
| RX | MEDLINE=95380343; PubMed=7651886; | |
| RA | Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S., | |
| RA | Grauwels L., van Leuven F., de Loof A.; | |
| RT | "Identification, characterization, and immunological localization of | |
| RT | a novel myotropic neuropeptide in the Colorado potato beetle, | |
| RT | Leptinotarsa decemlineata."; | |
| RL | Peptides 16:365-374(1995). | |
| CC | -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE | |
| CC | OVIDUCT. | |
| CC | Neuropeptide; Amidation. | |
| FT | MOD_RES | 7 |
| SQ | SEQUENCE | 7 AA; 705 MW; 6DD73768745B5DB0 CRC64; |
| | Query Match | 11.8%; Score 2; DB 1; Length 7; |
| | Best Local Similarity | 100.0%; Pred.No. 1.3e+05; |
| | Matches | 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 6 PL 7 | |
| Dd | | |
| | 5 PL 6 | |
| | | |
| RESULT 35 | | |
| PPH2 LYCES | | |
| ID | _PPH2 LYCES | STANDARD; PRT; 7 AA. |

```

RESULT 37
ACI_THUAL
ID ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415888;
RA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
  muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 933 MW; 6AA863733051F1B7 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
Db 7 GD 8

RESULT 38
AKHG_GRAYI
ID AKEG_GRAYI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
  of a peptide with adipokinetic activity from the corpora cardiaca of
  the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
  the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
  CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
  DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
  MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro; IPR002047; AKH.

```

```

DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QV 10
Db 1 QV 2

RESULT 39
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
  concentrating hormone family isolated and sequenced from a
  dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
  CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
  DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
  MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
Db 5 TP 6

RESULT 40
AKH_TABAT
ID AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
  (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]

```

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RCH FAMILY.
DR PR; A33995; A33995.
DR InterPro; IPRO02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 41
ALL6 CYDPO STANDARD; PRT; 8 AA.
ID -ALL6 CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PL 7
DB 2 PL 3

RESULT 42
COW2 CONPU STANDARD; PRT; 8 AA.
ID -COW2 CONPU STANDARD; PRT; 8 AA.
AC P88785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938889; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99 (1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 4 LL 5

RESULT 43
CPDI ENTFA
ID -CPDI ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPDI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPDI.";
RL Science 226:849-850 (1984).
CC -1- FUNCTION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPDI.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VM 11
DB 3 VM 4

RESULT 44
FARL PENMO STANDARD; PRT; 8 AA.
ID -FARL PENMO STANDARD; PRT; 8 AA.
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI (GDRNFLRP-amide).

```

OS Penaeus monodon (Peneid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]_
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaiyavithangkura P., Sithigorngul W., Petsom A.;
RA "Seven novel PMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 133B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)
CC -!- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
DB 1 GD 2

RESULT 45
HTF1_PERAM
ID HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach),
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]_
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RL bombardment mass spectrometry.";
RN Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]_
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]_
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RT beetle and the American cockroach are identical.";
```

```

Peptides 10:1287-1289(1989).
RL [4]_
RN SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grylloblatta portentosus, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A44960; A44960.
DR PIR; A49823; A49823.
DR PIR; S08995; S08995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QV 10
DB 1 QV 2

RESULT 46
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (Pea-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]_
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RL bombardment mass spectrometry.";
RN Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]_
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]_
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
```

```

RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RL beetle and the American cockroach are identical.";
RN Peptides 10:1287-1289(1989).
[4]
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrichosomic neuropeptides isolated from
RL the corpora cardiaca of the cockroaches Leucophaea maderae,
RX Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RL atom bombardment mass spectrometry.";
RC Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTRICHOSOMIC FACTORS ARE NEUROPEPTIDES THAT
RX ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
RL THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 47
LCK3 LEUMA
ID LCK3 LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin III (L.III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberiidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RL from Leucophaea maderae: members of a new family of
RX Cephalomyotropeptides."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -!- ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QG 16
DB 11

```

```

Db 2 QG 3

RESULT 48
LMT2 LOCMI
ID LMT2 LOCMI STANDARD; PRT; 8 AA.
AC P22356;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Casilifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RL additional neuropeptide of Locusta migratoria. Member of the
RX cephalomyotrophic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; PYROKININ.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 49
LPK LEUMA
ID LPK LEUMA STANDARD; PRT; 8 AA.
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberiidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RL leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RL neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS

```

```

CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPLR.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR, A23967; A23967.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QT 3
Db 1 QT 2

RESULT 50
NPB_BOVIN
ID_NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR, B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 4 QP 5

RESULT 51
UC26_MAIZE
ID_UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;

```

```

RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 2 EP 3

RESULT 52
UF06_MOUSE
ID_UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EP 14
Db 3 EP 4

RESULT 53
WP1_PERAT
ID_WP1_PERAT STANDARD; PRT; 8 AA.
AC P83195;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Wall protein-1 (PWP-1) (Fragment).
OS Perkinsus atlanticus.
CC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.
OX NCBI_TaxID=106964;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX MEDLINE=22044350; PubMed=12049410;
RA Montes J.F., Durfort M., Llado A., Garcia-Valero J.;

```

RT "Characterization and immunolocalization of a main proteinaceous
RT component of the cell wall of the protozoan parasite Perkinsus
RL atlanticus";
RL Parasitology 124:477-484(2002).
CC -!- FUNCTION: is a major protein component of the cell wall. May play
CC a key role in the organization of the cell wall and in promoting
CC the survival of this parasite.
CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
CC wall components.
CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
CC stages.
KW Cell wall.
FT NON_TER 8
SQ SEQUENCE 8 AA; 765 MW; F1787DD87B1AAB16 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ME 13
DB 1 ME 2

RESULT 54
BUK CLOPA STANDARD; PRT; 9 AA.
ID AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
CC phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetokinase family.
DR HAMAP; MF_00542; -, 1.
DR InterPro; IPR000890; Acetate kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 4 LL 5

RESULT 55
COW CONVE STANDARD; PRT; 9 AA.
ID AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT snail Conus ventricosus.";
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GD 17
DB 1 GD 2

RESULT 56
COXE THUOB STANDARD; PRT; 9 AA.
ID AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

```

Query Match      11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 3 QP 4

RESULT 57
DSIP_RABIT STANDARD; PRT; 9 AA.
AC P01158;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Delta sleep-inducing peptide (DSIP).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=77185324; PubMed=862769;
RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA Schoenenberger G.A.;
RT "The delta sleep inducing peptide (DSIP). Comparative properties of
RT the original and synthetic nonapeptide."
RL Experientia 33:548-552(1977).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=79054421; PubMed=568769;
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
RT analysis, sequence, synthesis and activity of the nonapeptide."
RL Pflugers Arch. 376:119-129(1978).
RN [3]
RP REVIEW.
RX MEDLINE=87175129; PubMed=3550726;
RA Graf M.V., Kastin A.J.;
RT "Delta-sleep-inducing peptide (DSIP): an update."
RL Peptides 7:1165-1187(1986).
CC -!- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
CC REDUCED MOTOR ACTIVITIES.
CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
CC STIMULATION OF THE THALAMUS.
CC -!- DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 8 of March 2001;
CC WWW="http://www.expasy.org/spotlight/articles/splt008.html".
DR PIR; A01422; QDRB.
SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

Query Match      11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GD 17
Db 4 GD 5

RESULT 58
FAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

```

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfield J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match      11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
Db 1 TP 2

RESULT 59
FAR3_PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match      11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 2 QP 3

RESULT 60
FAR4_PENMO STANDARD; PRT; 9 AA.

```



```

AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQFSMRURF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qp 6
Db 2 Qp 3

RESULT 61
FAR9 ASCSU
ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide Af9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
Db 6 PL 7

RESULT 62
FARA CALVO
ID FARA_CALVO STANDARD; PRT; 9 AA.

```

```

AC P41865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 10.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A44787; A44787.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
FT UNSURE 1 1 OR S OR A.
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4
Db 1 TP 2

RESULT 63
FRF1 SARBU
ID FRF1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 5 QP 6
DB 1 QP 2

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 64
KML3_BOMVA
ID KNL3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA "Cloning and post-translational processing of frog skin kininogens.";
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TP 4
DB 6 TP 7

RESULT 65
LMT3_LOCM1
ID LMT3 LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9
FT AVIATION 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TP 4
DB 7 TP 8

RESULT 67
OXYA_SQUAC
ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
```

```

RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
RL isolated from a cartilaginous fish, Squalus acanthias.";
RN Eur. J. Biochem. 29:12-19(1972).
RP [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
FT SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
   ||
Db 7 PL 8

RESULT 68
OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus).
OS Balaeoptera phyllus (finback whale), (Common rorqual),
OS Tachyglossus aculeatus aculeatus (Australian echidna), and
OS Hydroglossus collieri (spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit; PubMed=5150741;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RL principles from rabbits and rats.";
RN Biochimie 53:1099-1104(1971).
RP [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RL neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. phyalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A. aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;

```

```

RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H. colliei;
RX MEDLINE=7008110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holocephalian
RT elasmobranch fish, Hydrolagus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A91466; A91466.
DR PIR: A92774; A92774.
DR PIR: A93147; A93147.
DR PIR: A93408; A93408.
DR PIR: B90667; B90667.
DR PDB: 1XY1; 15-OCT-90.
DR PDB: 1XY2; 15-OCT-90.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD RES 9
FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PL 7
   ||
Db 7 PL 8

RESULT 69
PPH1_LYCES STANDARD; PRT; 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LeSAP1 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RL esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1005 MW; 3F17C04B5042CAA8 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;

```

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 16 GD 17
DB 2 GD 3

RESULT 70
RE42 LITRU
ID RE42 LITRU STANDARD; PRT; 9 AA.
AC P82075; P82093;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.2/4.3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=104895;
RN [1]
RN SEQUENCE AND MASS SPECTROMETRY.
RP TISSUE=SKIN SECRETION.
RC TISSUE=SKIN SECRETION.
RA Steinborner S.H., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RN [2]
RN SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
RN [1]
RN FUNCTION: Shows neither neuropeptide activity nor antibiotic
RN activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
CC terminal amidation.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 9
FT SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 3 LL 4

RESULT 71
TALL PICJA
ID TALL PICJA STANDARD; PRT; 9 AA.
AC P17440;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase I (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OC NCBI_TaxID=4903;
RN [1]
RN SEQUENCE.
MEDLINE=75145197; PubMed=1092268;
Tsolas O., Sun S.C.;
"Isolation of a peptide containing a histidyl-cysteinyl sequence
from the active center of transaldolase.";
Arch. Biochem. Biophys. 167:525-533(1975).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
FT SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 8 LL 9

RESULT 73

```

```

Sun S.C., Joris L., Tsolas O.;
"Purification of crystallization of transaldolase isozyme I and
evidence for different genetic origin of isozymes I and III in
Candida utilis.";
Arch. Biochem. Biophys. 178:69-78(1977).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
PIR; A12872; A12872.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
FT SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 8 LL 9

RESULT 72
TAL3 PICJA
ID TAL3 PICJA STANDARD; PRT; 9 AA.
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Pichia jadinii (Yeast) (Candida utilis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OC NCBI_TaxID=4903;
RN [1]
RN SEQUENCE.
MEDLINE=75145197; PubMed=1092268;
Tsolas O., Sun S.C.;
"Isolation of a peptide containing a histidyl-cysteinyl sequence
from the active center of transaldolase.";
Arch. Biochem. Biophys. 167:525-533(1975).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
FT NON_TER 9
FT SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LL 8
DB 8 LL 9

RESULT 73

```

THYF PIG
ID -THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9821;
RN [1]
RN SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
CC PIR; A01523; YFPG.
DR Pyrrolidone carboxylic acid.
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QG 16
DB 5 QG 6

RESULT 74
UF02 MOUSE STANDARD; PRT; 9 AA.
AC P38670;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ME 13
DB 1 ME 2

RESULT 75
ULAD HUMAN STANDARD; PRT; 9 AA.
ID ULAD HUMAN
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RP TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
DR SWISS-2DPAGE; P31929; HUMAN.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 11.8%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QT 3
DB 5 QT 6

Search completed: November 25, 2003, 18:17:22
Job time : 9.22872 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 40.9628 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 17
Sequence: 1 LQTPQPLQLQVMEPOGD 17

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

| | | | |
|---------|----|-----|------------|
| Minimum | DB | seq | length: 3 |
| Maximum | DB | seq | length: 20 |

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23:*

- ```

1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp_mhc.*
8: sp.organelle.*
9: sp.phase.*
10: sp.plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vterbrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteria.*
17: sp_archaea.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | %     |       | Length | DB     | ID     | Description  |
|------------|-------|-------|-------|--------|--------|--------|--------------|
|            |       | Query | Match |        |        |        |              |
| 1          | 4     | 23.5  | 12    | 11     | Q8CG32 | Q8CG32 | rattus sp.   |
| 2          | 4     | 23.5  | 18    | 4      | Q16167 | Q16167 | homo sapien  |
| 3          | 4     | 23.5  | 18    | 5      | Q3TWM9 | Q3TWM9 | tetrahymena  |
| 4          | 4     | 23.5  | 19    | 4      | Q1W178 | Q1W178 | homo sapien  |
| 5          | 4     | 23.5  | 20    | 2      | Q46499 | Q46499 | desulfovibr  |
| 6          | 4     | 23.5  | 20    | 6      | Q3TR56 | Q3TR56 | sus scrofa   |
| 7          | 4     | 23.5  | 20    | 10     | Q9S8Y7 | Q9S8Y7 | sus scrofa   |
| 8          | 3     | 17.6  | 7     | 12     | Q9YQ10 | Q9YQ10 | transmissib  |
| 9          | 3     | 17.6  | 8     | 4      | Q15893 | Q15893 | homo sapien  |
| 10         | 3     | 17.6  | 8     | 5      | Q94623 | Q94623 | mandauca sex |
| 11         | 3     | 17.6  | 8     | 11     | Q8K327 | Q8K327 | mus musculus |
| 12         | 3     | 17.6  | 8     | 11     | Q99F40 | Q99F40 | mus musculus |
| 13         | 3     | 17.6  | 9     | 2      | Q47556 | Q47556 | escherichia  |
| 14         | 3     | 17.6  | 9     | 13     | Q8AYL5 | Q8AYL5 | carassius a  |
| 15         | 3     | 17.6  | 9     | 13     | Q8AUM7 | Q8AUM7 | carassius a  |
| 16         | 3     | 17.6  | 9     | 15     | Q85723 | Q85723 | simian sarc  |

```
90 Q9TWK1 mytilus edu
91 Q9CWK0 mytilus edu
92 Q9TR99 canis famil
93 Q9TRR1 oryctolagus
94 Q9T2R0 solanum tub
95 Q9CTJ7 mus musculu
96 Q9R2D2 mus musculu
97 Q9PRU6 gallus gall
98 Q9KDD5 bacillus ha
99 Q8VME2 pseudomonas
100 Q9UCR7 homo sapien

ALIGNMENTS
ID Q8CG32 PRELIMINARY; PRT; 12 AA.
AC Q8CG32;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE L-histidine decarboxylase (fragment).
GN HDC.
OS Eukarya sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198284; PubMed=8928792;
RA Hocker M., Zhang Z., Fenstermacher D.A., Tagerud S., Chulak M.,
RA Joseph D., Wang T.C.;
RT "Rat histidine decarboxylase promoter is regulated by gastrin through
RT a protein kinase C pathway."
RL Am. J. Physiol. 270:G619-G633(1996).
DR EMBL; S83368; AAN86715.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1515 MW; 8783953D28FB5B05 CRC64;

Query Match 23.5%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MWEP 14
Db 1 MWEP 4

RESULT 2
Q16167 PRELIMINARY; PRT; 18 AA.
AC Q16167;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Serum albumin (fragment).
GN SERUM ALBUMIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94294404; PubMed=8022807;
RA Madison J., Galliano M., Watkins S., Minchiotti L., Porta F.,
RA Rossi A., Putnam F.W.;
RT "Genetic variants of human serum albumin in Italy: point mutants and a
RT carboxyl-terminal variant."
RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).
DR EMBL; S70799; AAB31177.1; -.
FT NON_TER 1
```

```
SQ SEQUENCE 18 AA; 2089 MW; 2CCF6C5B0B08690B CRC64;

Query Match 23.5%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 12 LLQV 15

RESULT 3
Q9TWM9 PRELIMINARY; PRT; 18 AA.
AC Q9TWM9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE NKTAG antigen (fragment).
OS Tetrahymena pyriformis.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=94323706; PubMed=7519359;
RA Leary J.H.3rd, Evans D.L., Jaso-Friedmann L.;
RT "Partial amino acid sequence of a novel protozoan parasite antigen
RT that inhibits non-specific cytotoxic cell activity."
RL Scand. J. Immunol. 40:158-164(1994).
SQ SEQUENCE 18 AA; 2082 MW; 13BCB737B1FF92A3 CRC64;

Query Match 23.5%; Score 4; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17
Db 9 PQGD 12

RESULT 4
Q8IWT8 PRELIMINARY; PRT; 19 AA.
AC Q8IWT8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aspecific BCL2 ARE-binding protein 2 (fragment).
GN ASBAP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Donini M., Schiavone N., Lapucci A., Papucci L., Witort E.,
RA Capaccioli S.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY140907; AAN25598.1; -.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2324 MW; 9352F39D59FC642D CRC64;

Query Match 23.5%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 14 LLQV 17
```

```

RESULT 5
Q46499
ID Q46499 PRELIMINARY; PRT; 20 AA.
AC Q46499;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Periplasmic (Fragment).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=M6;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49192; AAA91808.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D26C22999B CRC64;

Query Match 23.5%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
DB 10 PQPL 13

RESULT 6
Q9TR56
ID Q9TR56 PRELIMINARY; PRT; 20 AA.
AC Q9TR56;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE TAUROCHENOXYCHOLIC acid 6 alpha-hydroxylase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95377322; PubMed=7649186;
RA Araya Z., Hellman U., Hansson R.;
RT "Characterisation of taurochenodeoxycholic acid 6 alpha-hydroxylase
RT from pig liver microsomes."
RL Eur. J. Biochem. 231:855-861(1995).
SQ SEQUENCE 20 AA; 1893 MW; F12628269D54D8D CRC64;

Query Match 23.5%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
DB 11 LLQV 14

RESULT 7
Q9S8Y7
ID Q9S8Y7 PRELIMINARY; PRT; 20 AA.
AC Q9S8Y7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 2S storage albumin large subunit (Fragment).
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.

```

```

OX NCBI_TaxID=3726;
RN [1]_
RP SEQUENCE.
RX MEDLINE=92348373; PubMed=1639777;
RA Terras F.R., Schoofs H.M., De Boile M.F., van Leuven F., Rees S.B.,
RA Vanderleyden J., Cammue B.P., Broekaert W.F.;
RT "Analysis of two novel classes of plant antifungal proteins from
RT radish (Raphanus sativus L.) seeds."
RL J. Biol. Chem. 267:15301-15309(1992).
SQ SEQUENCE 20 AA; 2276 MW; DCB4B3960A1960B7 CRC64;

Query Match 23.5%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
DB 9 PLLQ 12

RESULT 8
Q9YQ10
ID Q9YQ10 PRELIMINARY; PRT; 7 AA.
AC Q9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=9909045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes."
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Rasschaert D., Lambert P., Levy L., Verde P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus."
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Rasschaert D., Gelfi J., Laude H.;
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression."
RL Biochimie 69:591-600(1987).
DR EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
DB 4 LLQ 6

RESULT 9
Q15893
ID Q15893 PRELIMINARY; PRT; 8 AA.
AC Q15893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```



```

DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQT 3
Db 5 LQT 7

RESULT 10
Q94623 PRELIMINARY; PRT; 8 AA.
ID Q94623
AC Q94623;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MSUP-2 protein (Fragment).
DE USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermis;
RX MEDLINE=97165493; PubMed=9013254;
RA Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
RT "Identification and mRNA developmental profiles of two ultraspiracle
RT isoforms in the epidermis and wings of Manduca sexta.";
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U57921; AAB64235.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 17.6%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEP 14
Db 1 MEP 3

RESULT 11
Q8K327 PRELIMINARY; PRT; 8 AA.
ID Q8K327
AC Q8K327;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE C-mer proto-oncogene (Fragment).
GN MER.
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22148657; PubMed=12153576;
RA Wong C.C.S., Lee W.M.;
RA "The proximal cis-acting elements Sp1, Sp3 and E2F regulate mouse mer
RT gene transcription in Sertoli cells.";
RL Eur. J. Biochem. 269:3789-3800(2002).
DR EMBL; AF517125; AAM77639.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 869 MW; FE2727376DD732C6 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8
Db 5 PLL 7

RESULT 12
Q99P40 PRELIMINARY; PRT; 8 AA.
ID Q99P40
AC Q99P40;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Repressor of GATA (Fragment).
DE ROG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RA Miao S., Ho I.;
RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-
RT Atc2/NF-Atc3 deficient Th cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335542; AAG59843.1; -.
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
Db 3 QTP 5

RESULT 13
Q47556 PRELIMINARY; PRT; 9 AA.
ID Q47556
AC Q47556;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Aspartate transcarbamoylase regulatory chain (Fragment).
GN PYRI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82275057; PubMed=7051000;
RA Pauza C.D., Karels M.J., Navre M., Schachman H.K.;

```

RT "Genes encoding Escherichia coli aspartate transcarbamoylase: The  
 RT pyrB-pyrI operon."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).  
 RN [2]  
 RP SEQUENCE OF 1-5 FROM N.A.  
 RX MEDLINE=83195078; PubMed=6302686;  
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,  
 RA Wild J.R.;  
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the  
 RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia  
 RT coli."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).  
 DR EMBL; J01670; AAA24475.1; -;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1085 MW; 99EFD723344AA1F1 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10  
 DB 7 LQV 9

RESULT 14  
 ID Q8AVL5 PRELIMINARY; PRT; 9 AA.  
 AC Q8AVL5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome P450 aromatase (Fragment).  
 GN CYP19A  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
 RT "Promoter characteristics of two CYP19 genes differentially expressed  
 RT in the brain and ovary of teleost fish."  
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
 DR EMBL; AF324897; AAN32618.1; -;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match 17.6%; Score 3; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9  
 DB 5 LLQ 7

RESULT 15  
 ID Q8AUM7 PRELIMINARY; PRT; 9 AA.  
 AC Q8AUM7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome P450 aromatase (Fragment).  
 GN CYP19A  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
 RT "Promoter characteristics of two CYP19 genes differentially expressed  
 RT in the brain and ovary of teleost fish."  
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
 DR EMBL; AF324895; AAN32616.1; -;  
 DR EMBL; AF324896; AAN32617.1; -;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 17.6%; Score 3; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9  
 DB 5 LLQ 7

RESULT 16  
 ID Q85723 PRELIMINARY; PRT; 9 AA.  
 AC Q85723;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE V-sis and p28-sis Genes (Fragment).  
 OS Simian sarcoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.  
 OX NCBI\_TaxID=11817;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84106822; PubMed=6319011;  
 RA Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;  
 RT "Expression of the PDGF-related transforming protein of simian sarcoma  
 RT virus in E. coli."  
 RL Cell 36:43-49(1984).  
 DR EMBL; K01473; AAA46816.1; -;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17  
 DB 6 QGD 8

RESULT 17  
 ID Q9R7J8 PRELIMINARY; PRT; 10 AA.  
 AC Q9R7J8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Vacuolating cytotoxin (Fragment).  
 GN VACA.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Helicobacteraceae; Helicobacter.  
 OX NCBI\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Kobe 500;  
 RA Shirasaka D.;  
 RT "Helicobacter pylori vacA gene, strain Kobe 500, partial cds."  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB017599; BAA33412.1; -;  
 FT NON TER 1  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1018 MW; 414390C76879CDD7 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQQ 16  
|||  
Db 7 PQQ 9

RESULT 18  
P83154 PRELIMINARY; PRT; 10 AA.  
ID P83154  
AC P83154; 20, Created)  
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).  
OS Anabaena sp. (strain 131).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
OX NCBI\_TaxID=29412;  
RN [1]  
RP SEQUENCE.  
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;  
RL Submitted (OCT-2001) to the SWISS-PROT data bank.  
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF  
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES  
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION  
CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN  
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN  
CC ORDER TO MEDATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.  
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS  
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT  
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM  
CC THE CORE.  
CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.  
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.  
KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1144 MW; 2F9B662B5B172737 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8  
|||  
Db 3 PLL 5

RESULT 19  
Q9H3R9 PRELIMINARY; PRT; 10 AA.  
ID Q9H3R9  
AC Q9H3R9;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Deoxyribonuclease II (Fragment).  
GN DNASE2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yasuda T.;  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB031422; BAB20386.1; -.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1067 MW; 3D5514DDD7272737 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8  
|||  
Db 3 PLL 5

RESULT 20  
Q9UJ48 PRELIMINARY; PRT; 10 AA.  
ID Q9UJ48  
AC Q9UJ48;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE latrophilin-2 (Fragment).  
GN LPHH1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA White G.R.M., Varley J.M., Heighway J.;  
RL Oncogene 17:3513-3519 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA White G.R.M., Varley J.M., Heighway J.;  
RT "Genomic structure and expression profile of LPHH1, a 7TM gene  
RT variably expressed in breast cancer cell lines.";  
RL Biochim. Biophys. Acta 1491:75-92(2000).  
DR EMBL; AJ244514; CAB60206.1; -.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9  
|||  
Db 7 LLQ 9

RESULT 21  
Q9QVK7 PRELIMINARY; PRT; 10 AA.  
ID Q9QVK7  
AC Q9QVK7; 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=91363409; PubMed=1888759;  
RA Flannery A.V., Macadam G.C., Beynon R.J.;  
RL "Immunological characterisation of different meprin species in mice.";  
RT Biochim. Biophys. Acta 1079:119-122(1991).  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1138 MW; FC01BFB5BAA866D1 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;

```
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QGD 17
Db 4 QGD 6

RESULT 22
Q8JLIS PRELIMINARY; PRT; 10 AA.
AC Q8JLIS;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MCLR (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=20090876; PubMed=10623832;
RA Adachi S., Morii E., Kim D.-k, Ogiwara H., Jippo T., Ito A., Lee Y.M.,
RA Kitamura Y.;
RT "Involvement of mi-transcription factor in expression of alpha-
RT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice.";
RL J. Immunol. 164:855-860(2000).
RW EMBL; AF176016; AAF37323.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 17.6%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15
Db 5 EPQ 7

RESULT 23
Q39957 PRELIMINARY; PRT; 10 AA.
AC Q39957;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]_TaxID=39839;
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B., Cuceanu N., Davidson F., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
RW EMBL; AF003175; AAC57986.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1067 MW; CC88FE2727273772 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
```

```
Db 4 PLL 6

RESULT 24
Q82625 PRELIMINARY; PRT; 10 AA.
AC Q82625;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Small ORF.
OS Infectious bursal disease virus (Gumboro virus).
OC Viruses; dsRNA viruses; Birnaviridae; Avibirnavirus.
OX NCBI_TaxID=10995;
RN [1]_TaxID=10995;
RP SEQUENCE FROM N.A.
RX MEDLINE=86259073; PubMed=3014441;
RA Hudson P.J., Mckern N.M., Power B.E., Azad A.A.;
RT "Genomic structure of the large RNA segment of infectious bursal
RT disease virus.";
RL Nucleic Acids Res. 14:5001-5012(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90016880; PubMed=2552417;
RA Spies U.;
RT "Nucleotide sequence of infectious bursal disease virus genome segment
RT A delineates two major open reading frames.";
RL Nucleic Acids Res. 17:7982-7982(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90278420; PubMed=2161902;
RA Bayliss C.D., Spies U., Shaw K., Peters R.W., Papageorgiou A.,
RA Muller H., Boursnell M.E.;
RT "A comparison of the sequences of segment A of four infectious bursal
RT disease virus strains and identification of a variable region in VP2.";
RL J. Gen. Virol. 71:1303-1312(1990).
RW EMBL; D00869; BAA00743.1; -.
DR EMBL; A33255; CAA02133.1; -.
SQ SEQUENCE 10 AA; 1316 MW; 58B57D16D7272727 CRC64;

Query Match 17.6%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ILQ 9
Db 5 ILQ 7

RESULT 25
Q75595 PRELIMINARY; PRT; 10 AA.
AC Q75595;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=T12B;
RA Lorentz E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RT "The TAT and C2-V3 Envelope Genes in the Molecular Epidemiology of
RT Human Immunodeficiency Virus-1.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RW EMBL; U57303; AAB17863.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;
```

```

Query Match 17.6%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEP 14
Db 1 MEP 3

RESULT 26
Q8X4E5 PRELIMINARY; PRT; 10 AA.
AC Q8X4E5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein z5903.
GN Z5903.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RW EMBL; AE005662; AAG59489.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 10 AA; 1161 MW; 98AC9BD2D6D7205A CRC64;

Query Match 17.6%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
Db 5 LQV 7

RESULT 27
Q48933 PRELIMINARY; PRT; 11 AA.
AC Q48933; P77701; Q48932;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alkyl hydroperoxide reductase C (Fragment).
GN AHPc.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35728, and ATCC35727;
RA Zhang Y., Detric V.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35735;
RX MEDLINE=96256622; PubMed=8655566;
RA Dhandayuthapani S., Zhang Y., Detric V.;
RT "Oxidative stress response and its role in sensitivity to isoniazid in
RT Mycobacteria: characterization and inducibility of ahpC by peroxides in
RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
```

```

RT tuberculosis".
RL J. Bacteriol. 178:3641-3649 (1996).
DR EMBL; U58031; AAB00320.1; -.
DR EMBL; U57979; AAA99830.1; -.
DR EMBL; U57978; AAA99829.1; -.
DR EMBL; U57762; AAB00317.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db 2 PLL 4

RESULT 28
Q9R7U8 PRELIMINARY; PRT; 11 AA.
AC Q9R7U8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNR protein (A regulatory protein for the expression of the Nir and
DE nor genes) (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95226457; PubMed=7711073;
RA Arai H., Igarashi Y., Kodama T.;
RT "The structural genes for nitric oxide reductase from Pseudomonas
RT aeruginosa.";
RL Biochim. Biophys. Acta 1261:279-284 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO1;
RX MEDLINE=95394152; PubMed=7664887;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of
RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76 (1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIQ 9
Db 2 LIQ 4

RESULT 29
Q44237 PRELIMINARY; PRT; 11 AA.
AC Q44237;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glutamine synthetase (Fragment).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
```

|           |                                                                   |                  |           |                                                                         |
|-----------|-------------------------------------------------------------------|------------------|-----------|-------------------------------------------------------------------------|
| RN        | (1)                                                               | NCBI_TaxID=9606; | OX        | NCBI_TaxID=9606;                                                        |
| RP        | SEQUENCE FROM N.A.                                                |                  | RN        | [1]                                                                     |
| RC        | STRAIN=PCC 7120;                                                  |                  | RP        | SEQUENCE FROM N.A.                                                      |
| RA        | Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;                |                  | RA        | Carri I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E., |
| RT        | "The apcf gene of Anabaena sp. strain PCC 7120 is regulated by    |                  | RA        | Meredith D.M.;                                                          |
| RL        | nitrogen and the apcf and glnA promoters overlap.";               |                  | RT        | "APC2 partial gene sequence.";                                          |
| RN        | Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.           |                  | RL        | Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.                 |
| RP        | (2)                                                               |                  | DR        | EMBL; AF110338; AAD29275.1; -                                           |
| RC        | STRAIN=PCC 7120;                                                  |                  | FT        | NON_TER 1                                                               |
| RA        | Scappino L.A.;                                                    |                  | FT        | NON_TER 11                                                              |
| RL        | Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.           |                  | SQ        | SEQUENCE 11 AA; 1326 MW; 75881D7B8441EAB4 CRC64;                        |
| DR        | EMBL; U21853; AAA65652.1; -                                       |                  |           | Query Match 17.6%; Score 3; DB 4; Length 11;                            |
| FT        | NON_TER 11                                                        |                  |           | Best Local Similarity 100.0%; Pred. No. 6.8e+03;                        |
| SQ        | SEQUENCE 11 AA; 1316 MW; 2000580E332CB06C7 CRC64;                 |                  |           | Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |
|           | Query Match 17.6%; Score 3; DB 2; Length 11;                      |                  |           |                                                                         |
|           | Best Local Similarity 100.0%; Pred. No. 6.8e+03;                  |                  |           |                                                                         |
|           | Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;        |                  |           |                                                                         |
| Qy        | 3 TPQ 5                                                           |                  | Qy        | 1 LQT 3                                                                 |
| Db        | 3 TPQ 5                                                           |                  | Db        | 9 LQT 11                                                                |
|           |                                                                   |                  |           |                                                                         |
| RESULT 30 |                                                                   |                  | RESULT 32 |                                                                         |
| Q56972    |                                                                   |                  | Q8TDA8    |                                                                         |
| ID        | Q56972 PRELIMINARY; PRT; 11 AA.                                   |                  | ID        | Q8TDA8 PRELIMINARY; PRT; 11 AA.                                         |
| AC        | Q56972;                                                           |                  | AC        | Q8TDA8;                                                                 |
| DT        | 01-NOV-1996 (TREMBLrel. 01, Created)                              |                  | DT        | 01-JUN-2002 (TREMBLrel. 21, Created)                                    |
| DT        | 01-NOV-1996 (TREMBLrel. 01, Last sequence update)                 |                  | DT        | 01-JUN-2002 (TREMBLrel. 21, Last sequence update)                       |
| DT        | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)               |                  | DT        | 01-JUN-2002 (TREMBLrel. 21, Last annotation update)                     |
| DE        | Lcrkb protein (Fragment).                                         |                  | DE        | Glutathione synthetase (Fragment).                                      |
| GN        | LCKRB.                                                            |                  | OS        | Homo sapiens (Human).                                                   |
| OS        | Yersinia pestis.                                                  |                  | OS        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;       |
| OG        | Plasmid Lcr.                                                      |                  | OC        | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.              |
| OC        | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; |                  | OC        | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.              |
| OC        | Enterobacteriaceae; Yersinia.                                     |                  | OX        | NCBI_TaxID=9606;                                                        |
| OX        | NCBI_TaxID=632;                                                   |                  | RN        | [1]                                                                     |
| RN        | (1) SEQUENCE FROM N.A.                                            |                  | RP        | SEQUENCE FROM N.A.                                                      |
| RC        | STRAIN=358;                                                       |                  | RA        | Cho Y.-W., Lee Y.-Y., Lim C.-J.;                                        |
| RX        | MEDLINE=92250432; PubMed=1577700;                                 |                  | RT        | "Cloning and characterization of glutathione synthetase gene from       |
| RA        | Rimpilainen M., Forsberg A., Wolf-Watz H.;                        |                  | RT        | human placenta DNA.";                                                   |
| RT        | "A novel protein LcrQ, involved in the low-calcium response of    |                  | RL        | Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.                 |
| RT        | Yersinia pseudotuberculosis shows extensive homology to YopH.";   |                  | DR        | EMBL; AF485789; AAL91591.1; -                                           |
| RL        | J. Bacteriol. 174:3355-3363 (1992).                               |                  | FT        | NON_TER 11                                                              |
| DR        | EMBL; X78303; CAA55113.1; -                                       |                  | FT        | NON_TER 11                                                              |
| KW        | Plasmid.                                                          |                  | SQ        | SEQUENCE 11 AA; 1235 MW; 1CE28D1E35B86374 CRC64;                        |
| FT        | NON_TER 11                                                        |                  |           | Query Match 17.6%; Score 3; DB 4; Length 11;                            |
| FT        | NON_TER 11                                                        |                  |           | Best Local Similarity 100.0%; Pred. No. 6.8e+03;                        |
| SQ        | SEQUENCE 11 AA; 1377 MW; 0478BFEC1A04B54 CRC64;                   |                  |           | Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |
|           | Query Match 17.6%; Score 3; DB 2; Length 11;                      |                  |           |                                                                         |
|           | Best Local Similarity 100.0%; Pred. No. 6.8e+03;                  |                  |           |                                                                         |
|           | Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;        |                  |           |                                                                         |
| Qy        | 11 MME 13                                                         |                  | Qy        | 7 LLQ 9                                                                 |
| Db        | 1 MME 3                                                           |                  | Db        | 8 LLQ 10                                                                |
|           |                                                                   |                  |           |                                                                         |
| RESULT 31 |                                                                   |                  | RESULT 33 |                                                                         |
| Q9UNL8    |                                                                   |                  | Q9UCR1    |                                                                         |
| ID        | Q9UNL8 PRELIMINARY; PRT; 11 AA.                                   |                  | ID        | Q9UCR1 PRELIMINARY; PRT; 11 AA.                                         |
| AC        | Q9UNL8;                                                           |                  | AC        | Q9UCR1;                                                                 |
| DT        | 01-MAY-2000 (TREMBLrel. 13, Created)                              |                  | DT        | 01-MAY-2000 (TREMBLrel. 13, Created)                                    |
| DT        | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                 |                  | DT        | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                       |
| DT        | 01-MAY-2000 (TREMBLrel. 13, Last annotation update)               |                  | DT        | 01-JUN-2002 (TREMBLrel. 21, Last annotation update)                     |
| DE        | APC2 protein (Fragment).                                          |                  | DE        | AUTOTAXIN (Fragment).                                                   |
| GN        | Homo sapiens (Human).                                             |                  | OS        | Homo sapiens (Human).                                                   |
| OS        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                  | OS        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;       |
| OC        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                  | OC        | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.              |
| OC        | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |                  | OX        | NCBI_TaxID=9606;                                                        |
|           |                                                                   |                  | RN        | [1]                                                                     |
|           |                                                                   |                  | RP        | SEQUENCE.                                                               |
|           |                                                                   |                  | RX        | MEDLINE=92129337; PubMed=1733949;                                       |
|           |                                                                   |                  | RA        | Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,       |
|           |                                                                   |                  | RA        | Schiffmann E., Liotta L.A.;                                             |
|           |                                                                   |                  | RT        | "Identification, purification, and partial sequence analysis of         |
|           |                                                                   |                  | RT        | autotaxin, a novel motility-stimulating protein.";                      |
|           |                                                                   |                  | RL        | J. Biol. Chem. 267:2524-2529 (1992).                                    |
|           |                                                                   |                  | FT        | NON_TER 1                                                               |

FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;  
Query Match 17.6%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QPL 7  
Db 3 QPL 5  
RESULT 34  
Q81VG8 PRELIMINARY; PRT; 11 AA.  
ID Q81VG8  
AC Q81VG8  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Low density lipoprotein receptor related protein 1 (Fragment).  
GN LRP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Schulz S., Schagdarsurenjin U., Greiser P., Birkenmeier G.,  
RA Muller-Werdan U., Hagemann M., Riemann D., Werdan K., Glaser C.;  
RT "The LDL receptor-related protein (LRP1/A2MR) and coronary  
RT atherosclerosis - novel genomic variants and functional  
RT consequences.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y18524; CAD57169.1; -.  
KW Receptor; Lipoprotein.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;  
Query Match 17.6%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PLL 8  
Db 5 PLL 7  
RESULT 35  
P83168 PRELIMINARY; PRT; 11 AA.  
ID P83168  
AC P83168  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Alpha-2-antiplasmin (Alpha-2-plasmin inhibitor) (Alpha-2-  
DE AP) (Fragment).  
OS Struthio camelus (Ostrich).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;  
OC Struthio.  
OX NCBI\_TaxID=8801;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Plasma;  
RX MEDLINE=21328857; PubMed=11435135;  
RA Thomas A.R., Naude R.J., Oelofsen W., Naganuma T., Muramoto K.;  
RT "Purification and partial characterisation of alpha(2)-antiplasmin and  
RT plasmin(ogen) from ostrich plasma.";  
RL Comp. Biochem. Physiol. 129B:809-820(2001).  
CC -!- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND  
CC TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

KW Serpin; Serine protease inhibitor.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1261 MW; 9B08C06B32C73B5A CRC64;  
Query Match 17.6%; Score 3; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 LQV 10  
Db 1 LQV 3  
RESULT 36  
Q8ADI8 PRELIMINARY; PRT; 11 AA.  
ID Q8ADI8  
AC Q8ADI8  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Truncated vif protein.  
GN VIF.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=98UG57135;  
RX MEDLINE=22375625; PubMed=12487816;  
RA Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,  
RA Kigozi G., Kwanuka N., Phillips J.B., Meehan M., Lutalo T.,  
RA Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,  
RA McCutchan F.E.;  
RT "Among 46 Near Full Length HIV Type 1 Genome Sequences from Rakai  
RT District, Uganda, Subtype D and AD Recombinants Predominate.";  
RL AIDS Res. Hum. Retroviruses 18:1281-1290(2002).  
DR EMBL; AF484508; AAN73711.1; -.  
SQ SEQUENCE 11 AA; 1492 MW; 75C18E6F82D6C364 CRC64;  
Query Match 17.6%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 QVM 11  
Db 6 QVM 8  
RESULT 37  
Q9SPT5 PRELIMINARY; PRT; 12 AA.  
ID Q9SPT5  
AC Q9SPT5  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Topoisomerase II (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20023730; PubMed=10561074;  
RA Reddy M.K., Nair S., Tewari K.K., Mudgil Y., Yadav B.S., Sopory S.K.;  
RT "Cloning and characterization of a cDNA encoding topoisomerase II in  
RT pea and analysis of its expression in relation to cell  
RT proliferation.";  
RL Plant Mol. Biol. 41:125-137(1999).  
DR EMBL; AF144649; AAD30165.1; -.  
KW Isomerase.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1346 MW; 2A1F261B98B6D737 CRC64;

|                       |                                                                       |              |                    |        |                                 |  |  |  |  |
|-----------------------|-----------------------------------------------------------------------|--------------|--------------------|--------|---------------------------------|--|--|--|--|
| Query Match           |                                                                       | 17.6%;       | Score 3;           | DB 10; | Length 12;                      |  |  |  |  |
| Best Local Similarity |                                                                       | 100.0%;      | Pred. No. 7.4e+03; |        |                                 |  |  |  |  |
| Matches               |                                                                       | 3;           | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |
| QY                    | 1 LQT 3                                                               |              |                    |        |                                 |  |  |  |  |
|                       |                                                                       |              |                    |        |                                 |  |  |  |  |
| Db                    | 6 LQT 8                                                               |              |                    |        |                                 |  |  |  |  |
| RESULT 38             |                                                                       |              |                    |        |                                 |  |  |  |  |
| P82328                |                                                                       |              |                    |        |                                 |  |  |  |  |
| ID                    | P82328                                                                | PRELIMINARY; | PRT;               | 12 AA. |                                 |  |  |  |  |
| AC                    | P82328;                                                               |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2000 (TrEMBLrel. 14, Created)                                  |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)                     |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)                   |              |                    |        |                                 |  |  |  |  |
| DE                    | Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment). |              |                    |        |                                 |  |  |  |  |
| OS                    | Pisum sativum (Garden pea).                                           |              |                    |        |                                 |  |  |  |  |
| OC                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;    |              |                    |        |                                 |  |  |  |  |
| OC                    | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; |              |                    |        |                                 |  |  |  |  |
| OC                    | eurosid I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.          |              |                    |        |                                 |  |  |  |  |
| OX                    | NCBI_TaxID=3888;                                                      |              |                    |        |                                 |  |  |  |  |
| RN                    | [1]                                                                   |              |                    |        |                                 |  |  |  |  |
| RP                    | SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.              |              |                    |        |                                 |  |  |  |  |
| RC                    | STRAIN=cv. DE GRACE; TISSUE=LEAF;                                     |              |                    |        |                                 |  |  |  |  |
| RX                    | MEDLINE=20181728; PubMed=10715320;                                    |              |                    |        |                                 |  |  |  |  |
| RA                    | Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,      |              |                    |        |                                 |  |  |  |  |
| RA                    | Adamska I., van Wijk K.J.;                                            |              |                    |        |                                 |  |  |  |  |
| RT                    | "Proteomics of the chloroplast: systematic identification and         |              |                    |        |                                 |  |  |  |  |
| RT                    | targeting analysis of luminal and peripheral thylakoid proteins.";    |              |                    |        |                                 |  |  |  |  |
| RL                    | Plant Cell 12:319-341(2000).                                          |              |                    |        |                                 |  |  |  |  |
| CC                    | -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.       |              |                    |        |                                 |  |  |  |  |
| CC                    | -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.         |              |                    |        |                                 |  |  |  |  |
| CC                    | -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN    |              |                    |        |                                 |  |  |  |  |
| CC                    | PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.                                 |              |                    |        |                                 |  |  |  |  |
| KW                    | Chloroplast; Thylakoid membrane.                                      |              |                    |        |                                 |  |  |  |  |
| FT                    | NON TER 12 12                                                         |              |                    |        |                                 |  |  |  |  |
| SQ                    | SEQUENCE 12 AA; 1264 MW; 96691CBC663B1B01 CRC64;                      |              |                    |        |                                 |  |  |  |  |
| Query Match           |                                                                       |              |                    |        |                                 |  |  |  |  |
| Best Local Similarity |                                                                       | 17.6%;       | Score 3;           | DB 10; | Length 12;                      |  |  |  |  |
| Matches               |                                                                       | 3;           | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |
| QY                    | 6 PLL 8                                                               |              |                    |        |                                 |  |  |  |  |
|                       |                                                                       |              |                    |        |                                 |  |  |  |  |
| Db                    | 10 PLL 12                                                             |              |                    |        |                                 |  |  |  |  |
| RESULT 39             |                                                                       |              |                    |        |                                 |  |  |  |  |
| Q9EQV3                |                                                                       |              |                    |        |                                 |  |  |  |  |
| ID                    | Q9EQV3                                                                | PRELIMINARY; | PRT;               | 12 AA. |                                 |  |  |  |  |
| AC                    | Q9EQV3;                                                               |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-MAR-2001 (TrEMBLrel. 16, Created)                                  |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)                     |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)                   |              |                    |        |                                 |  |  |  |  |
| DE                    | Alpha-sarcoglycan (Fragment).                                         |              |                    |        |                                 |  |  |  |  |
| GN                    | SGCA.                                                                 |              |                    |        |                                 |  |  |  |  |
| OS                    | Mus musculus (Mouse).                                                 |              |                    |        |                                 |  |  |  |  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |              |                    |        |                                 |  |  |  |  |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |              |                    |        |                                 |  |  |  |  |
| OX                    | NCBI_TaxID=10090;                                                     |              |                    |        |                                 |  |  |  |  |
| RN                    | [1]                                                                   |              |                    |        |                                 |  |  |  |  |
| RP                    | SEQUENCE FROM N.A.                                                    |              |                    |        |                                 |  |  |  |  |
| RC                    | TISSUE=Liver;                                                         |              |                    |        |                                 |  |  |  |  |
| RX                    | MEDLINE=21099368; PubMed=11179961;                                    |              |                    |        |                                 |  |  |  |  |
| RA                    | Wakabayashi-Takai E., Noguchi S., Ozawa E.;                           |              |                    |        |                                 |  |  |  |  |
| RT                    | "Identification of myogenesis-dependent transcriptional enhancers in  |              |                    |        |                                 |  |  |  |  |
| RT                    | promoter region of mouse gamma-sarcoglycan gene.";                    |              |                    |        |                                 |  |  |  |  |
| RL                    | Eur. J. Biochem. 268:948-957(2001).                                   |              |                    |        |                                 |  |  |  |  |
| DR                    | EMBL; AB044625; BAB18770.1; -.                                        |              |                    |        |                                 |  |  |  |  |
| FT                    | NON TER 12 12                                                         |              |                    |        |                                 |  |  |  |  |
| SQ                    | SEQUENCE 12 AA; 1257 MW; D382726D594361B2 CRC64;                      |              |                    |        |                                 |  |  |  |  |
| Query Match           |                                                                       |              |                    |        |                                 |  |  |  |  |
| Best Local Similarity |                                                                       | 17.6%;       | Score 3;           | DB 11; | Length 12;                      |  |  |  |  |
| Matches               |                                                                       | 3;           | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |
| QY                    | 6 PLL 8                                                               |              |                    |        |                                 |  |  |  |  |
|                       |                                                                       |              |                    |        |                                 |  |  |  |  |
| Db                    | 9 PLL 11                                                              |              |                    |        |                                 |  |  |  |  |
| RESULT 40             |                                                                       |              |                    |        |                                 |  |  |  |  |
| Q8QDY5                |                                                                       |              |                    |        |                                 |  |  |  |  |
| ID                    | Q8QDY5                                                                | PRELIMINARY; | PRT;               | 12 AA. |                                 |  |  |  |  |
| AC                    | Q8QDY5;                                                               |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2002 (TrEMBLrel. 21, Created)                                  |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)                     |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)                   |              |                    |        |                                 |  |  |  |  |
| DE                    | Vif protein (Fragment).                                               |              |                    |        |                                 |  |  |  |  |
| GN                    | VIF.                                                                  |              |                    |        |                                 |  |  |  |  |
| OS                    | Human immunodeficiency virus 1.                                       |              |                    |        |                                 |  |  |  |  |
| OC                    | Viruses; Retroid viruses; Retroviridae; Lentivirus.                   |              |                    |        |                                 |  |  |  |  |
| OC                    | NCBI_TaxID=11676;                                                     |              |                    |        |                                 |  |  |  |  |
| RN                    | [1]                                                                   |              |                    |        |                                 |  |  |  |  |
| RP                    | SEQUENCE FROM N.A.                                                    |              |                    |        |                                 |  |  |  |  |
| RC                    | STRAIN=98UA0116;                                                      |              |                    |        |                                 |  |  |  |  |
| RA                    | Masharsky A.E., Eremin V.F., Kozlov A.P.;                             |              |                    |        |                                 |  |  |  |  |
| RT                    | "Molecular cloning and analysis of full-length human immunodeficiency |              |                    |        |                                 |  |  |  |  |
| RT                    | virus type 1 genomes of prevalent strains among IDUs in countries of  |              |                    |        |                                 |  |  |  |  |
| RT                    | the FSU.";                                                            |              |                    |        |                                 |  |  |  |  |
| RL                    | Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.               |              |                    |        |                                 |  |  |  |  |
| DR                    | EMBL; AF413969; AAL78396.1; -.                                        |              |                    |        |                                 |  |  |  |  |
| FT                    | NON_TER 12 12                                                         |              |                    |        |                                 |  |  |  |  |
| SQ                    | SEQUENCE 12 AA; 1648 MW; 28D5C18B6F82D6C3 CRC64;                      |              |                    |        |                                 |  |  |  |  |
| Query Match           |                                                                       |              |                    |        |                                 |  |  |  |  |
| Best Local Similarity |                                                                       | 17.6%;       | Score 3;           | DB 15; | Length 12;                      |  |  |  |  |
| Matches               |                                                                       | 3;           | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |
| QY                    | 9 QVM 11                                                              |              |                    |        |                                 |  |  |  |  |
|                       |                                                                       |              |                    |        |                                 |  |  |  |  |
| Db                    | 6 QVM 8                                                               |              |                    |        |                                 |  |  |  |  |
| RESULT 41             |                                                                       |              |                    |        |                                 |  |  |  |  |
| Q8QE47                |                                                                       |              |                    |        |                                 |  |  |  |  |
| ID                    | Q8QE47                                                                | PRELIMINARY; | PRT;               | 12 AA. |                                 |  |  |  |  |
| AC                    | Q8QE47;                                                               |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2002 (TrEMBLrel. 21, Created)                                  |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)                     |              |                    |        |                                 |  |  |  |  |
| DT                    | 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)                   |              |                    |        |                                 |  |  |  |  |
| DE                    | Vif protein (Fragment).                                               |              |                    |        |                                 |  |  |  |  |
| GN                    | VIF.                                                                  |              |                    |        |                                 |  |  |  |  |
| OS                    | Human immunodeficiency virus 1.                                       |              |                    |        |                                 |  |  |  |  |
| OC                    | Viruses; Retroid viruses; Retroviridae; Lentivirus.                   |              |                    |        |                                 |  |  |  |  |
| OC                    | NCBI_TaxID=11676;                                                     |              |                    |        |                                 |  |  |  |  |
| RN                    | [1]                                                                   |              |                    |        |                                 |  |  |  |  |
| RP                    | SEQUENCE FROM N.A.                                                    |              |                    |        |                                 |  |  |  |  |
| RC                    | STRAIN=98UA0116;                                                      |              |                    |        |                                 |  |  |  |  |
| RA                    | Masharsky A.E., Eremin V.F., Kozlov A.P.;                             |              |                    |        |                                 |  |  |  |  |
| RT                    | "Molecular cloning and analysis of full-length human immunodeficiency |              |                    |        |                                 |  |  |  |  |
| RT                    | virus type 1 genomes of prevalent strains among IDUs in countries of  |              |                    |        |                                 |  |  |  |  |
| RT                    | the FSU.";                                                            |              |                    |        |                                 |  |  |  |  |
| RL                    | Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.               |              |                    |        |                                 |  |  |  |  |
| DR                    | EMBL; AF413969; AAL78396.1; -.                                        |              |                    |        |                                 |  |  |  |  |
| FT                    | NON_TER 12 12                                                         |              |                    |        |                                 |  |  |  |  |
| SQ                    | SEQUENCE 12 AA; 1648 MW; 28D5C18B6F82D6C3 CRC64;                      |              |                    |        |                                 |  |  |  |  |
| Query Match           |                                                                       |              |                    |        |                                 |  |  |  |  |
| Best Local Similarity |                                                                       | 17.6%;       | Score 3;           | DB 15; | Length 12;                      |  |  |  |  |
| Matches               |                                                                       | 3;           | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |  |  |  |  |
| QY                    | 9 QVM 11                                                              |              |                    |        |                                 |  |  |  |  |
|                       |                                                                       |              |                    |        |                                 |  |  |  |  |



```
Db 6 QVM 8

RESULT 42
Q8QDY4
ID Q8QDY4 PRELIMINARY; PRT; 12 AA.
AC Q8QDY4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413999; AAL78469.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
Db |||
6 QVM 8

RESULT 43
Q8QE41
ID Q8QE41 PRELIMINARY; PRT; 12 AA.
AC Q8QE41;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413972; AAL78402.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
Db |||
6 QVM 8

RESULT 44
Q8QE45
ID Q8QE45 PRELIMINARY; PRT; 12 AA.
AC Q8QE45;
```

```
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413970; AAL78398.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
Db |||
6 QVM 8

RESULT 45
Q8QE43
ID Q8QE43 PRELIMINARY; PRT; 12 AA.
AC Q8QE43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RC STRAIN=98UA0116;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF413971; AAL78400.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
Db |||
6 QVM 8

RESULT 46
Q8QDY6
ID Q8QDY6 PRELIMINARY; PRT; 12 AA.
AC Q8QDY6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Fragment).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
```

```

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98BY10443;
RA Masharsky A.E., Eremin V.F., Kozlov A.P.;
RT "Molecular cloning and analysis of full-length human immunodeficiency
RT virus type 1 genomes of prevalent strains among IDUs in countries of
RT the FSU.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF4113997; AAL78465.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1620 MW; 2A05C18E6F82D6C3 CRC64;

Query Match 17.6%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QVM 11
Db [1]
6 QVM 8

RESULT 47
Q9UEE2 PRELIMINARY; PRT; 13 AA.
AC Q9UEE2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ERGB transcription factor (Fragment).
GN FL11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RT "Molecular analysis on the breakpoint region of a t(11;22)
RT translocation in Ewing's sarcoma.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012625; BAA32806.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQP 6
Db [1]
4 PQP 6

RESULT 48
Q14182 PRELIMINARY; PRT; 13 AA.
AC Q14182;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
GN DNTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87213162; PubMed=3579900;
RA Koiwai O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA

```

```

RT expressible in mammalian cells.";
RL Biochem. Biophys. Res. Commun. 144:185-190 (1987).
DR EMBL; M26144; AAA74588.1; -.
KW Transference. 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPL 7
Db [1]
8 QPL 10

RESULT 49
Q9UPB6 PRELIMINARY; PRT; 13 AA.
AC Q9UPB6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Multiple inositol polyphosphate phosphatase (Fragment).
GN MIPP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99189241; PubMed=10087200;
RA Chi H., Tiller G.E., Dasouki M.J., Romano P.R., Wang J., O'Keefe R.J.,
RA Puzas J.E., Rosier R.N., Reynolds P.R.;
RT "Multiple inositol polyphosphate phosphatase: evolution as a distinct
RT group within the histidine phosphatase family and chromosomal
RT localization of the human and mouse genes to chromosomes 10q23 and
RT 19.";
RL Genomics 56:324-336 (1999).
DR EMBL; AF046915; AAD02438.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1325 MW; C7DF7B7BF157D772 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
Db [1]
4 LQV 6

RESULT 50
Q9UM46 PRELIMINARY; PRT; 13 AA.
AC Q9UM46;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hereditary haemochromatosis protein (Fragment).
GN HLA-H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Hashimoto K., Hirai M., Kurosawa Y.;
RT "Identification of a mouse homolog for the human hereditary
RT haemochromatosis candidate gene.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL: U80914; AAD00449.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1531 MW; 4352B39C9503BB13 CRC64;

Query Match
 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LQV 10
Db 11 LQV 13

RESULT 51
Q16007 PRELIMINARY; PRT; 13 AA.
ID Q16007;
AC Q16007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Lysosomal acid beta-galactosidase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91369478; PubMed=1909871;
RA Morreau H., Bonten E., Zhou X.Y., d'Azzo A.;
RT "Organization of the gene encoding human lysosomal beta-
 galactosidase."
RL DNA Cell Biol. 10:495-504(1991).
DR EMBL; S59584; AAB19814.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1482 MW; D70DAEE928194412 CRC64;

Query Match
 17.6%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db 10 PLL 12

RESULT 52
Q81ZRO PRELIMINARY; PRT; 13 AA.
ID Q81ZRO;
AC Q81ZRO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Truncated axonemal dynein heavy chain 8 isoform 4 (Fragment).
GN DNAB8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22233532; PubMed=12297094;
RA Samant S.A., Ogunkua O., Hui L., Fossella J., Pilder S.H.;
RT "The t complex distorter 2 candidate gene, Dnahc8, encodes at least
 two testis-specific axonemal dynein heavy chains that differ
 extensively at their amino and carboxyl termini."
RL Dev. Biol. 250:24-43(2002).
DR EMBL; AF527623; AAN34634.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1604 MW; 4569A2F01AA92727 CRC64;

Query Match
 17.6%; Score 3; DB 4; Length 13;

```

```

Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
Db 8 LLQ 10

RESULT 53
Q9U7D6 PRELIMINARY; PRT; 13 AA.
ID Q9U7D6;
AC Q9U7D6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ycf24 protein (Fragment).
OS GN YCF24.
OS Neospora caninum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Neospora.
OX NCBI_TaxID=29176;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Nci;
RX MEDLINE=20074141; PubMed=10608442;
RA Lang-Unnasch N., Aiello D.P.;
RT "Sequence evidence for an altered genetic code in the Neospora caninum
 plastid."
RL Int. J. Parasitol. 29:1557-1562(1999).
DR EMBL; AF138960; AAF14260.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FDCD40D CRC64;

Query Match
 17.6%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db 1 PLL 3

RESULT 54
O97122 PRELIMINARY; PRT; 13 AA.
ID O97122;
AC O97122;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Ycf24 protein (Fragment).
GN YCF24.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Aiello D.P., Lang-Unnasch N.;
RT "Analysis of the rpoB gene product of Toxoplasma gondii."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF095904; AAD17841.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FDCD40D CRC64;

Query Match
 17.6%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8
Db 1 PLL 3

```

```

RESULT 55
Q9R2Z4 PRELIMINARY; PRT; 14 AA.
ID Q9R2Z4;
AC Q9R2Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133577; CAB39387.1; -
DR EMBL; AJ133577; CAB39387.1; -
DR EMBL; AJ133572; CAB39382.1; -
DR EMBL; AJ133573; CAB39383.1; -
FT NON TER 1
SQ SEQUENCE 14 AA; 1599 MW; C7C4BEB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
Db 12 LLQ 14

RESULT 56
Q9R5I7 PRELIMINARY; PRT; 14 AA.
ID Q9R5I7;
AC Q9R5I7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Fimbrial antigen F165 subunit 1 (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
EX MEDLINE=92381496; PubMed=1355108;
RA Harel J., Forget C., Saint-Amand J., Daigle F., Dubreuil D.,
RA Jacques M., Fairbrother J.;
RT "Molecular cloning of a determinant coding for fimbrial antigen
RT F165(1), a Pfs-like fimbrial antigen from porcine septicaemic
RT Escherichia coli.";
RL J. Gen. Microbiol. 138:1495-1502(1992).
SQ SEQUENCE 14 AA; 1431 MW; 3B5981F6811863D8 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPQ 5
Db 4 TPQ 6

RESULT 57

```

```

Q9R2Z5 PRELIMINARY; PRT; 14 AA.
ID Q9R2Z5;
AC Q9R2Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133567; CAB55353.1; -
DR EMBL; AJ133568; CAB39378.1; -
DR EMBL; AJ133569; CAB39379.1; -
DR EMBL; AJ133570; CAB39380.1; -
DR EMBL; AJ133571; CAB39381.1; -
DR EMBL; AJ133574; CAB39384.1; -
DR EMBL; AJ133575; CAB39385.1; -
DR EMBL; AJ133576; CAB39386.1; -
FT NON TER 1
SQ SEQUENCE 14 AA; 1611 MW; C7C0EFB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQ 9
Db 12 LLQ 14

RESULT 58
Q8RK22 PRELIMINARY; PRT; 14 AA.
ID Q8RK22;
AC Q8RK22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transposase (Fragment).
GN TNPA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC29-5; TRANSPOSON=Tn5041B;
RA Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
RT "Distribution of distinct microvariants of Tn5041 in environmental
RT bacteria.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ422232; CAD19590.1; -
FT NON TER 14
SQ SEQUENCE 14 AA; 1535 MW; 866834EPB82164C1 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLL 8

```

```

Db 10 PLL 12

RESULT 59
Q9X715
ID Q9X715 PRELIMINARY; PRT; 14 AA.
AC Q9X715;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133578; CAB39388.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1595 MW; C7C0F96DA1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9
Db 12 LLQ 14

RESULT 60
Q9WW79
ID Q9WW79 PRELIMINARY; PRT; 14 AA.
AC Q9WW79;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Flagellin A (Fragment).
GN FLAA.
OS Campylobacter coli.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=195;
RN [1]
RP SEQUENCE FROM N.A.
RA Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133579; CAB39377.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1611 MW; C7C0EPB7A1739156 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9

```

```

Db 12 LLQ 14

RESULT 61
Q8GMC4
ID Q8GMC4 PRELIMINARY; PRT; 14 AA.
AC Q8GMC4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rpos (Fragment).
GN RPOS.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LT2;
RX MEDLINE=22167056; PubMed=12177346;
RA Kotewicz M.L., Li B., Levy D.D., LeClerc J.E., Shifflet A.W.,
RA Cebula T.A.;
RT "Evolution of multi-gene segments in the mutS-rpos intergenic region
RT of Salmonella enterica serovar Typhimurium LT2.";
RL Microbiology 148:2531-2540(2002).
DR EMBL; AY050714; AAL24442.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1632 MW; 032FD6D26DD06C54 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
Db 1 LQT 3

RESULT 62
Q9TWW0
ID Q9TWW0 PRELIMINARY; PRT; 14 AA.
AC Q9TWW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Histone C (fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=93064852; PubMed=1437281;
RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
RT "Sequence differences between histones of procyclic Trypanosoma brucei
RT brucei and higher eukaryotes.";
RL Parasitology 105:97-104(1992).
SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8976C4EC7 CRC64;

Query Match 17.6%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3
Db 1 LQT 3

RESULT 63
Q9ZRS3
ID Q9ZRS3 PRELIMINARY; PRT; 14 AA.
AC Q9ZRS3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

```

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Knotted-like homobox protein (Fragment).  
 GN KNAF1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. C24;  
 RA Raap M., Heyer A.G.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ131822; CAA10513.1; --  
 DE DNA-binding; Homobox; Nuclear protein.  
 KW  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1722 MW; 9B3ADC59F1EB8D4A CRC64;  
  
 Query Match 17.6%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 TPQ 5  
 Db 11 TPQ 13  
  
 RESULT 64  
 Q8V1H7 PRELIMINARY; PRT; 14 AA.  
 ID Q8V1H7  
 AC Q8V1H7  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Truncated HBAg.  
 DE Hepatitis B virus.  
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FH10;  
 RA Wen Y.M., Liu F., Ma Z.M.;  
 RT "Structural and functional analysis of hepatitis B virus genomes in  
 RT fulminant hepatitis B patients.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF461362; AAL66336.1; --  
 SQ SEQUENCE 14 AA; 1427 MW; 2F487846CB391E28 CRC64;  
  
 Query Match 17.6%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 6 PLL 8  
 Db 11 PLL 13  
  
 RESULT 65  
 Q9PY99 PRELIMINARY; PRT; 14 AA.  
 ID Q9PY99  
 AC Q9PY99  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE NON-structural protein (Truncated NON-structural protein).  
 OS Murine hepatitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11138;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MHV-2;

RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;  
 RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2:  
 RT an experimental model system of acute meningitis and hepatitis in  
 RT mice.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PENN 97-1;  
 RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;  
 RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2:  
 RT an experimental model system of acute meningitis and hepatitis in  
 RT mice.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF201929; AAP19387.1; --  
 DE EMBL; AF208066; AAF69340.1; --  
 SQ SEQUENCE 14 AA; 1534 MW; C2FD164C12169242 CRC64;  
  
 Query Match 17.6%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 8 LQV 10  
 Db 12 LQV 14  
  
 RESULT 66  
 Q88400 PRELIMINARY; PRT; 14 AA.  
 ID Q88400  
 AC Q88400;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Tax protein (Fragment).  
 DE TAX.  
 GN Simian T-lymphotropic virus 1.  
 OS Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.  
 OX NCBI\_TaxID=33747;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94082462; PubMed=8259665;  
 RA Saksena N.K., Herve V., Durand J.P., LeGuanno B., Diop O.M.,  
 RA Digoutte J.P., Mathiot C., Muller M.C., Love J.L., Benz P.M.,  
 RA Erensay S., Barre-Sinoussi F., Poiesz B.J.;  
 RT "Seroepidemiologic, molecular, and phylogenetic analyses of simian T-  
 RT cell leukemia viruses (STLV-I) from various naturally infected monkey  
 RT species from central and western Africa.";  
 RL Virology 198:297-310(1993).  
 DR EMBL; L20363; AAA47870.1; --  
 DR InterPro; IPR004120; Tax.  
 DR Pfam; PF02959; Tax; 1  
 FT NON\_TER 1  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1394 MW; 8BA7726C9C6D387A CRC64;  
  
 Query Match 17.6%; Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 15 QGD 17  
 Db 5 QGD 7  
  
 RESULT 67  
 Q9R5A0 PRELIMINARY; PRT; 15 AA.  
 ID Q9R5A0  
 AC Q9R5A0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE DNA topoisomerase I (Fragment).  
 OS Micrococcus luteus (Micrococcus lysodeikticus).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcineae; Micrococcaceae; Micrococcus.  
 OX NCBI\_TaxID=1270;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93249439; PubMed=8387285;  
 RA Anderluzzi D., Pedrini A.M.;  
 RT "Structural similarities between M. luteus and E. coli DNA  
 RT topoisomerase I.";  
 RL Biochem. Biophys. Res. Commun. 192:657-664(1993).  
 SQ SEQUENCE 15 AA; 1602 MW; 2B5457836F151383 CRC64;

Query Match 17.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4  
 Db |||  
 6 QTP 8

## RESULT 68

Q9X637  
 ID Q9X637 PRELIMINARY; PRT; 15 AA.  
 AC Q9X637;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE MERT (Fragment).  
 GN MERT.  
 OS Klebsiella oxytoca.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=571;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 RT bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 RT gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=509H;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 RT mer operon.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF131272; RAD37141.1; -.  
 DR InterPro; IPR003457; Transprt\_Mert.  
 DR Pfam; PF02411; MERT; 1.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 17.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15  
 Db |||  
 3 EPQ 5

## RESULT 69

Q9X637  
 ID Q9X637 PRELIMINARY; PRT; 15 AA.  
 AC Q9X637;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE MERT (Fragment).  
 GN MERT.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 RT bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 RT mer operon.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF131272; RAD37141.1; -.  
 DR InterPro; IPR003457; Transprt\_Mert.  
 DR Pfam; PF02411; MERT; 1.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 17.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15  
 Db |||  
 3 EPQ 5

Q9X635  
 ID Q9X635 PRELIMINARY; PRT; 15 AA.  
 AC Q9X635;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE MERT (Fragment).  
 GN MERT.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 RT bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 RT gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=390;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the  
 RT mer operon.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF131272; RAD37139.1; -.  
 DR InterPro; IPR003457; Transprt\_Mert.  
 DR Pfam; PF02411; MERT; 1.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 17.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQ 15  
 Db |||  
 3 EPQ 5

RESULT 70  
 Q9UMT6  
 ID Q9UMT6 PRELIMINARY; PRT; 15 AA.  
 AC Q9UMT6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE VEGF related factor (fragment).  
 GN VRF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,  
 RA Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,  
 RA Hayward N., Weber G.;  
 RT "Cloning and characterization of a novel human gene related to  
 RT vascular endothelial growth factor.";  
 RL Genome Res. 6:122-129(1996).  
 DR EMBL; U43370; AAA91464.1; -.  
 FT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1708 MW; 5D0AE30FE481A71E CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8  
Db 3 PLL 5

RESULT 71

ID P78482 PRELIMINARY; PRT; 15 AA.

AC P78482;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE APOB protein (Fragment).

GN APOB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88018019; PubMed=3659919;

RA Chen S.-H., Habib G., Yang C.-Y., Gu Z.-W., Lee B.R., Weng S.-A.,  
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseanu M.,  
Gotto A.M., Jr., Li W.-H., Chan L.;  
RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-  
specific in-frame stop codon.";

RL Science 238:363-366 (1987).

DR EMBL; M18036; AARS1754.1; -.

FT NON\_TER 1

SQ SEQUENCE 15 AA; 1842 MW; 9172790C16559AE8 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3  
Db 10 LQT 12

RESULT 72

ID Q96RX1 PRELIMINARY; PRT; 15 AA.

AC Q96RX1;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Leucocyte differentiation antigen CD84 (Fragment).

GN CD84.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20208572; PubMed=10746783;

RA Palou E., Piroto F., Sole J., Freed J.H., Peral B., Vilardell C.,  
Vilella R., Vives J., Gaya A.;  
RT "Genomic characterization of CD84 reveals the existence of five  
isoforms differing in their cytoplasmic domains.";

RL Tissue Antigens 55:118-127 (2000).

DR EMBL; AF114490; AAK68906.1; -.

FT NON\_TER 15

SQ SEQUENCE 15 AA; 1820 MW; 1F23F01D9B227D19 CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQT 3  
Db 13 LQT 15

RESULT 73

ID Q9UC60 PRELIMINARY; PRT; 15 AA.

AC Q9UC60;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=95392215; PubMed=7663175;

RA De Pauw P., Neyt C., Vanderwinkel E., Wattiez R., Falmagne P.;  
RT "Characterization of human serum N-acetylmuramyl-L-alanine amidase  
purified by affinity chromatography.";

RL Protein Expr. Purif. 6:371-378 (1995).

SQ SEQUENCE 15 AA; 1600 MW; 9016B00FFF9F9E780A CRC64;

Query Match 17.6%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLL 8  
Db 3 PLL 5

RESULT 74

ID Q9TRP1 PRELIMINARY; PRT; 15 AA.

AC Q9TRP1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE LOW MR zona pellucida binding protein (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE.

RX MEDLINE=92378826; PubMed=1510840;

RA Parry R.V., Barker P.J., Jones R.;  
RT "Characterization of low Mr zona pellucida binding proteins from boar  
spermatozoa and seminal plasma.";

RL Mol. Reprod. Dev. 33:108-115 (1992).

SQ SEQUENCE 15 AA; 1736 MW; 668FA50BB6120B7C CRC64;

Query Match 17.6%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQ 9  
Db 11 LLQ 13

RESULT 75

ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.

AC Q9TNQ1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)



DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex  
DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin  
DE (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94240094; PubMed=8183884;  
RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;  
RT "Characterization of an incompletely assembled major  
RT histocompatibility class I molecule (H-2KB) associated with unusually  
RT long peptides: implications for antigen processing and presentation.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).  
KW MHC.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;  
  
Query Match 17.6%; Score 3; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 LLQ 9  
Db 4 LLQ 6

Search completed: November 25, 2003, 18:25:11  
Job time : 44.0128 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 55.0691 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPOPLQVMPEQGD 17

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A.Geneseq 19Jun03.\*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 17    | 100.0       | 17     | 22 | Colostrin derive   |
| 2          | 17    | 100.0       | 17     | 22 | Colostrin peptid   |
| 3          | 17    | 100.0       | 17     | 22 | Colostrin peptid   |
| 4          | 17    | 100.0       | 17     | 22 | Ewe colostrin pe   |
| 5          | 17    | 100.0       | 17     | 22 | Colostrin consti   |
| 6          | 17    | 100.0       | 17     | 23 | Colostrin consti   |
| 7          | 17    | 100.0       | 17     | 23 | Neural cell regula |
| 8          | 17    | 100.0       | 18     | 22 | Ewe colostrin pe   |
| 9          | 11    | 64.7        | 11     | 22 | Colostrin peptid   |

acquired immunological deficiencies.

|          |    |                                                                           |                                                     |
|----------|----|---------------------------------------------------------------------------|-----------------------------------------------------|
| XX       | SQ | Sequence                                                                  | 17 AA;                                              |
|          |    | Query Match                                                               | 100.0%; Score 17; DB 22; Length 17;                 |
|          |    | Best Local Similarity                                                     | 100.0%; Pred. No. 5.2e-11;                          |
|          |    | Matches                                                                   | 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY       |    | 1 LQTQPQLQVMPEPGD 17                                                      |                                                     |
|          |    |                                                                           |                                                     |
| Dd       |    | 1 LQTQPQLQVMPEPGD 17                                                      |                                                     |
|          |    |                                                                           |                                                     |
| RESULT 2 |    |                                                                           |                                                     |
| AAB72501 |    | ID AAB72501 standard; Peptide; 17 AA.                                     |                                                     |
| XX       |    | AC AC                                                                     |                                                     |
| XX       |    | AAB72501;                                                                 |                                                     |
| XX       |    | DT 09-MAY-2001 (first entry)                                              |                                                     |
| XX       |    | Colostrinin peptide #2.                                                   |                                                     |
| XX       |    | Dermatological; oxidative stress regulator; colostrinin.                  |                                                     |
| XX       |    | Unidentified.                                                             |                                                     |
| XX       |    | WO200112650-A2.                                                           |                                                     |
| XX       |    | 22-FEB-2001.                                                              |                                                     |
| XX       |    | 17-AUG-2000; 2000WO-US22665.                                              |                                                     |
| XX       |    | 17-AUG-1999; 99US-0149310.                                                |                                                     |
| XX       |    | (TEXA ) UNIV TEXAS SYSTEM.                                                |                                                     |
| PI       |    | Stanton GJ, Hughes TK, Boldogh I;                                         |                                                     |
| XX       |    | WPI; 2001-218342/22.                                                      |                                                     |
| PT       |    | Modulating oxidative stress level in a cell, involves contacting the      |                                                     |
| PT       |    | cell with an oxidative stress regulator selected from colostrinin, its    |                                                     |
| PT       |    | constituent peptide, analog or their combinations -                       |                                                     |
| PS       |    | Claim 6; Page 25; 48pp; English.                                          |                                                     |
| CC       |    | The present invention relates to a method for modulating the oxidative    |                                                     |
| CC       |    | stress level in a cell or a patient, comprising contacting the cell with, |                                                     |
| CC       |    | or administering to the patient, an oxidative stress regulator selected   |                                                     |
| CC       |    | from colostrinin, or its constituent peptide (e.g. the present peptide),  |                                                     |
| CC       |    | to change the level of an oxidizing species in the cell. The method can   |                                                     |
| CC       |    | be used to treat oxidative damage to skin, by decreasing or preventing an |                                                     |
| CC       |    | increase in the level of damage to a biomolecule of the patient.          |                                                     |
| XX       |    |                                                                           |                                                     |
| SQ       |    | Sequence                                                                  | 17 AA;                                              |
|          |    | Query Match                                                               | 100.0%; Score 17; DB 22; Length 17;                 |
|          |    | Best Local Similarity                                                     | 100.0%; Pred. No. 5.2e-11;                          |
|          |    | Matches                                                                   | 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY       |    | 1 LQTQPQLQVMPEPGD 17                                                      |                                                     |
|          |    |                                                                           |                                                     |
| Dd       |    | 1 LQTQPQLQVMPEPGD 17                                                      |                                                     |
|          |    |                                                                           |                                                     |
| RESULT 3 |    |                                                                           |                                                     |
| AAB72533 |    | ID AAB72533 standard; Peptide; 17 AA.                                     |                                                     |
| XX       |    | AC AAB72533;                                                              |                                                     |
| XX       |    | DT 09-MAY-2001 (first entry)                                              |                                                     |
| XX       |    |                                                                           |                                                     |



CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 17; DB 23; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLLQVMPEQGD 17  
 Db 1 LQTPQPLLQVMPEQGD 17  
 RESULT 6  
 AAM51037  
 ID AAM51037 standard; Peptide; 17 AA.  
 AC AAM51037;  
 DT 30-MAY-2002 (first entry)  
 XX Colostrinin constituent peptide.  
 DE Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 17 /note= "optional C-terminal amidation"  
 FT  
 PN WO200213849-A1.  
 XX  
 XX 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2002-269150/31.  
 XX  
 XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -  
 XX  
 XX Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-4, interleukin-6, interleukin-10 and  
 CC interleukin-12. It was one of the best overall inducers in almost  
 CC all cytokine and blood cell proliferation experiments conducted.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 17; DB 23; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLLQVMPEQGD 17  
 Db 1 LQTPQPLLQVMPEQGD 17  
 RESULT 7  
 AAO14578  
 ID AAO14578 standard; peptide; 17 AA.  
 AC AAO14578;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX Neural cell regulatory colostrinin peptide 2.  
 DE  
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX Unidentified.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 17 /note= "Optional C-terminal amide"  
 FT  
 PN WO200213851-A1.  
 XX  
 XX 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US22777.  
 XX  
 XX 17-AUG-2000; 2000WO-US22777.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I, Stanton JG, Hughes TK;  
 XX WPI; 2002-269152/31.  
 XX  
 XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -  
 XX  
 XX Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 17; DB 23; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVMMPEQGD 17  
 |||||  
 Db 1 LQTPQLQVMMPEQGD 17  
 |||||

# RESULT 8

AAE59341  
 ID AAB59341 standard; Peptide; 18 AA.

XX AC AAB59341;

DT 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment derived sequence #1.

DE Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 17; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-11;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVMMPEQGD 17  
 |||||  
 Db 2 LQTPQLQVMMPEQGD 18  
 |||||

# RESULT 9

AAE07195 standard; peptide; 12 AA.

AAE07185

ID AAE07185 standard; peptide; 11 AA.

XX AC AAE07185;

XX 06-NOV-2001 (first entry)

XX Colostrinin peptide 1.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.

XX Unidentified.

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 1 related to the invention.

XX SQ Sequence 11 AA;

Query Match 64.7%; Score 11; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLLQVMMPEQ 15  
 |||||  
 Db 1 QPLLQVMMPEQ 11  
 |||||

# RESULT 10

AAE07195

```

XX AC AAE07195;
XX AC
XX DT 06-NOV-2001 (first entry)
XX DE Modified colostrinin cyclic peptide #1.
XX DE
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral; cyclic.
XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT Modified-site 1
XX FT /notes "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Gln found at the C-terminal end"
XX FT
XX PN WO200155199-A1.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 26-JAN-2001; 2001WO-GB00329.
XX XX
XX PR 26-JAN-2000; 2000GB-0001825.
XX XX
XX PA (REG-) REGEN THERAPEUTICS PLC.
XX PI
XX PI Georgiades JA;
XX XX
XX DR WPI; 2001-488775/53.
XX XX
XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX PS
XX PS Example 2; Page 8; 40pp; English.
XX CC
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is modified colostrinin cyclic peptide #1 related to
XX CC the invention.
XX SQ
XX SQ Sequence 12 AA;
XX SQ
XX SQ Query Match 64.7%; Score 11; DB 22; Length 12;
XX SQ Best Local Similarity 100.0%; Pred. No. 5.8e-05;
XX SQ Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX QY 5 QPLLQVMMEPQ 15
XX QY |||||
XX DB 2 QPLLQVMMEPQ 12
XX DB

```

```

RESULT 11
AAR21055
ID AAR21055 standard; Peptide; 8 AA.
XX
XX AC AAR21055;
XX AC
XX DT 25-MAR-2003 (updated)
XX DT 01-JUN-1992 (first entry)
XX DE Gamma-carboxylase, N-terminus.
XX KW Degenerate; Vitamin K dependent proteins; PCR.
XX OS Homo sapiens.
XX PN WO9201795-A.
XX PD 06-FEB-1992.
XX PF 22-JUL-1991; 91WO-US05177.
XX PR 14-MAR-1991; 91US-0669735.
XX PR 23-JUL-1990; 90US-0557220.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Berkner KL;
XX DR WPI; 1992-064951/08.
XX PT Gamma-carboxylase protein compens. - used in recombinant prodn.
XX PT of active vitamin-K dependent proteins
XX PS Claim 6; Table 9; 91pp; English.
XX CC Nucleotide sequences encoding gamma-carboxylase were obtd. using PCR,
XX CC and oligonucleotides designed from amino acid sequences determined
XX CC by missequencing of partially purified material. SEQ ID No 19
XX CC (peptide 5) is one of seven alternative sequences for the N-terminus
XX CC of gamma carboxylase, due to the degeneracy of the genetic code.
XX CC Obtaining the full DNA and protein sequence of gamma-carboxylase
XX CC will allow proteins such as Factor VII, Factor IX, prothrombin,
XX CC (activated) protein C, protein S, protein Z, or osteocalcin to be
XX CC easily produced by recombinant techniques.
XX CC See also AAR21049-56, AAR23010.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ
XX SQ Sequence 8 AA;
XX SQ
XX SQ Query Match 35.3%; Score 6; DB 13; Length 8;
XX SQ Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX SQ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX QY 3 TPQPLL 8
XX QY |||||
XX DB 1 TPQPLL 6
XX DB
XX DB
XX DB
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 34497.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.

```

XX WO200157273-A2.  
 PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00664.  
 PF 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 DR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-48898/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PI analysing gene expression in human adult liver -  
 XX Claim 27; SEQ ID No 34497; 658pp; English.  
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 QPLLQV 10  
 Db 3 QPLLQV 8  
 RESULT 13  
 ABB40529  
 ID ABB40529 standard; Peptide; 18 AA.  
 XX AC ABB40529;  
 XX DT 04-FEB-2002 (first entry)  
 XX DE Peptide #8035 encoded by human foetal liver single exon probe.  
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
 XX Homo sapiens.  
 OS WO200157277-A2.  
 PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00669.  
 XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 DR Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human fetal liver -  
 XX Claim 27; SEQ ID NO 33164; 639pp + sequence listing; English.  
 XX The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 QPLLQV 10  
 Db 3 QPLLQV 8  
 RESULT 14  
 ABB24849  
 ID ABB24849 standard; Protein; 18 AA.  
 XX AC ABB24849;  
 XX DT 23-JAN-2002 (first entry)  
 XX DE Protein #6848 encoded by probe for measuring heart cell gene expression.  
 XX Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 XX Homo sapiens.  
 OS WO200157274-A2.  
 PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00666.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX



DR WPI; 2001-488899/53.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 XX  
 PS Claim 15; SEQ ID No 26619; 530pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLLQV 10  
 Db |||||  
 3 QPLLQV 8  
 RESULT 15  
 AAM61355  
 ID AAM61355 standard; Protein; 18 AA.  
 AC  
 XX  
 AC AAM61355;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33460.  
 XX  
 KW Human; brain expressed exon; gene expression analysis; probe;  
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157275-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00667.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2001-483446/52.  
 XX  
 PF Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains -  
 XX  
 PS Example 4; SEQ ID NO: 33460; 650pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLLQV 10  
 Db |||||  
 3 QPLLQV 8  
 RESULT 16  
 AAM74093  
 ID AAM74093 standard; Protein; 18 AA.  
 XX  
 AC AAM74093;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34399.  
 XX  
 KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157276-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00668.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2001-488900/53.  
 XX  
 PF Human genome-derived single exon nucleic acid probes useful for  
 XX analyzing gene expression in human bone marrow -  
 XX  
 PS Example 4; SEQ ID NO: 34399; 658pp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLLQV 10  
 Db |||||

```

Db 3 QPLLQV 8

RESULT 17
AAM20225
ID AAM20225 standard; Protein; 18 AA.
XX
XX AC AAM20225;
XX
XX DT 12-OCT-2001 (first entry)
XX
XX DE Peptide #6659 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX OS Homo sapiens.
XX
XX FN WO200157278-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00670.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX DR WPI; 2001-488901/53.
XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human cervical epithelial cells -
XX
XX PS Claim 27; SEQ ID No 25051; 487pp; English.
XX
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SNP: see AAI10068-AA128459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 18 AA;

Query Match 35.3%; Score 6; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQV 10
 |||||
Db 3 QPLLQV 8

RESULT 18
AAM34255
ID AAM34255 standard; Protein; 18 AA.
XX
XX AC AAM34255;
XX
XX DT 17-OCT-2001 (first entry)
XX

Query Match 35.3%; Score 6; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQV 10
 |||||
Db 3 QPLLQV 8

RESULT 19
ABG43991
ID ABG43991 standard; Peptide; 18 AA.
XX
XX AC ABG43991;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 33656.
XX
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX
XX OS Homo sapiens.
XX

```

```

XX
DE Peptide #8292 encoded by probe for measuring placental gene expression.
XX
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX
XX OS Homo sapiens.
XX
XX FN WO200157272-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00663.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX DR WPI; 2001-488901/53.
XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX
XX PS Claim 27; SEQ ID No 34524; 654pp; English.
XX
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders.
XX
XX SQ Sequence 18 AA;

Query Match 35.3%; Score 6; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQV 10
 |||||
Db 3 QPLLQV 8

RESULT 19
ABG43991
ID ABG43991 standard; Peptide; 18 AA.
XX
XX AC ABG43991;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 33656.
XX
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX
XX OS Homo sapiens.
XX

```

PN WO200186003-A2.  
 XX 15-NOV-2001.  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2002-114183/15.  
 XX  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 XX  
 PS Claim 27; SEQ ID No 33656; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 35.3%; Score 6; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLIQV 10

Db 3 QELLQV 8  
 RESULT 20  
 AAW17515  
 ID AAW17515 standard; Peptide; 7 AA.  
 XX  
 AC AAW17515;  
 XX 31-OCT-1997 (first entry)  
 XX Protein kinase C related kinase 1 peptide PRK1-3 (465-471).  
 DE  
 XX Signal transduction; cell signalling; modulator; immunomodulator;  
 KW protein kinase C related kinase 1; receptor for activated kinase C;  
 KW RACK; PRK1; cognate; graft rejection; autoimmune disease;  
 KW allergy; asthma; therapy.  
 XX  
 OS Homo sapiens.  
 XX WO9714038-A1.  
 XX 17-APR-1997.  
 XX 10-OCT-1996; 96WO-US16195.  
 XX 18-JUN-1996; 96US-0665647.  
 PR 10-OCT-1995; 95US-0541964.  
 PR 31-JAN-1996; 96US-0594447.  
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.  
 PA  
 XX Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;  
 PI Vasquez NJ, Voronova A;  
 XX WPI; 1997-236030/21.  
 DR  
 XX Identifying a modulator of intracellular signal transduction - by  
 PT determining the interaction of a signal generating peptide with the  
 PT test substance, allows modulation of the immune system  
 XX  
 PS Example 4; Page 34; 74pp; English.  
 XX  
 CC This sequence is a peptide, designated PRK1-3, that corresponds  
 CC to amino acid residues 465-471 of protein kinase C related kinase  
 CC 1 (PRK1). It was tested as a signal generating peptide in a  
 CC claimed method for identifying modulators of intracellular signal  
 CC transduction. This method assesses the ability of candidate  
 CC modulators to affect the interaction between a signal-generating  
 CC protein (see AAW15778-79, AAW15781, AAW15784-85, AAW17452-78), and a  
 CC cognate binding protein involved in modulating the signal  
 CC transduction function. Identified substances are useful as  
 CC immunomodulators (claimed). They reduce T-cell activity, reduce  
 CC the rate of graft rejection, reduce the severity of an autoimmune  
 CC disorder, ameliorate allergy and/or asthma, or diminish a cytokine  
 CC response (claimed).  
 XX  
 SQ Sequence 7 AA;  
 Query Match 29.4%; Score 5; DB 18; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 MEPQG 16  
 Db 1 MEPQG 5  
 RESULT 21  
 AAG87925  
 ID AAG87925 standard; Peptide; 10 AA.  
 XX

```

AC AAG87925;
XX
XX 11-SEP-2001 (first entry)
XX
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 2874.
XX
DE Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200142276-A1.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB04773.
XX
XX 13-DEC-1999; 99GB-0029471.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-367863/38.
XX
XX Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
XX Example 5; Page 426; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;

Query Match 29.4%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred.No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQPL 7
Db 3 TPQPL 7

RESULT 22
AAB44382
ID AAB44382 standard; Protein; 13 AA.
XX
XX AAB44382;
AC
XX
XX 14-FEB-2001 (first entry)
XX
DE Human secreted protein encoded by gene 49 clone HPWA82.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.
XX
XX Homo sapiens.
XX
XX WO2000058358-A1.
XX
XX 05-OCT-2000.
PD
XX
XX 23-MAR-2000; 2000WO-US07725.
PP

```

PR 27-DEC-2000; 2000US-0173419.  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shimkets RA, Leach M;  
 PI  
 XX WPI; 2001-465210/50.  
 XX  
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 PT  
 XX Disclosure; Page 4120; 4143pp; English.  
 PS  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.  
 XX  
 SQ Sequence 14 AA;  
  
 Query Match 29.4%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 PQLL 8  
 Db |||||  
 7 PQLL 11  
  
 RESULT 24  
 AAM98788  
 ID AAM98788 standard; Peptide; 14 AA.  
 AC AAM98788;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 DE Human peptide #2063 encoded by a SNP oligonucleotide.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200147944-A2.  
 PN  
 XX 05-JUL-2001.  
 PD  
 XX 28-DEC-2000; 2000WO-US35498.  
 PF  
 XX 28-DEC-1999; 99US-0173419.  
 PR  
 PR 27-DEC-2000; 2000US-0173419.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA

XX Shimkets RA, Leach M;  
 PI  
 XX WPI; 2001-465210/50.  
 XX  
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 PT  
 XX Disclosure; Page 4120; 4143pp; English.  
 PS  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.  
 XX  
 SQ Sequence 14 AA;  
  
 Query Match 29.4%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 PQLL 8  
 Db |||||  
 8 PQLL 12  
  
 RESULT 25  
 AAE33717  
 ID AAE33717 standard; peptide; 4 AA.  
 XX  
 AC AAE33717;  
 XX  
 XX 16-APR-2003 (first entry)  
 DT  
 DE GNA33 mAb 25 recognition VR2 peptide.  
 XX  
 XX Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;  
 KW MenB; immune response; infection; vaccine; antibacterial.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200283711-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 11-APR-2002; 2002WO-US11501.  
 PF  
 XX 17-APR-2001; 2001US-284554P.  
 PR  
 PR 03-OCT-2001; 2001US-326838P.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
 XX  
 XX Granoff D, Moe G, Rappuoli R;  
 PI  
 XX WPI; 2003-120415/11.  
 DR  
 XX New GNA33 peptides that elicit production of antibodies exhibiting  
 PT complement-mediated bactericidal activity against a Neisseria  
 PT meningitidis serogroup B (MenB), useful for diagnosing or preventing

(as vaccine) MenB infection -

Example 3; Page 47; 70pp; English.

The invention relates to novel genome derived antigen 33 (GNA33) peptides which are capable of eliciting the production of antibodies that exhibit complement-mediated bactericidal activity and/or opsonic activity against a surface-exposed epitope on loop 4 of PorA of *Neisseria meningitidis* serogroup B (MenB) P1.2 serosubtype. GNA33 sequences are useful for eliciting an immune response against MenB bacterium in a mammalian subject. They are useful for detecting MenB antibodies in a biological sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium infection. Sequences of the invention are used as vaccines. The present sequence is GNA33 mAb 25 recognition VR2 peptide.

XX SQ Sequence 4 AA;

Query Match 23.5%; Score 4; DB 24; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQ 5  
Db 1 QTPQ 4

RESULT 26

AAU07164 ID AAU07164 standard; peptide; 5 AA.

XX AC AAU07164;

XX DT 24-OCT-2001 (first entry)

XX DE Substituted Phenanthrene-9,10-dione R3 peptide group #15.

XX KW Phenanthrene-9,10-dione; T-cell mediated disorder; autoimmune disease;  
organ graft rejection; immunosuppressive; CD45 inhibitor; R3 peptide.

XX KW Synthetic.

XX OS WO200146125-A2.

XX PN 28-JUN-2001.

XX PD 18-DEC-2000; 2000WO-GB04854.

XX PF 21-DEC-1999; 99US-0172788.

XX PR (ASTR ) ASTRAZENECA AB.

XX PA (ASTR ) ASTRAZENECA UK LTD.

XX PI Chapelaine MJ, Knapenberger K, Steelman G, Suchard S, Sygowski L;  
Urbanek R, Veale CA;

XX DR WPI; 2001-502468/55.

XX Method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones -

XX Claim 1; Page 37; 42pp; English.

The invention relates to a method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones. The substituted phenanthrene-9,10-diones have been shown to inhibit the phosphatase activity of CD45 (leukocyte common antigen) which leads to proliferation of T-cells. Available treatments for autoimmune disorders and organ graft rejection have therapeutic disadvantages. For example, cyclosporin A, the drug most commonly used at present, has renal and CNS toxicity. The present sequence represents an N-linked peptide forming the R3 group of a substituted phenanthrene-9,10-dione.

PT XX (as vaccine) MenB infection -

PS PS Example 3; Page 47; 70pp; English.

XX CC The invention relates to novel genome derived antigen 33 (GNA33) peptides which are capable of eliciting the production of antibodies that exhibit complement-mediated bactericidal activity and/or opsonic activity against a surface-exposed epitope on loop 4 of PorA of *Neisseria meningitidis* serogroup B (MenB) P1.2 serosubtype. GNA33 sequences are useful for eliciting an immune response against MenB bacterium in a mammalian subject. They are useful for detecting MenB antibodies in a biological sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium infection. Sequences of the invention are used as vaccines. The present sequence is GNA33 mAb 25 recognition VR2 peptide.

XX SQ Sequence 4 AA;

Query Match 23.5%; Score 4; DB 24; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQ 5  
Db 1 QTPQ 4

RESULT 26

AAU07164 ID AAU07164 standard; peptide; 5 AA.

XX AC AAU07164;

XX DT 24-OCT-2001 (first entry)

XX DE Substituted Phenanthrene-9,10-dione R3 peptide group #15.

XX KW Phenanthrene-9,10-dione; T-cell mediated disorder; autoimmune disease;  
organ graft rejection; immunosuppressive; CD45 inhibitor; R3 peptide.

XX KW Synthetic.

XX OS WO200146125-A2.

XX PN 28-JUN-2001.

XX PD 18-DEC-2000; 2000WO-GB04854.

XX PF 21-DEC-1999; 99US-0172788.

XX PR (ASTR ) ASTRAZENECA AB.

XX PA (ASTR ) ASTRAZENECA UK LTD.

XX PI Chapelaine MJ, Knapenberger K, Steelman G, Suchard S, Sygowski L;  
Urbanek R, Veale CA;

XX DR WPI; 2001-502468/55.

XX Method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones -

XX Claim 1; Page 37; 42pp; English.

The invention relates to a method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones. The substituted phenanthrene-9,10-diones have been shown to inhibit the phosphatase activity of CD45 (leukocyte common antigen) which leads to proliferation of T-cells. Available treatments for autoimmune disorders and organ graft rejection have therapeutic disadvantages. For example, cyclosporin A, the drug most commonly used at present, has renal and CNS toxicity. The present sequence represents an N-linked peptide forming the R3 group of a substituted phenanthrene-9,10-dione.

PT XX (as vaccine) MenB infection -

PS PS Example 3; Page 47; 70pp; English.

XX CC The invention relates to novel genome derived antigen 33 (GNA33) peptides which are capable of eliciting the production of antibodies that exhibit complement-mediated bactericidal activity and/or opsonic activity against a surface-exposed epitope on loop 4 of PorA of *Neisseria meningitidis* serogroup B (MenB) P1.2 serosubtype. GNA33 sequences are useful for eliciting an immune response against MenB bacterium in a mammalian subject. They are useful for detecting MenB antibodies in a biological sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium infection. Sequences of the invention are used as vaccines. The present sequence is GNA33 mAb 25 recognition VR2 peptide.

XX SQ Sequence 4 AA;

Query Match 23.5%; Score 4; DB 24; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPQ 5  
Db 1 QTPQ 4

RESULT 26

AAU07164 ID AAU07164 standard; peptide; 5 AA.

XX AC AAU07164;

XX DT 24-OCT-2001 (first entry)

XX DE Substituted Phenanthrene-9,10-dione R3 peptide group #15.

XX KW Phenanthrene-9,10-dione; T-cell mediated disorder; autoimmune disease;  
organ graft rejection; immunosuppressive; CD45 inhibitor; R3 peptide.

XX KW Synthetic.

XX OS WO200146125-A2.

XX PN 28-JUN-2001.

XX PD 18-DEC-2000; 2000WO-GB04854.

XX PF 21-DEC-1999; 99US-0172788.

XX PR (ASTR ) ASTRAZENECA AB.

XX PA (ASTR ) ASTRAZENECA UK LTD.

XX PI Chapelaine MJ, Knapenberger K, Steelman G, Suchard S, Sygowski L;  
Urbanek R, Veale CA;

XX DR WPI; 2001-502468/55.

XX Method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones -

XX Claim 1; Page 37; 42pp; English.

The invention relates to a method of treating immunologically-related diseases, autoimmune disorders and organ graft rejection comprises administration of substituted phenanthrene-9,10-diones. The substituted phenanthrene-9,10-diones have been shown to inhibit the phosphatase activity of CD45 (leukocyte common antigen) which leads to proliferation of T-cells. Available treatments for autoimmune disorders and organ graft rejection have therapeutic disadvantages. For example, cyclosporin A, the drug most commonly used at present, has renal and CNS toxicity. The present sequence represents an N-linked peptide forming the R3 group of a substituted phenanthrene-9,10-dione.

AC AAY21560;  
 XX  
 DT 04-AUG-1999 (first entry)  
 XX  
 DE Target hexapeptide used in skin lightening composition.  
 XX  
 KW Skin lightening; targeting molecule.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9912518-A1.  
 XX  
 PD 18-MAR-1999.  
 XX  
 PF 19-JUN-1998; 98WO-EP04012.  
 XX  
 PR 09-SEP-1997; 97GB-0019195.  
 XX  
 PA (UNIL ) UNILEVER NV.  
 PA (UNIL ) UNILEVER PLC.  
 XX  
 PI Raghupathi S, Ramaiah A, Raman G, Wagh SS;  
 XX  
 DR WPI; 1999-357348/30.  
 XX  
 PT New cosmetic composition for lightening skin comprising peptide with  
 PT isoelectric point of 2-5.5  
 XX  
 PS Claim 8; Page 9; 14pp; English.  
 XX  
 CC The invention provides a cosmetic composition for lightening the skin  
 CC that comprises 0.1-10 wt.% of a peptide with an isoelectric point of  
 CC 2-5.5. The peptide in the composition is attached to a hydrophobic amino  
 CC acid residue or a targeting molecule or vehicle. The present sequence is  
 CC a hexapeptide that can act as the targeting molecule. The composition is  
 CC useful for lightening the skin. The skin lightening effected by the  
 CC composition is reversible and has no known side effects and is active  
 CC during both the day and night unlike the prior art.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 23.5%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLL 8  
 Db 2 QPLL 5  
 RESULT 29  
 ID AAW84430  
 AC AAW84430 standard; Peptide; 6 AA.  
 XX  
 AC AAW84430;  
 XX  
 DT 22-MAR-1999 (first entry)  
 XX  
 DE HIV-1 nucleic acid binding protein zinc finger 2 peptide.  
 XX  
 KW zinc finger; nucleotide-binding protein; cell proliferative disorder;  
 KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome;  
 KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;  
 KW transgenic plant.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9854311-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 27-MAY-1998; 98WO-US10801.  
 XX

PR 27-MAY-1997; 97US-0863813.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Barbas CF, Gottesfeld JM, Wright PE;  
 XX  
 DR WPI; 1999-059831/05.  
 XX  
 PT New zinc finger nucleotide-binding protein variant that modulates  
 PT selected nucleotide sequence - used for treatment of proliferative  
 PT and viral diseases by gene therapy, and can be made selective for  
 PT any target sequence  
 XX  
 PS Example 10; Fig 9; 158pp; English.  
 XX  
 CC AAW84422-41 represent the peptides obtained from randomised finger 2  
 CC sequences of zinc finger nucleotide-binding proteins that bind to HIV-1  
 CC target sequences. The peptides were produced in the course of the  
 CC invention. The specification describes zinc finger nucleotide-binding  
 CC protein variants with at least two zinc finger modules that bind to a  
 CC cellular nucleotide sequence and modulate its function. Zinc finger  
 CC proteins, and compositions containing them, are used to increase or  
 CC reduce transcription of a gene linked to the cellular nucleotide  
 CC sequence. The proteins are used specifically for treating or preventing  
 CC cell proliferative disorders (in humans, animals or plants, including  
 CC those induced by viruses), particularly where expressed from nucleic  
 CC acid by gene therapy (including ex vivo methods). Typical diseases that  
 CC can be treated are many forms of cancer, psoriasis, pemphigus vulgaris,  
 CC Bechet's syndrome and lipid histiocytosis, also treatment of human  
 CC immune deficiency virus (HIV) and other viral infections, and production  
 CC of transgenic plants resistant to bacterial and viral diseases. The  
 CC present oligonucleotide is used in the course of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 23.5%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PQPL 7  
 Db 1 PQPL 4  
 RESULT 30  
 ID AAE33713  
 AC AAE33713 standard; peptide; 6 AA.  
 XX  
 AC AAE33713;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE N. meningitidis serogroup B Pl.2 serosubtype Por A loop4 peptide #3.  
 XX  
 KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;  
 KW MenB; immune response; infection; vaccine; antibacterial.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO200283711-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002WO-US11501.  
 XX  
 PR 17-APR-2001; 2001US-284554P.  
 PR 03-OCT-2001; 2001US-326838P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
 XX  
 PI Granoff D, Moe G, Rappuoli R;  
 XX

DR WPI; 2003-120415/11.  
 XX  
 PT New GNA33 peptides that elicit production of antibodies exhibiting  
 PT complement-mediated bactericidal activity against a Neisseria  
 PT meningitidis serogroup B (MenB), useful for diagnosing or preventing  
 XX (as vaccine) MenB infection -  
 PS  
 XX Example 3; Page 46; 70pp; English.  
 CC The invention relates to novel genome derived antigen 33 (GNA33) peptides  
 CC which are capable of eliciting the production of antibodies that exhibit  
 CC complement-mediated bactericidal activity and/or opsonic activity against  
 CC a surface-exposed epitope on loop 4 of PorA of Neisseria meningitidis  
 CC serogroup B (MenB) Pl.2 serosubtype. GNA33 sequences are useful for  
 CC eliciting an immune response against MenB bacterium in a mammalian  
 CC subject. They are useful for detecting MenB bacterium in a biological  
 CC sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium  
 CC infection. Sequences of the invention are used as vaccines. The present  
 CC sequence is N. meningitidis serogroup B Pl.2 serosubtype Por A loop4  
 XX peptide.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 23.5%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QTPQ 5  
 DB 1 QTPQ 4  
 RESULT 31  
 AAP90659  
 ID AAP90659 standard; protein; 7 AA.  
 XX  
 AC AAP90659;  
 XX  
 DT 10-MAR-2003 (updated)  
 DT 26-MAY-1990 (first entry)  
 XX  
 XX New antihypertensive peptide.  
 XX  
 XX Antihypertensive peptide; angiotensin-converting enzyme;  
 KW ACE.  
 KW  
 XX Synthetic.  
 OS  
 PN JP01083096-A.  
 XX  
 PD 28-MAR-1989.  
 XX  
 PF 25-SEP-1987; 87JP-0241646.  
 XX  
 PR 25-SEP-1987; 87JP-0241646.  
 XX  
 PA (AJIN ) AJINOMOTO KK.  
 XX  
 DR WPI; 1989-136272/18.  
 XX  
 XX New antihypertensive peptide(s) -  
 PT used to inhibit angiotensin-converting enzyme  
 XX  
 PS Disclosure; Page -; 20pp; Japanese.  
 XX  
 CC The peptide and its salts inhibit angiotensin-converting  
 CC enzyme (ACE) and are useful as antihypertensives. They may be  
 CC administered orally, parenterally or rectally in the form of tablets,  
 CC capsules, granules, powder, syrup, suspension, suppositories,  
 CC ointment, cream, gel, plaster, inhalation compn. or  
 CC injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.  
 CC (Updated on 10-MAR-2003 to add missing OS field.)  
 XX

SQ Sequence 7 AA;  
 Query Match 23.5%; Score 4; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PQPL 7  
 DB 1 PQPL 4  
 RESULT 32  
 AAR38240  
 ID AAR38240 standard; peptide; 7 AA.  
 XX  
 AC AAR38240;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 08-OCT-1993 (first entry)  
 XX  
 DE Alzheimer paired helical filament tau protein epitope 47-53.  
 XX  
 KW Alzheimer tau protein; phosphorylation-dependent; PHF;  
 KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 4..5  
 FT /label= Phosphorylation\_motif  
 XX  
 PN WO9311231-A1.  
 XX  
 PD 10-JUN-1993.  
 XX  
 PF 07-DEC-1992; 92WO-EP02829.  
 XX  
 PR 06-DEC-1991; 91EP-0120974.  
 PR 16-NOV-1992; 92EP-0119551.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;  
 PI Steiner B;  
 XX  
 DR WPI; 1993-197050/24.  
 XX  
 PT Tau protein epitope(s), specific antibodies and protein kinase(s)  
 PT - used in the prevention, diagnosis and treatment of Alzheimer's  
 PT disease  
 XX  
 PS Claim 5; Page 89; 148pp; English.  
 XX  
 CC This is one of 26 preferred epitopes which occur in a phosphorylated  
 CC state in tau protein from Alzheimer paired helical filaments. The  
 CC epitopes all include phosphorylatable serine residues in Ser-Pro  
 CC motifs, Ile-Gly-Ser motifs or Cys-Gly-Ser motifs and/or  
 CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern  
 CC of tau protein phosphorylation differs between Alzheimer's and  
 CC non-Alzheimer's individuals. Knowledge of the phosphorylated  
 CC epitopes and antibodies which recognise them may be useful in  
 CC diagnosis, treatment and prevention of Alzheimer's Disease. The  
 CC protein kinases present in mammalian brain which phosphorylate the  
 CC different epitopes are also claimed but no sequences are given.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 7 AA;  
 Query Match 23.5%; Score 4; DB 14; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTP 4



```

Db |||||
 2 LQTP 5

RESULT 33
AAR37559
ID AAR37559 standard; peptide; 7 AA.
AC AAR37559;
XX
XX
XX 25-MAR-2003 (updated)
DT 07-OCT-1993 (first entry)
XX
XX Phosphorylated tau protein epitope.
DE
XX Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
KW treatment; formation; inhibition; inhibitor.
XX Homo sapiens.
OS
XX EP544942-A1.
PN
XX 09-JUN-1993.
PD
XX 06-DEC-1991; 91EP-0120974.
PF
XX 06-DEC-1991; 91EP-0120974.
PR
XX (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
PA
XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
PI WPI; 1993-183841/23..
XX
XX Phosphorylated tau protein epitope associated with Alzheimer's
PT disease - is used as protein kinase inhibitor for treatment and
PT diagnosis
XX
XX Claim 4; Page 16; 34pp; English.
PS
XX The sequence is that of an epitope of tau protein which specifically
CC occurs in a phosphorylated state in tau protein from Alzheimer's
CC paired helical fragments. It may be used as part of a method for the
CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
CC also be used in an in vitro model for the study of the generation of
CC the Alzheimer state of proteins and the testing of substances which
CC prevent the conversion of normal to Alzheimer tau protein. The
CC epitope occurs at residues 47-53 of human tau protein.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 7 AA;
SQ

Query Match 23.5%; Score 4; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db |||||
 2 LQTP 5

RESULT 34
AAW27488
ID AAW27488 standard; peptide; 7 AA.
XX
XX AAW27488;
XX
XX 14-APR-1998 (first entry)
DT
XX Tyrosinase cytoplasmic domain derived peptide SEQ ID NO:3.
DE
XX Tyrosinase cytoplasmic domain; trypsin; epidermal melanocyte;
KW phosphorylation; pigmentation; modulator; protein kinase C-beta;

KW hyperpigmentation; hypopigmentation; hair; skin; fur; wool.
XX Synthetic.
OS Homo sapiens.
XX WO9735998-A1.
PN
XX 02-OCT-1997.
PD
XX 27-MAR-1997; 97WO-US04752.
PF
XX 28-MAR-1996; 96US-0623364.
PR
XX (UYBO-) UNIV BOSTON.
PA
XX Gilchrist BA, Park H;
XX WPI; 1997-489658/45.
DR
XX Modulating activation of tyrosinase in epidermal melanocytes - by
PT regulating phosphorylation of specific serine or threonine residues
PT in cytoplasmic domain, useful to reduce or increase skin
PT pigmentation
XX
XX Example 5; Page 23; 40pp; English.
PS
XX A method has been developed of modulating, specifically preventing, the
CC activation of tyrosinase in vertebrate epidermal melanocytes. The method
CC comprises modulating, specifically inhibiting, the protein kinase C beta
CC (PKC beta) mediated phosphorylation of a Ser or Thr residue in the
CC tyrosinase's cytoplasmic domain. The present sequence represents a
CC tyrosinase cytoplasmic domain derived peptide. The method can be used
CC to therapeutically or cosmetically alter, particularly reduce, skin,
CC hair, wool or fur pigmentation, e.g. to treat hyperpigmentation or
CC hypopigmentation. Pigmentation can be reduced without surgery, or the
CC use of harsh chemicals.
XX
XX Sequence 7 AA;
SQ

Query Match 23.5%; Score 4; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8
Db |||||
 1 QPLL 4

RESULT 35
AAW17516
ID AAW17516 standard; Peptide; 7 AA.
XX
XX AAW17516;
AC
XX 31-OCT-1997 (first entry)
DT
XX Protein kinase C related kinase 2 peptide PRK2-3 (467-473).
DE
XX Signal transduction; cell signalling; modulator; immunomodulator;
KW protein kinase C related kinase 2; receptor for activated kinase C;
KW RACK; PRK2; cognate; graft rejection; autoimmune disease;
KW allergy; asthma; therapy.
XX
XX Homo sapiens.
OS
XX WO9714038-A1.
PN
XX 17-APR-1997.
PD
XX 10-OCT-1996; 96WO-US16195.
PF
XX 18-JUN-1996; 96US-0665647.
PR
XX 10-OCT-1995; 95US-0541964.
PR

```

```

PR 31-JAN-1996; 96US-0594447.
XX (TERR-) TERRAPIN TECHNOLOGIES INC.
XX
PI Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;
PI Vasquez NJ, Voronova A;
XX
DR WPI; 1997-236030/21.
XX
XX Identifying a modulator of intracellular signal transduction - by
PT determining the interaction of a signal generating peptide with the
PT test substance, allows modulation of the immune system
XX
PS Example 4; Page 34; 74pp; English.
XX
XX This sequence is a peptide, designated PRK2-3, that corresponds
CC to amino acid residues 467-473 of protein kinase C related kinase
CC 2 (PRK2). It was tested as a signal generating peptide in a
CC claimed method for identifying modulators of intracellular signal
CC transduction. This method assesses the ability of candidate
CC modulators to affect the interaction between a signal-generating
CC protein (see AAM15778-79, AAM15781, AAM15784-85, AAM17452-78), and a
CC cognate binding protein involved in modulating the signal
CC transduction function. Identified substances are useful as
CC immunomodulators (claimed). They reduce T-cell activity, reduce
CC the rate of graft rejection, reduce the severity of an autoimmune
CC disorder, ameliorate allergy and/or asthma, or diminish a cytokine
CC response (claimed).
XX
SQ Sequence 7 AA;
Query Match 23.5%; Score 4; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16
DB 2 EPQG 5

RESULT 36
AAG79271
ID AAG79271 standard; peptide; 7 AA.
XX
AC AAG79271;
XX
XX 03-JAN-2002 (first entry)
XX
DE Peptide which binds specifically to the kinase domain receptor.
XX
KW Kinase domain receptor; KDR; vascular endothelial growth factor; VEGF;
KW VEGF antibody; angiogenesis; cancer; diabetic retinopathy; psoriasis;
KW hemangioblastoma; Kaposi's sarcoma.
XX
OS Synthetic.
XX
XX WO200172829-A2.
XX
XX 04-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-IB00577.
XX
XX 31-MAR-2000; 2000US-193396P.
XX
XX (INSP) INST PASTEUR.
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX (UYPA-) UNIV PARIS 13 NORD.
XX
XX Tournaire R, Demangel C, Derbin C, Perret G, Mazie J, Plouet J;
XX Vassy R;
XX
XX WPI; 2001-616471/71.
XX
PT Novel peptides inhibiting binding of vascular endothelial growth factor
PT (VEGF) to kinase domain receptor, or inhibiting binding of anti-VEGF
PT antibody to VEGF, useful for treating diabetic retinopathy and
PT psoriasis -
XX
PS Claim 6; Page 19; 55pp; English.
XX
XX AAG79260-73 represent peptides which affect vascular endothelial growth
CC factor (VEGF) binding to antibodies or the kinase domain receptor (KDR).
CC Peptides AAG79260-66 were selected by their ability to bind to an
CC anti-VEGF antibody, and peptides AAG79267-73 were selected for their
CC ability to bind to CHO cells expressing a KDR which binds VEGF. The
CC peptides inhibit the binding of VEGF to KDR, and inhibit binding of
CC anti-VEGF antibody to VEGF. The peptides are useful for inhibiting
CC angiogenesis and for treating diseases including cancer, diabetic
CC retinopathy, psoriasis, hemangioblastoma, and Kaposi's sarcoma.
XX
SQ Sequence 7 AA;
Query Match 23.5%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQTP 4
DB 4 IQTP 7

RESULT 37
AAM45859
ID AAM45859 standard; Peptide; 7 AA.
XX
AC AAM45859;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2130.
XX
DE
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
XX Example 4; Page 108; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated

```

CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 23.5%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
 ||||  
 Db 4 PQPL 7

RESULT 38  
 AAM45914  
 ID AAM45914 standard; Peptide; 7 AA.

XX AC AAM45914;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #2195.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX PS Example 4; Page 108; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response

CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 23.5%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
 ||||  
 Db 4 PQPL 7

RESULT 39  
 AAM45919  
 ID AAM45919 standard; Peptide; 7 AA.

XX AC AAM45919;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #2190.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX PS Example 4; Page 108; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including

CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;  
 SQ Query Match 23.5%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
 Db |||||  
 4 PQPL 7

RESULT 40  
 AAM45924  
 ID AAM45924 standard; Peptide; 7 AA.

XX AC AAM45924;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #2195.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW endodermoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.  
 OS Synthetic.

XX CA2290722-AL.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, a  
 CC oligodendroglioma, endodermoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;  
 SQ Query Match 23.5%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
 Db |||||  
 4 PQPL 7

RESULT 41  
 AAM45929  
 ID AAM45929 standard; Peptide; 7 AA.

XX AC AAM45929;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #2200.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW endodermoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.  
 OS Synthetic.

XX CA2290722-AL.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KB;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX Example 4; Page 108; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, a  
 CC oligodendroglioma, endodermoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 23.5%; Score 4; DB 22; Length 7;

```

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
Db 4 PQPL 7

RESULT 42
AAE33721
ID AAE33721 standard; peptide; 7 AA.
AC AAE33721;
XX
XX
DT 16-APR-2003 (first entry)
XX
XX
DE N. meningitidis serogroup B Pl.2 serosubtype VR2 loop 4 peptide #2.
XX
XX
KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;
KW MenB; immune response; infection; vaccine; antibacterial.
XX
XX
OS Neisseria meningitidis.
XX
XX
PN WO200283711-A2.
XX
XX
PD 24-OCT-2002.
XX
XX
PF 11-APR-2002; 2002WO-US11501.
XX
XX
PR 17-APR-2001; 2001US-284554P.
PR 03-OCT-2001; 2001US-326838P.
XX
XX
PA (CHIR) CHIRON CORP.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
XX
PI Granoff D, Moe G, Rappuoli R;
XX
XX
DR WPI; 2003-120415/11.
XX
XX
PT New GNA33 peptides that elicit production of antibodies exhibiting
PT complement-mediated bactericidal activity against a Neisseria
PT meningitidis serogroup B (MenB), useful for diagnosing or preventing
PT (as vaccine) MenB infection -
XX
XX
PS Example 4; Page 48; 70pp; English.
XX
XX
CC The invention relates to novel genome derived antigen 33 (GNA33) peptides
CC which are capable of eliciting the production of antibodies that exhibit
CC complement-mediated bactericidal activity and/or opsonic activity against
CC a surface-exposed epitope on loop 4 of PorA of Neisseria meningitidis
CC serogroup B (MenB) Pl.2 serosubtype. GNA33 sequences are useful for
CC eliciting an immune response against MenB bacterium in a mammalian
CC subject. They are useful for detecting MenB antibodies in a biological
CC sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium
CC infection. Sequences of the invention are used as vaccines. The present
CC sequence is N. meningitidis serogroup B Pl.2 serosubtype VR2 loop 4
CC peptide.
XX
XX
SQ Sequence 7 AA;

Query Match 23.5%; Score 4; DB 24; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTPQ 5
Db 4 QTPQ 7

RESULT 43
AAP90673
ID AAP90673 standard; protein; 8 AA.
XX

```

```

AC AAP90673;
XX
XX
DT 10-MAR-2003 (updated)
DT 26-MAY-1990 (first entry)
XX
XX
DE New antihypertensive peptide.
XX
XX
KW Antihypertensive peptide; angiotensin-converting enzyme;
KW ACE.
XX
XX
OS Synthetic.
XX
XX
PN JP01083096-A.
XX
XX
PD 28-MAR-1989.
XX
XX
PF 25-SEP-1987; 87JP-0241646.
XX
XX
PR 25-SEP-1987; 87JP-0241646.
XX
XX
PA (AJIN) AJINOMOTO KK.
XX
XX
DR WPI; 1989-136272/18.
XX
XX
PT New antihypertensive peptide(s) -
PT used to inhibit angiotensin-converting enzyme
XX
XX
PS Disclosure; Page -; 20pp; Japanese.
XX
XX
CC The peptide and its salts inhibit angiotensin-converting
CC enzyme (ACE) and are useful as antihypertensives. They may be
CC administered orally, parenterally or rectally in the form of tablets,
CC capsules, granules, powder, syrup, suspension, suppositories,
CC ointment, cream, gel, plaster, inhalation compsn. or
CC injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
CC (Updated on 10-MAR-2003 to add missing OS field.)
XX
XX
SQ Sequence 8 AA;

Query Match 23.5%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
Db 2 PQPL 5

RESULT 44
AAR03875
ID AAR03875 standard; Protein; 8 AA.
XX
XX
AC AAR03875;
XX
XX
DT 17-FEB-1993 (first entry)
XX
XX
DE Hypotensive peptide (14).
XX
XX
KW Hypotensor; salt.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "pyroGlutamic acid"
FT FT
XX
XX
PN JP02062828-A.
XX
XX
PD 02-MAR-1990.
XX
XX
PF 26-AUG-1988; 88JP-0211696.
XX
XX
PR 26-AUG-1988; 88JP-0211696.

```

XX (AJIN ) AJINOMOTO KK.  
 XX WPI; 1990-111933/15.  
 XX New peptide used as active ingredient of hypotensive agent -  
 PT which may be prep'd. e.g. as tablets, capsules, powder, syrup,  
 PT injection prepn. etc.  
 XX Claim; Page ?; 9pp; Japanese.  
 XX The peptides given in AAR03862-76 and their salts can be used as  
 CC components of hypotensive agents.  
 CC The hypotensor may be in the form of tablets, capsules, powder,  
 CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of  
 CC the peptide.  
 XX SQ Sequence 8 AA;  
 Query Match 23.5%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PQPL 7  
 Db |||||  
 2 PQPL 5  
 RESULT 45  
 AAR93206  
 ID AAR93206 standard; peptide; 8 AA.  
 XX AAR93206;  
 AC AAR93206;  
 DT 04-OCT-1996 (first entry)  
 DE New contraceptive peptide #2 derived from Zona Pellucida ZP3 protein.  
 KW Zona pellucida; ZP3; vaccine; humoral response; contraception; epitope;  
 KW pathogenic T cell response; ovary; assay; autoimmune; antibody;  
 KW passive immunisation.  
 XX Synthetic.  
 XX WO9606113-A1.  
 XX 29-FEB-1996.  
 XX 18-AUG-1995; 95WO-EP03311.  
 XX 22-AUG-1994; 94EP-0202392.  
 XX (ALKU ) AKZO NOBEL NV.  
 XX Bunschoten EJ, Grootenhuis AJ, Van DUIN M;  
 DR WPI; 1996-151331/15.  
 XX Immuno:contraceptive peptide(s) derived from Zona Pellucida protein  
 PT ZP3 - used to prepare contraceptive vaccine and in assays to measure  
 PT autoimmune antibodies  
 XX Claim 4; Page 31; 43pp; English.  
 XX Peptides AAR93205-9 are examples of peptides derived from the sequence  
 CC of the Zona Pellucida protein ZP3 which contain the amino acid sequences  
 CC AAR93210 or AAR93214-5. The peptides are esp. based on amino acids 23-30  
 CC of the ZP3 protein. The novel peptides can be used in vaccines to induce  
 CC a humoral response against the ZP3 protein e.g. for contraception, esp.  
 CC as they do not raise a pathogenic T cell response since they do not  
 CC contain T cell epitopes. The novel peptides thus avoid potential ovarian  
 CC damage caused by some peptides used as vaccines. The peptides are also  
 CC useful in assays for detecting autoimmune antibodies or for generating

CC antibodies for passive immunisation.  
 XX SQ Sequence 8 AA;  
 Query Match 23.5%; Score 4; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PQPL 7  
 Db |||||  
 1 PQPL 4  
 RESULT 46  
 AAM23045  
 ID AAM23045 standard; Peptide; 8 AA.  
 XX AAM23045;  
 AC AAM23045;  
 DT 22-OCT-2001 (first entry)  
 XX HIV peptide SEQ ID NO 930.  
 DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 KW human immunodeficiency virus; vaccine.  
 KW Human immunodeficiency virus.  
 OS Synthetic.  
 XX WO200155177-A2.  
 XX 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-DK00059.  
 XX 28-JAN-2000; 2000EP-0610017.  
 XX 31-JAN-2000; 2000US-0179333.  
 XX (STAT-) STATENS SERUM INST.  
 XX Fomsgaard A, Brunak S, Buus S, Corbet S, Laemolier SL, Hansen J;  
 PI WPI; 2001-476184/51.  
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in  
 PT anti-HIV vaccines -  
 XX Example 4; Page 70; 383pp; English.  
 XX The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents.  
 XX SQ Sequence 8 AA;  
 Query Match 23.5%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 PQGD 17  
 Db |||||  
 1 PQGD 4  
 RESULT 47  
 AAM23046  
 ID AAM23046 standard; Peptide; 8 AA.  
 XX AAM23046;  
 AC AAM23046;

```

XX DT 22-OCT-2001 (first entry)
XX DE HIV peptide SEQ ID NO 931.
XX KW Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-DK00059.
XX PR 28-JAN-2000; 2000EP-0610017.
XX PR 31-JAN-2000; 2000US-0179333.
XX PA (STAT-) STATENS SERUM INST.
XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX DR WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 48
XX AAM23047
XX ID AAM23047 standard; Peptide; 8 AA.
XX AC AAM23047;
XX XX 22-OCT-2001 (first entry)
XX DT HIV peptide SEQ ID NO 932.
XX DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-DK00059.
XX PR 28-JAN-2000; 2000EP-0610017.
XX PR 31-JAN-2000; 2000US-0179333.
XX PA (STAT-) STATENS SERUM INST.
XX PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX DR WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 48
XX AAM23047
XX ID AAM23047 standard; Peptide; 8 AA.
XX AC AAM23047;
XX XX 22-OCT-2001 (first entry)
XX DT HIV peptide SEQ ID NO 932.
XX DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX OS Human immunodeficiency virus.
XX OS Synthetic.
XX PN WO200155177-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-DK00059.
XX PR 28-JAN-2000; 2000EP-0610017.

```

```

PR 31-JAN-2000; 2000US-0179333.
XX (STAT-) STATENS SERUM INST.
XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX WPI; 2001-476184/51.
XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
XX PT anti-HIV vaccines -
XX PS Example 4; Page 70; 383pp; English.
XX CC The invention relates to identification of cytotoxic T cell lymphocyte
XX CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX CC are a major protective mechanism against viral diseases. Antibodies may
XX CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX CC prevent infection of cells in the host, but CTL will limit viral
XX CC production by killing the cell. The CTL epitopes are useful in medicine,
XX CC in the manufacture of vaccines or diagnostic agents.
XX SQ Sequence 8 AA;
XX Query Match 23.5%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 14 PQGD 17
XX Db 1 PQGD 4
XX RESULT 49
XX ABG91967
XX ID ABG91967 standard; Peptide; 8 AA.
XX AC ABG91967;
XX DT 04-DEC-2002 (first entry)
XX DE Human antibody fragment #151.
XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX KW metastasis; hypervariable region; autoimmune disease; thrombosis;
XX KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX KW myocardial infarction; retinopathic disease; abnormal platelet function;
XX KW sulphated tyrosine-dependent protein-protein interaction.
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX XX 11-JUL-2002.
XX PD 31-DEC-2001; 2001WO-US49442.
XX PF 29-DEC-2000; 2000US-258948P.
XX PR 29-DEC-2000; 2000US-0751181.
XX XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Santhone E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX DR WPI; 2002-674776/72.
XX XX Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer -
XX PS Disclosure; Page 294; 310pp; English.
XX

```

CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody.  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-adhesion or  
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
 CC increasing mortality of tumour or leukaemia cells, for increasing the  
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
 CC or anti-leukaemia agents, or for decreasing the number of tumour or  
 CC leukaemia cells in a patient, or in the manufacture of a medicament for  
 CC the above mentioned purposes. The epitopes are useful for diagnosing and  
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
 CC inflammatory diseases, cardiovascular diseases such as myocardial  
 CC infarction, retinopathic diseases and other diseases mediated by abnormal  
 CC platelet function and diseases caused by sulphated tyrosine-dependent  
 CC protein-protein interactions. This sequence represents a human antibody  
 CC fragment of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
 ||||  
 DB 4 LQTP 7

# RESULT 50

ABG91998  
 ID ABG91998 standard; Peptide; 8 AA.

XX AC ABG91998;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #182.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US49442.

XX PR 29-DEC-2000; 2000US-258948P.

XX PR 29-DEC-2000; 2000US-0751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer -

PS Disclosure; Page 302; 310pp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-adhesion or  
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
 CC increasing mortality of tumour or leukaemia cells, for increasing the  
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
 CC or anti-leukaemia agents, or for decreasing the number of tumour or  
 CC leukaemia cells in a patient, or in the manufacture of a medicament for  
 CC the above mentioned purposes. The epitopes are useful for diagnosing and  
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
 CC inflammatory diseases, cardiovascular diseases such as myocardial  
 CC infarction, retinopathic diseases and other diseases mediated by abnormal  
 CC platelet function and diseases caused by sulphated tyrosine-dependent  
 CC protein-protein interactions. This sequence represents a human antibody  
 CC fragment of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
 ||||  
 DB 4 LQTP 7

# RESULT 51

ABG78276  
 ID ABG78276 standard; Peptide; 8 AA.

XX AC ABG78276;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #151.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US49440.

XX PR 29-DEC-2000; 2000US-0751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favour of other  
 PT cells -

XX Claim 34; Page 218; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv



CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
 Db 4 LQTP 7

RESULT 52  
 ABG78307

ID ABG78307 standard; Peptide; 8 AA.

XX AC ABG78307;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #182.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX Homo sapiens.

XX WO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US49440.

XX 29-DEC-2000; 2000US-0751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Feretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 FT or fragment, or construct of fragment with enhanced binding  
 FT characteristics so as to selectively bind target cell in favour of other  
 FT cells -

PS Claim 34; Page 226; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention.

SQ Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
 Db 4 LQTP 7

RESULT 53

AAO17346

ID AAO17346 standard; peptide; 8 AA.

XX AC AAO17346;

XX 08-JUL-2002 (first entry)

XX Alpha-isomaltosylglucosaccharide synthase related peptide #17.

XX Alpha-isomaltosylglucosaccharide synthase; enzyme; sweetener; food;  
 KW drink; cosmetics; pharmaceutical; cyclic tetrasaccharide.

OS Bacillus globisporus.

XX WO200210361-A1.

XX 07-FEB-2002.

XX 25-JUL-2001; 2001WO-JP06412.

XX 01-AUG-2000; 2000JP-0233364.

PR 02-AUG-2000; 2000JP-0234937.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kubota M, Tsusaki K, Higashiyama T, Fukuda S, Miyake T;

XX WPI; 2002-315302/35.

XX Alpha-Isomaltosylglucosaccharide synthase capable of transferring  
 FT Alpha-glucosyl from saccharide, useful in producing cyclic  
 FT tetrasaccharides and related carbohydrates industrially for application  
 FT in compositions e.g. as drugs -

PS Disclosure; Page 204; 209pp; Japanese.

XX The present invention relates to an alpha-isomaltosylglucosaccharide  
 CC synthase which is capable of transferring alpha-glucosyl from a  
 CC saccharide to form a specific saccharide which carries an alpha-1,6  
 CC glucosyl linkage at its non-reducing end and an alpha-1,4 glucosyl  
 CC linkage at ends other than the non-reducing end and has a degree of  
 CC glucose polymerization of at most 3, but without substantially elevating  
 CC the reducing ability. The synthase is useful in producing cyclic  
 CC tetrasaccharides and related carbohydrates industrially for application  
 CC in compositions e.g. as sweeteners, low calorie food materials, taste  
 CC improvers, flavour improvers, quality improvers, water-separation  
 CC inhibitors, stabilizers, excipients, binding agents and pulverisation  
 CC bases, especially in foods, drinks, cosmetics and pharmaceuticals. The  
 CC present sequence is a peptide described in the exemplification of the  
 CC invention.

XX Sequence 8 AA;

Query Match 23.5%; Score 4; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17  
|||||  
Db 5 PQGD 8

RESULT 54  
ABB05026  
ID ABB05026 standard; peptide; 8 AA.  
XX  
AC ABB05026;  
XX  
DT 22-MAR-2002 (first entry)  
XX  
DE Bacillus globisporus peptide SEQ ID NO:7.  
XX  
KW Bacillus globisporus; alpha-isomaltosyltransferase; saccharide;  
KW cyclic tetrasaccharide; alpha-isomaltosyl transfer; food; drink;  
KW glucose polymerisation; cosmetic; pharmaceutical; sweetening agent.  
XX  
OS Sporosarcina globisporus.  
XX  
PN WO200190338-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 22-MAY-2001; 2001WO-JF04276.  
XX  
PR 22-MAY-2000; 2000JP-0149484.  
XX  
PS 28-JUL-2000; 2000JP-0229557.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Kubota M, Nishimoto T, Aga H, Fukuda S, Miyake T;  
XX  
DR WPI; 2002-089929/12.  
XX  
PT Microorganism-produced alpha-isomaltosyltransferase capable of forming  
PT cyclic tetrasaccharide of specific structure and its derivatives, for  
PT use in food, pharmaceutical and cosmetic industries -  
XX  
PS Disclosure; Page 156; 158pp; Japanese.  
XX

The present invention describes an alpha-isomaltosyltransferase, capable  
of producing a cyclic tetrasaccharide with a (1,6)-alpha-D-  
glucopyranosyl-(1,3)-alpha-D-glucopyranosyl-(1,6)-alpha-D-glucopyranosyl  
structure via a reaction involving alpha-isomaltosyl transfer from a  
saccharide having specific linkages and degree of glucose polymerisation.  
The alpha-isomaltosyltransferase can be used to produce a cyclic  
tetrasaccharide of specific structure and its derivatives for  
formulation into compositions for foods and drinks, cosmetics and  
pharmaceuticals, both of which can be applied in sweetening agents, low  
tooth-decaying and low calorie food materials, flavour improvers,  
quality improvers, water retainers, aroma retainers, stabiliser,  
excipients, adhesives or powdering base. The cheap, industrially-  
producing, easily handleable, substantially non-reducing or lowly  
reducing saccharides can prevent starch from aging, protein from  
denaturation and fat from deterioration as well as colouring, and are  
no hygroscopic, with acid and heat stability, which can undergo  
aminocarbonyl reaction. The present sequence represents a peptide  
isolated from Bacillus globisporus (also called Sporosarcina globisporus)  
which is used in the exemplification of the present invention.

QY 14 PQGD 17  
|||||

Sequence 8 AA;  
Query Match 23.5%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 PQGD 8

RESULT 55  
AAP90672  
ID AAP90672 standard; protein; 9 AA.  
XX  
AC AAP90672;  
XX  
DT 10-MAR-2003 (updated)  
DT 26-MAY-1990 (first entry)  
XX  
DE New antihypertensive peptide.  
XX  
KW Antihypertensive peptide; angiotensin-converting enzyme;  
KW ACE.  
XX  
OS Synthetic.  
XX  
PN JP01083096-A.  
XX  
PD 28-MAR-1989.  
XX  
PF 25-SEP-1987; 87JP-0241646.  
XX  
PR 25-SEP-1987; 87JP-0241646.  
XX  
PA (AJIN ) AJINOMOTO KK.  
XX  
DR WPI; 1989-136272/18.  
XX  
PT New antihypertensive peptide(s) -  
PT used to inhibit angiotensin-converting enzyme  
XX  
PS Disclosure; Page -; 20pp; Japanese.  
XX

The peptide and its salts inhibit angiotensin-converting  
enzyme (ACE) and are useful as antihypertensives. They may be  
administered orally, parenterally or rectally in the form of tablets,  
capsules, granules, powder, syrup, suspension, suppositories,  
ointment, cream, gel, plaster, inhalation compsn. or  
injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.  
(Updated on 10-MAR-2003 to add missing OS field.)

QY 4 PQPL 7  
|||||  
Db 3 PQPL 6

Sequence 9 AA;  
Query Match 23.5%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 56  
AAR84629  
ID AAR84629 standard; Peptide; 9 AA.  
XX  
AC AAR84629;  
XX  
DT 02-JUN-1996 (first entry)  
XX  
DE Wheat acetyl-Coenzyme-A-carboxylase peptide sequence.  
XX  
KW Acetyl Coenzyme A carboxylase; ACCase; plasmid pK11;  
KW transgenic plant; modified oil content;  
KW polyhydroxyalkanoate polymer; herbicide resistance;  
KW monocot crop improvement.  
XX  
OS Triticum aestivum.  
XX  
PN WO9529246-A1.

XX 02-NOV-1995.  
 XX 21-APR-1994; 94WO-GB00846.  
 XX 21-APR-1994; 94WO-GB00846.  
 XX (ZENE ) ZENECA LTD.  
 XX Bright SWJ, Elborough KM, Fentem PA, Slabas AR;  
 XX WPI; 1995-382994/49.  
 XX DNA encoding acetyl Coenzyme A carboxylase - used for developing  
 XX plants with controlled expression of Accase, e.g. for controlling  
 XX fatty acid synthesis.  
 XX Disclosure; Fig 3; 61pp; English.  
 XX Wheat acetyl Coenzyme A carboxylase (ACCase) was partially  
 XX purified from wheat germ and a dominant 220 KDa band was identified  
 XX as ACCase by column chromatography and SDS-PAGE. After  
 XX purification in the gel, the protein was hydrolysed using  
 XX Endoproteinase LysC, and resulting peptides were purified by  
 XX electrophoresis and loaded onto an ABI 477A pulse liquid  
 XX protein sequencer. Sequence data of 4 peptides (this peptide and  
 XX peptides AAR84625, AAR84627 and AAR84631) were compared with plasmid  
 XX PK111-deduced amino acid sequences (AAR84630, AAR84626, AAR84628 and  
 XX AAR84632) so as to authenticate PK111 (see AAR04948) as wheat ACCase  
 XX partial cDNA. More specifically, this peptide corresponds to  
 XX amino acids 319-327 of the PK111 deduced AA sequence AAR84619  
 XX (i.e. AAR84630). Partial cDNA clone PK111 (NCIF 40553) can be  
 XX used to create a sense/antisense expression cassette to  
 XX transform rape and other oilseed plants (canola, soybean,  
 XX sunflower) to downregulate production of the ACCase enzyme.  
 XX The transgenic plants have a lower or a modified oil content.  
 XX Down-regulation of oil synthesis can be used to divert the  
 XX substrate, acetyl Coenzyme A, into synthesis of alternative  
 XX storage materials (starch, protein or novel polymers e.g.  
 XX polyhydroxyalkanoates). Full-length ACCase clones can be used  
 XX to create transgenic plants over-expressing ACCase, and  
 XX therefore with increased oil content. ACCase over-expression in  
 XX monocot plants such as wheat, barley, maize and rice, which are  
 XX normally sensitive to herbicides, results in  
 XX aryloxyphenoxy-propionate and alkylketone herbicide resistance in  
 XX the transgenic plants (dicots are normally resistant to these  
 XX herbicides).  
 XX SQ Sequence 9 AA;  
 Query Match 23.5%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 EPOQ 16  
 Db 4 EPOQ 7  
 RESULT 57  
 AAW17493  
 ID AAW17493 standard; Peptide; 9 AA.  
 XX AAW17493;  
 XX AAW17493;  
 XX 31-OCT-1997 (first entry)  
 XX Protein kinase C-theta peptide theta V3-2 (337-345).  
 XX Signal transduction; cell signalling; modulator; immunomodulator;  
 XX protein kinase C; receptor for activated kinase C; RACK;  
 XX PKC-theta; cognate; graft rejection; autoimmune disease;  
 XX allergy; asthma; therapy.

XX Homo sapiens.  
 XX WO9714038-A1.  
 XX 17-APR-1997.  
 XX 10-OCT-1996; 96WO-US16195.  
 XX 18-JUN-1996; 96US-0665647.  
 XX 10-OCT-1995; 95US-0541964.  
 XX 31-JAN-1996; 96US-0594447.  
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.  
 XX Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;  
 XX Vasquez NJ, Voronova A;  
 XX WPI; 1997-236030/21.  
 XX Identifying a modulator of intracellular signal transduction - by  
 XX determining the interaction of a signal generating peptide with the  
 XX test substance, allows modulation of the immune system  
 XX Example 4; Page 33; 74pp; English.  
 XX This sequence is a peptide, designated theta V3-2, that corresponds  
 XX to amino acid residues 337-345 in the V3 region of protein kinase C  
 XX (PKC)-theta. It was tested as a signal generating peptide in a  
 XX claimed method for identifying modulators of intracellular signal  
 XX transduction. This method assesses the ability of candidate  
 XX modulators to affect the interaction between a signal-generating  
 XX protein, such as a PKC isozyme peptide (see AAW15781, AAW15781,  
 XX AAW15784-85, AAW17452-78), and a cognate binding protein involved in  
 XX are useful as immunomodulators (claimed). Identified substances  
 XX activity, reduce the rate of graft rejection, reduce the severity  
 XX of an autoimmune disorder, ameliorate allergy and/or asthma, or  
 XX diminish a cytokine response (claimed).  
 XX SQ Sequence 9 AA;  
 Query Match 23.5%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 EPOQ 16  
 Db 4 EPOQ 7  
 RESULT 58  
 AAW60385  
 ID AAW60385 standard; peptide; 9 AA.  
 XX AAW60385;  
 XX 24-AUG-1998 (first entry)  
 XX Tumour homing peptide of the invention.  
 XX Tumour homing peptide; in vivo panning;  
 XX alpha-V-containing integrin binding motif; tumour.  
 XX Synthetic.  
 XX WO9810795-A2.  
 XX 19-MAR-1998.  
 XX 10-SEP-1997; 97WO-US16086.  
 XX 10-SEP-1996; 96US-0710067.

```

XX PA (BURN-) BURNHAM INST.
XX PI Pasqualini R, Ruoslahti E;
XX DR WPI; 1998-207151/18.
XX PT Tumour homing molecules and their conjugates - useful for, e.g.
XX PT directing linked moiety to tumour containing angiogenic vasculature
XX PS Example 3; Page 74; 105pp; English.
XX CC AAW60303-99 represent peptides recovered from human breast cancer.
XX CC The peptides are tumour homing peptides, and are identified by in
XX CC vivo panning. The in vivo panning comprises administering a library
XX CC of diverse peptides to a subject having a tumour, collecting a sample of
XX CC the tumour, identifying a peptide that homes to the tumour, collecting a
XX CC sample of normal tissue corresponding to the tumour, and determining
XX CC that the peptide that homes to the tumour is not present in the normal
XX CC tissue. The tumour homing peptides can be linked to a moiety (e.g.
XX CC doxorubicin), and used to direct the moiety to a tumour.
XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 4 LLQV 7

RESULT 59
AAW52801
ID AAW52801 standard; peptide; 9 AA.
AC AAW52801;
XX 07-JUL-1998 (first entry)
XX Signal region from human gp75 (brown locus protein).
XX Sorting signal region; intracellular transport; endosome;
XX endoplasmic reticulum; genetic immunisation.
XX Homo sapiens.
XX WO9804720-A1.
XX 05-FEB-1998.
XX 18-JUL-1997; 97WO-US12675.
XX 26-JUL-1996; 96US-0022710.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX Bartido SM, Houghton A, Yu Y;
XX WPI; 1998-130707/12.
XX Nucleic acid for genetic immunisation including subcellular
XX localisation signal - provides better loading of major
XX histocompatibility complex molecules and increased immune response
XX Claim 4; Page 22; 31pp; English.
XX Peptides AAW52801-05 represent sorting signal regions for various
XX proteins. AAW52801-04 direct intracellular transport to the endosomes,
XX while AAW52805 directs intracellular transport to the endoplasmic
XX reticulum. The specification describes a nucleic acid construct for
XX genetic immunisation which comprises sequence encoding an antigenic
XX protein or peptide, and sequence encoding a second protein or peptide
XX that acts as a sorting signal to direct intracellular transport of the
XX antigen to the endosome or endoplasmic reticulum. The constructs or
XX vaccines including them are used to induce an immune response against the
XX antigen.
XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8
Db 4 QPLL 7

RESULT 60
AAW52802
ID AAW52802 standard; peptide; 9 AA.
AC AAW52802;
XX 07-JUL-1998 (first entry)
XX Signal region from human tyrosinase (albino locus protein).
XX Sorting signal region; intracellular transport; endosome;
XX endoplasmic reticulum; genetic immunisation.
XX Homo sapiens.
XX WO9804720-A1.
XX 05-FEB-1998.
XX 18-JUL-1997; 97WO-US12675.
XX 26-JUL-1996; 96US-0022710.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX Bartido SM, Houghton A, Yu Y;
XX WPI; 1998-130707/12.
XX Nucleic acid for genetic immunisation including subcellular
XX localisation signal - provides better loading of major
XX histocompatibility complex molecules and increased immune response
XX Claim 5; Page 22; 31pp; English.
XX Peptides AAW52801-05 represent sorting signal regions for various
XX proteins. AAW52801-04 direct intracellular transport to the endosomes,
XX while AAW52805 directs intracellular transport to the endoplasmic
XX reticulum. The specification describes a nucleic acid construct for
XX genetic immunisation which comprises sequence encoding an antigenic
XX protein or peptide, and sequence encoding a second protein or peptide
XX that acts as a sorting signal to direct intracellular transport of the
XX antigen to the endosome or endoplasmic reticulum. The constructs or
XX vaccines including them are used to induce an immune response against the
XX antigen.
XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8
Db 4 QPLL 7

```

## RESULT 61

AAV47643  
ID AAY47643 standard; Peptide; 9 AA.

XX  
AC AAY47643;

XX  
DT 01-DEC-1999 (first entry)

XX  
DE Immunogenic peptide having a human leukocyte antigen binding motif #2254.  
XX  
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW Immune response; T cell activation; major histocompatibility complex;  
KW Cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.

XX  
OS Synthetic.

XX  
OS Homo sapiens.

XX  
PN WO9945954-A1.

XX  
PD 16-SEP-1999.

XX  
PF 13-MAR-1998; 98WO-US05039.

XX  
PR 13-MAR-1998; 98WO-US05039.

XX  
PA (EPIM-) EPIMUNE INC.

XX  
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX  
DR WPI; 1999-551214/46.

XX  
PT New immunogenic peptides with HLA binding motif, useful in treatment  
PT and diagnosis of cancers and viral diseases

XX  
PS Claim 1; Page 117; 150pp; English.

XX  
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also  
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
CC response against the antigen from which the peptide is derived.  
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
CC normally induced by an antigen in the form of a peptide fragment bound  
CC to a HLA molecule, rather than the intact foreign antigen itself, and  
CC are particularly important in tumour rejection and in fighting viral  
CC infections. The peptides are therefore useful therapeutically to treat  
CC or prevent viral infections and cancers in mammals (especially humans)  
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
CC They can be administered as vaccines to elicit an immune response in  
CC individuals susceptible or otherwise at risk of viral infection or  
CC cancer, or used to treat chronic or acute conditions. They are also  
CC useful diagnostically, and can be used to induce a cytotoxic T cell  
CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
CC produce CTLs ex vivo for infusion back into a patient. The  
CC polynucleotides encoding the immunogenic peptides are also useful  
CC therapeutically and for immunisation as above.

XX  
SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10

Db 6 LLQV 9

## RESULT 62

AAW93711

XX ID AAW93711 standard; Peptide; 9 AA.

XX  
AC AAW93711;

XX  
DT 28-JUN-1999 (first entry)

XX  
DE Human breast cancer derived tumour homing peptide 83.

XX  
KW Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;  
KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;  
KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;  
KW prognosis; inflammation; regeneration; wounded tissue; targeting;  
KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;  
KW occlusive thrombus; human.

XX  
OS Homo sapiens.

XX  
PN WO9913329-A1.

XX  
PD 18-MAR-1999.

XX  
PF 08-SEP-1998; 98WO-US18895.

XX  
PR 25-AUG-1998; 98US-0139802.

XX  
PR 10-SEP-1997; 97US-0926914.

XX  
PA (BURN-) BURNHAM INST.

XX  
PI Pasqualini R, Ruoslahti E;

XX  
DR WPI; 1999-215158/18.

XX  
PT Identifying molecules that home to angiogenic vasculature used as  
PT targets for anticancer agents

XX  
PS Example II; Page 104; 180pp; English.

XX  
CC This invention describes novel peptides which home to angiogenic  
CC vasculature, specifically of a tumour and which have anti-tumour,  
CC anti-inflammatory, anti-angiogenic and anti-arthritis activity. Such  
CC molecules are identified by treating a purified NGR receptor with a test  
CC compound and identifying compounds that bind specifically to the NGR  
CC receptor. The peptides of the invention are inhibitors of angiogenesis  
CC and can be used to produce conjugates for delivering agents to  
CC angiogenic vasculature, particularly anticancer drugs or an imaging  
CC agent, for diagnosis or prognosis. These conjugates may be directed to  
CC non-tumour angiogenic vasculature, e.g. that present in inflammatory,  
CC regenerating or wounded tissue, e.g. for treatment of macular  
CC degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides  
CC provide specific targeting to tumours, especially their supporting  
CC vasculature, since the NGR receptor is exposed to the circulation only in  
CC angiogenic vasculature. Precise targeting should reduce the systemic  
CC toxicity of anticancer drugs in the conjugates. Complete killing of all  
CC target cells may not be essential since partial denudation of endothelium  
CC may result in an occlusive thrombus, and endothelial cells are unlikely  
CC to become resistant to anticancer agents nor to lose the targeting  
CC receptor. AAW93622-W93809 and AAW93843-44 are examples of tumour homing  
CC peptides used in the invention.

XX  
SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10

Db 4 LLQV 7

## RESULT 63

AAB21802

ID AAB21802 standard; Peptide; 9 AA.  
 XX AC AAB21802;  
 XX  
 XX 22-MAR-2001 (first entry)  
 XX  
 XX Human breast tumour homing peptide #87.  
 DE  
 XX Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;  
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200042973-A2.  
 XX  
 XX 27-JUL-2000.  
 XX  
 XX 21-JAN-2000; 2000WO-US01602.  
 XX  
 XX 22-JAN-1999; 99US-0235902.  
 XX  
 XX (BURN-) BURNHAM INST.  
 XX  
 XX Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;  
 FI  
 XX WPI; 2000-499174/44.  
 XX  
 XX Homing pro-apoptotic conjugate comprising a tumor homing molecule that  
 PT selectively homes to a mammalian cell type or tissue linked to an  
 PT antimicrobial peptide, useful for the treatment of prostate cancer -  
 XX  
 XX Example 5; Page 90; 118pp; English.  
 XX  
 XX The present invention relates to homing pro-apoptotic conjugates,  
 CC comprising of a tumour homing molecule that selectively homes to a  
 CC mammalian cell type or tissue, linked to an antimicrobial peptide. The  
 CC homing pro-apoptotic conjugates are selectively internalised by the  
 CC mammalian cell type or tissue and exhibits high toxicity, especially to  
 CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell  
 CC toxicity when not linked to the tumor homing molecule. The conjugates are  
 CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and  
 CC prostate cancer or melanoma. The present sequence is a homing peptide  
 CC isolated in the present invention, which can be conjugated to an  
 CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the  
 CC present invention.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 23.5%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 LLQV 10  
 Db 4 LLQV 7  
 RESULT 64  
 AAY95224  
 ID AAY95224 standard; Peptide; 9 AA.  
 XX AC AAY95224;  
 XX  
 XX 29-AUG-2000 (first entry)  
 XX  
 XX Anti-platelet glycoprotein Ib human H1b-5 VL CDR3.  
 DE  
 XX Variable light chain; single chain antibody; scFv; human; H1b-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic; CDR3;  
 KW complementarity determining region.  
 XX  
 XX Homo sapiens.  
 OS

XX WO200026667-A1.  
 XX  
 XX 11-MAY-2000.  
 XX  
 XX 29-OCT-1999; 99WO-US25495.  
 XX  
 XX 30-OCT-1998; 98US-0106275.  
 XX  
 XX (MILL/) MILLER J L.  
 XX  
 XX Miller JL;  
 XX  
 XX WPI; 2000-365744/31.  
 XX  
 XX Isolated nucleic acid molecule encoding anti-human platelet  
 PT glycoprotein Ib alpha molecule useful for producing antibodies which  
 PT inhibit platelet aggregation -  
 XX  
 XX Claim 21; Fig 8; 89pp; English.  
 XX  
 XX The present sequence is that of complementarity determining region  
 CC 3 (CDR3) of the light chain variable region (VL) of human single  
 CC chain antibody (scFv) H1b-5, which is directed against platelet  
 CC glycoprotein Ib (GPIb). The H1b series of scFv antibodies was  
 CC isolated from a human synthetic VH and VL scFv library on the  
 CC basis of their binding to platelet GPIb. Whether displayed as  
 CC surface proteins on a phagemid or secreted as free scFv by  
 CC Escherichia coli, the H1b scFv clones are capable of inhibiting  
 CC von Willebrand factor-dependent aggregation of platelets. The scFv  
 CC are composed of native human protein sequences and are therefore  
 CC attractive potential reagents for therapeutic purposes. They  
 CC provide a new class of antithrombotic agents, useful for the  
 CC prevention of platelet-dependent thrombi in diseased arteries,  
 CC bypass grafts, dialysis etc., and can also be used as diagnostic  
 CC reagents. Methods of inhibiting aggregation of platelets, of  
 CC binding human platelet GPIb alpha and of selecting a VH or VL  
 CC region of an antibody that inhibits platelet aggregation are  
 CC claimed. Fragments of the scFv VH or VL chain, including CDR  
 CC fragments, are also claimed.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 23.5%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LQTP 4  
 Db 4 LQTP 7  
 RESULT 65  
 AAY67365  
 ID AAY67365 standard; peptide; 9 AA.  
 XX AC AAY67365;  
 XX  
 XX 25-APR-2000 (first entry)  
 XX  
 XX Melanosomal protein sorting signal.  
 DE  
 XX  
 XX Therapeutic antigen; cytotoxic T lymphocyte; CTL; CTL immune response;  
 KW cellular immune response induction method; vaccine; human; tumour;  
 KW melanoma glycoprotein 75; melanosomal protein sorting signal.  
 XX  
 XX Unidentified.  
 OS  
 XX WO9963945-A2.  
 XX  
 XX 16-DEC-1999.  
 XX  
 XX 11-JUN-1999; 99WO-US13146.  
 XX

XX 12-JUN-1998; 98US-0089055.  
 PR 30-OCT-1998; 98US-0106339.  
 XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
 PA PI Nikolic-Zugic J, Dyall R, Houghton AN;  
 XX WPI; 2000-126432/11.  
 DR Induction of a cellular immune response to a weakly immunogenic  
 PT protein, used to target and kill tumour cells -  
 XX Disclosure; Page 7; 44pp; English.  
 PS This sequence represents a sorting signal which may be coupled to the  
 CC antigen used in the method of the invention. The invention relates to a  
 CC method for inducing a cytotoxic T lymphocyte (CTL) immune response to a  
 CC non/weakly-immunogenic proteins which are expressed on tumour cells. The  
 CC method for inducing a cellular immune response to a non-immunogenic or  
 CC weakly immunogenic target peptide expressed on tumour cells of a  
 CC mammalian subject comprises administering antigen to induce a cellular  
 CC immune response to the target peptide. The antigen comprises an  
 CC immunogenic portion having a major histocompatibility complex (MHC)  
 CC binding domain which binds to the MHC and an immune recognition domain  
 CC which is recognized by T-cells. The antigen is derived from the target  
 CC peptide such that the MHC-binding portion binds to MHC with a greater  
 CC affinity than the target peptide without material alteration of the  
 CC immune recognition portion. The methods are used for inducing a cellular  
 CC immune response to a non-immunogenic or weakly immunogenic target peptide  
 CC expressed on tumour cells of a mammalian subject. The antigens and  
 CC immunogens of the invention, as well as polynucleotides encoding them,  
 CC are used in vaccine compositions against tumour cells.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 23.5%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPLL 8  
 DB |||||  
 4 QPLL 7  
 RESULT 66  
 AAE06380  
 ID AAE06380 standard; peptide; 9 AA.  
 XX  
 AC AAE06380;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human breast tumour homing peptide #86.  
 XX  
 KW Chimeric prostate-homing pro-apoptotic peptide; prostate-homing peptide;  
 KW antimicrobial peptide; prostate cancer; breast tumour homing molecule;  
 KW cytostatic; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153342-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 16-JAN-2001; 2001WO-US01362.  
 XX  
 PR 21-JAN-2000; 2000US-0489582.  
 PA (BUEN-) BUENHAM INST.  
 XX  
 PI Ruoslahti EI, Pasqualini R, Arap W, Breddesen DE, Ellerby HM;  
 XX

DR WPI; 2001-451901/48.  
 XX Novel chimeric prostate-homing pro-apoptotic peptide, used to treat  
 PT prostate cancer, comprises a prostate-homing peptide linked to an  
 PT antimicrobial peptide -  
 XX Example 5; Page 89; 176pp; English.  
 PS  
 XX The patent discloses novel chimeric prostate-homing pro-apoptotic  
 CC peptide which comprises a prostate-homing peptide linked to an  
 CC antimicrobial peptide, where the chimeric peptide is selectively  
 CC internalised by and exhibits high toxicity to prostate tissue and  
 CC where the antimicrobial peptide has low mammalian cell toxicity when  
 CC not linked to prostate-homing peptide. The chimeric peptide is used  
 CC to direct an antimicrobial peptide in vivo to a prostate cancer, to  
 CC induce selective toxicity in vivo in a prostate cancer, and to treat  
 CC a patient with prostate cancer. The present sequence is human breast  
 CC tumour homing peptide. This sequence is useful in the homing of  
 CC pro-apoptotic conjugates of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 23.5%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LLQV 10  
 DB |||||  
 4 LLQV 7  
 RESULT 67  
 ABJ15201  
 ID ABJ15201 standard; Peptide; 9 AA.  
 XX  
 AC ABJ15201;  
 XX  
 DT 02-JAN-2003 (first entry)  
 XX  
 DE Immunogenic HIV peptide #51.  
 XX  
 KW HIV; gene therapy; vaccine; immunogenic HIV peptide;  
 KW cytotoxic T lymphocyte; HIV infection.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN WO200269691-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US06314.  
 XX  
 PR 01-MAR-2001; 2001US-272565P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 XX  
 PI McNicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;  
 XX  
 DR WPI; 2002-750429/81.  
 XX  
 PT New immunogenic HIV peptide having one or more epitopes immunoreactive  
 PT with cytotoxic T lymphocytes, useful for diagnosing, treating and  
 PT monitoring HIV infection in humans -  
 XX Claim 6; Page 44; 65pp; English.  
 PS  
 XX The invention comprises immunogenic HIV peptides which contain one or  
 CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from  
 CC an HIV-positive individual. The immunogenic HIV peptides of the invention  
 CC are useful for diagnosing, treating and monitoring HIV infection. The  
 CC present amino acid sequence represents an immunogenic HIV peptide of the  
 CC invention.

```

XX Sequence 9 AA;
SQ
 Query Match 23.5%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
Db 1 LQTP 4

RESULT 68
ABG91962
ID ABG91962 standard; Peptide; 9 AA.
XX
AC ABG91962;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #146.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
XX
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
PS Disclosure; Page 293; 310pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of tumour or leukaemia cells, for increasing the
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC protein-protein interactions. This sequence represents a human antibody

```

```

CC fragment of the invention.
XX
SQ Sequence 9 AA;
 Query Match 23.5%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
Db 4 LQTP 7

RESULT 69
ABG91975
ID ABG91975 standard; Peptide; 9 AA.
XX
AC ABG91975;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #159.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US49442.
XX
PR 29-DEC-2000; 2000US-258948P.
XX
PR 29-DEC-2000; 2000US-0751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
PS Disclosure; Page 296; 310pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
CC increasing mortality of diseased cells to damage by anti-disease, anti-cancer
CC or anti-leukaemia agents, or for decreasing the number of tumour or
CC leukaemia cells in a patient, or in the manufacture of a medicament for
CC the above mentioned purposes. The epitopes are useful for diagnosing and
CC treating diseases such as cancer, leukaemia, autoimmune diseases,
CC inflammatory diseases, cardiovascular diseases such as myocardial
CC infarction, retinopathic diseases and other diseases mediated by abnormal
CC platelet function and diseases caused by sulphated tyrosine-dependent
CC platelet function and diseases caused by sulphated tyrosine-dependent

```



CC protein-protein interactions. This sequence represents a human antibody  
 CC fragment of the invention.

XX Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
 Db 4 LQTP 7  
 ||||

#### RESULT 70

ABG94766  
 ID ABG94766 standard; Peptide; 9 AA.

XX AC

XX AC ABG94766;

XX 02-DEC-2002 (first entry)

XX Replikin sequence identified by the 3-point recognition method #39.  
 KW Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;  
 KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;  
 KW Surface Antigen S Precursor Protein.

XX Human papillomavirus type 71.

XX US2002120106-A1.

XX 29-AUG-2002.

XX 26-OCT-2001; 2001US-0984056.

XX 27-MAR-2001; 2001US-278761P.

XX 09-JUL-2001; 2001US-303396P.

XX 04-SEP-1998; 98US-0146755.

XX 27-MAR-2001; 2001US-0817144.

XX (BOGO/) BOGOCH S.

PA (BOGO/) BOGOCH E S.

XX Bogoch S, Bogoch ES;

XX WPI; 2002-691212/74.

XX Isolated Bacillus anthracis and small pox virus peptides (I), also  
 known as replikins, useful for formulating vaccines for treating  
 anthrax or small pox, comprise 7 to 50 amino acids -

XX Disclosure; Page 3; 16pp; English.

CC The invention relates to isolated Bacillus anthracis and small pox virus  
 CC peptides, also known as replikins, comprising 7 to 50 amino acids  
 CC including at least one lysine residue located six to ten residues from a  
 CC second lysine residue, at least one histidine residue, and at least 8%  
 CC lysine residues. The peptides were identified using the 3-point-  
 CC recognition method and based on the replikin sequence isolated from  
 CC glioblastoma cells malignin peptide which is of non-human origin.  
 CC Also included are anti-replikin antibodies (or antibody cocktail),  
 CC a method of stimulating the immune system of a subject to  
 CC produce antibodies to Bacillus anthracis or small pox comprising  
 CC administering an effective amount of at least one or more Bacillus  
 CC anthracis or small pox replikin and an antisense nucleic acid molecule  
 CC complementary to a mRNA encoding a Bacillus anthracis polypeptide  
 CC (e.g. Anthrax Lethal Factor Protein pX01-107) comprising a replikin  
 CC sequence, an antisense nucleic acid molecule complementary to a mRNA  
 CC encoding a Small Pox Virus polypeptide (e.g. Surface Antigen S Precursor  
 CC Protein comprising a replikin sequence). The peptides are useful for  
 CC stimulating the immune system of a subject to produce antibodies that  
 CC bind specifically to Anthrax or small pox polypeptides containing a

CC replikin sequence. The peptides are useful for generating antibodies that  
 CC can be used in the treatment and/or prevention of anthrax or small pox.  
 CC The peptides are also useful for formulating vaccines for treating  
 CC anthrax or small pox. The present sequence is a replikin sequence  
 CC isolated by the 3-point-recognition system and sharing structural  
 CC similarity with the replikin sequence isolated from glioblastoma cells  
 CC malignin.

XX Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLLQ 9  
 Db 4 PLLQ 7  
 ||||

#### RESULT 71

ABG78271

ID ABG78271 standard; Peptide; 9 AA.

XX AC

XX AC ABG78271;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #146.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX Homo sapiens.

XX WO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US49440.

XX 29-DEC-2000; 2000US-0751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 Plaksain D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favour of other  
 PT cells -

XX Claim 34; Page 217; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention.

QY 1 LQTP 4

```

KW HLA.
XX Homo sapiens.
XX WO200216593-A2.
XX 28-FEB-2002.
XX PD
XX PF 22-AUG-2001; 2001WO-US26276.
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX PA
XX (AGEN-) AGENSYS INC.
XX PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX PI Challita-eid FM, Jakobovits A;
XX DR WPI; 2002-425659/45.
XX CC New compositions comprising a gene (designated 158P1D7), its encoded
XX PT protein or their modulators, useful for treating or diagnosing cancers,
XX PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans) -
XX PS Disclosure; Page 129; 181pp; English.
XX CC The invention relates to a novel nucleic acid, designated 158P1D7. The
XX CC compositions are useful for treating or diagnosing cancers, particularly
XX CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX CC horses or humans). The compositions are also useful for monitoring
XX CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX CC of the invention can be used in gene therapy to treat the said disorders.
XX CC This sequence represents a human leukocyte antigen (HLA) peptide relating
XX CC to the 158P1D7 protein of the invention.
XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db ||||
6 LLQV 9

RESULT 75
ABJ01433
XX ID ABJ01433 standard; Peptide; 9 AA.
XX AC ABJ01433;
XX DT 19-SEP-2002 (first entry)
XX DE
XX DE 158P1D7 related HLA peptide SEQ ID No 133.
XX KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX KW HLA.
XX OS Homo sapiens.
XX PN WO200216593-A2.
XX XX
XX PD 28-FEB-2002.
XX PF 22-AUG-2001; 2001WO-US26276.
XX XX
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX PA
XX (AGEN-) AGENSYS INC.

```

```

XX PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX PI Challita-eid FM, Jakobovits A;
XX XX
XX DR WPI; 2002-425659/45.
XX CC New compositions comprising a gene (designated 158P1D7), its encoded
XX PT protein or their modulators, useful for treating or diagnosing cancers,
XX PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans) -
XX PS Disclosure; Page 130; 181pp; English.
XX CC The invention relates to a novel nucleic acid, designated 158P1D7. The
XX CC compositions are useful for treating or diagnosing cancers, particularly
XX CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX CC horses or humans). The compositions are also useful for monitoring
XX CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX CC of the invention can be used in gene therapy to treat the said disorders.
XX CC This sequence represents a human leukocyte antigen (HLA) peptide relating
XX CC to the 158P1D7 protein of the invention.
XX SQ Sequence 9 AA;

Query Match 23.5%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db ||||
1 LLQV 4

```

Search completed: November 25, 2003, 18:15:39  
Job time : 57.0691 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 : Search time 33.8191 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQPLLOWMEPQGD 17

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 17    | 100.0       | 17     | 15 | US-10-281-652-2     |
| 2          | 6     | 35.3        | 12     | 12 | US-10-286-457-195   |
| 3          | 6     | 35.3        | 18     | 9  | US-09-864-761-40147 |
| 4          | 5     | 29.4        | 12     | 12 | US-10-137-867-452   |
| 5          | 4     | 23.5        | 5      | 12 | US-10-168-758-15    |
| 6          | 4     | 23.5        | 6      | 11 | US-09-500-700-104   |
| 7          | 4     | 23.5        | 7      | 9  | US-09-822-270-12    |
| 8          | 4     | 23.5        | 7      | 12 | US-10-342-371-12    |
| 9          | 4     | 23.5        | 8      | 10 | US-09-894-018-76    |
| 10         | 4     | 23.5        | 8      | 12 | US-10-089-549-17    |
| 11         | 4     | 23.5        | 9      | 7  | US-08-344-824-282   |
| 12         | 4     | 23.5        | 9      | 9  | US-09-765-086-102   |
| 13         | 4     | 23.5        | 9      | 9  | US-09-834-765-48    |
| 14         | 4     | 23.5        | 9      | 9  | US-09-834-765-130   |
| 15         | 4     | 23.5        | 9      | 9  | US-09-834-765-356   |
| 16         | 4     | 23.5        | 9      | 9  | US-09-834-765-462   |
| 17         | 4     | 23.5        | 9      | 9  | US-09-834-765-546   |
| 18         | 4     | 23.5        | 9      | 9  | US-09-898-541-1     |
| 19         | 4     | 23.5        | 9      | 9  | US-09-898-541-2     |
| 20         | 4     | 23.5        | 9      | 10 | US-09-984-056-56    |
| 21         | 4     | 23.5        | 9      | 10 | US-09-984-057-56    |
| 22         | 4     | 23.5        | 9      | 11 | US-09-972-656-30    |
| 23         | 4     | 23.5        | 9      | 12 | US-10-375-992-102   |
| 24         | 4     | 23.5        | 9      | 12 | US-10-105-232-56    |
| 25         | 4     | 23.5        | 9      | 12 | US-10-189-437-56    |
| 26         | 4     | 23.5        | 9      | 12 | US-10-277-292-101   |
| 27         | 4     | 23.5        | 9      | 12 | US-10-277-292-133   |
| 28         | 4     | 23.5        | 9      | 12 | US-10-137-867-288   |
| 29         | 4     | 23.5        | 9      | 12 | US-10-280-340-101   |
| 30         | 4     | 23.5        | 9      | 12 | US-10-280-340-133   |
| 31         | 4     | 23.5        | 9      | 15 | US-10-264-374-102   |
| 32         | 4     | 23.5        | 10     | 7  | US-08-344-824-393   |
| 33         | 4     | 23.5        | 10     | 8  | US-08-424-550B-597  |
| 34         | 4     | 23.5        | 10     | 9  | US-09-834-765-468   |
| 35         | 4     | 23.5        | 10     | 10 | US-09-908-322-53    |
| 36         | 4     | 23.5        | 10     | 10 | US-09-867-852-93    |
| 37         | 4     | 23.5        | 10     | 11 | US-09-783-931-53    |
| 38         | 4     | 23.5        | 10     | 12 | US-09-573-822C-108  |
| 39         | 4     | 23.5        | 10     | 12 | US-10-277-292-169   |
| 40         | 4     | 23.5        | 10     | 12 | US-10-277-292-179   |
| 41         | 4     | 23.5        | 10     | 12 | US-10-277-292-286   |
| 42         | 4     | 23.5        | 10     | 12 | US-10-277-292-436   |
| 43         | 4     | 23.5        | 10     | 12 | US-10-277-292-436   |
| 44         | 4     | 23.5        | 10     | 12 | US-10-137-867-274   |
| 45         | 4     | 23.5        | 10     | 12 | US-10-280-340-169   |
| 46         | 4     | 23.5        | 10     | 12 | US-10-280-340-179   |
| 47         | 4     | 23.5        | 10     | 12 | US-10-280-340-286   |
| 48         | 4     | 23.5        | 10     | 12 | US-10-280-340-424   |
| 49         | 4     | 23.5        | 10     | 12 | US-10-280-340-436   |
| 50         | 4     | 23.5        | 10     | 15 | US-10-185-815-89    |
| 51         | 4     | 23.5        | 11     | 9  | US-09-829-855-233   |
| 52         | 4     | 23.5        | 11     | 9  | US-09-829-855-234   |
| 53         | 4     | 23.5        | 11     | 12 | US-10-076-047A-57   |
| 54         | 4     | 23.5        | 12     | 9  | US-09-281-717-39    |
| 55         | 4     | 23.5        | 12     | 11 | US-09-954-385-193   |
| 56         | 4     | 23.5        | 13     | 11 | US-09-992-238-27    |
| 57         | 4     | 23.5        | 13     | 11 | US-09-992-238-77    |
| 58         | 4     | 23.5        | 14     | 9  | US-09-829-855-217   |
| 59         | 4     | 23.5        | 14     | 12 | US-10-271-078-53    |
| 60         | 4     | 23.5        | 14     | 12 | US-10-367-405-18    |
| 61         | 4     | 23.5        | 14     | 12 | US-10-256-865-15    |
| 62         | 4     | 23.5        | 14     | 15 | US-10-120-604-26    |
| 63         | 4     | 23.5        | 14     | 15 | US-10-120-604-69    |
| 64         | 4     | 23.5        | 14     | 15 | US-10-120-604-85    |
| 65         | 4     | 23.5        | 14     | 15 | US-10-294-891-25    |
| 66         | 4     | 23.5        | 15     | 12 | US-10-161-791-405   |
| 67         | 4     | 23.5        | 15     | 12 | US-10-360-836-9     |
| 68         | 4     | 23.5        | 15     | 12 | US-10-360-836-10    |
| 69         | 4     | 23.5        | 15     | 12 | US-10-360-836-11    |
| 70         | 4     | 23.5        | 15     | 12 | US-10-281-652-34    |
| 71         | 4     | 23.5        | 15     | 15 | US-10-194-985-29    |
| 72         | 4     | 23.5        | 16     | 12 | US-10-299-043-2     |
| 73         | 4     | 23.5        | 16     | 15 | US-10-174-105A-181  |
| 74         | 4     | 23.5        | 17     | 9  | US-09-861-708-1     |
| 75         | 4     | 23.5        | 18     | 9  | US-09-864-761-34833 |
| 76         | 4     | 23.5        | 18     | 9  | US-09-864-761-45132 |
| 77         | 4     | 23.5        | 18     | 12 | US-10-029-386-32086 |
| 78         | 4     | 23.5        | 18     | 12 | US-10-029-386-34082 |
| 79         | 4     | 23.5        | 18     | 12 | US-10-145-206-153   |
| 80         | 4     | 23.5        | 18     | 12 | US-10-350-405-138   |
| 81         | 4     | 23.5        | 18     | 15 | US-10-194-985-26    |
| 82         | 4     | 23.5        | 19     | 9  | US-09-864-761-35260 |
| 83         | 4     | 23.5        | 19     | 9  | US-09-864-761-43517 |
| 84         | 4     | 23.5        | 19     | 10 | US-09-989-903-53    |
| 85         | 4     | 23.5        | 19     | 10 | US-09-943-075A-4    |
| 86         | 4     | 23.5        | 19     | 10 | US-09-135-238B-17   |
| 87         | 4     | 23.5        | 19     | 15 | US-10-068-564-53    |
| 88         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 89         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 90         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 91         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 92         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 93         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 94         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 95         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 96         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 97         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 98         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 99         | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |
| 100        | 4     | 23.5        | 19     | 15 | US-10-225-567A-950  |

Sequence 462, App  
Sequence 546, App  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 56, Appl  
Sequence 56, Appl  
Sequence 30, Appl  
Sequence 102, App  
Sequence 56, Appl  
Sequence 56, Appl  
Sequence 101, App  
Sequence 133, App  
Sequence 286, App  
Sequence 101, App  
Sequence 133, App  
Sequence 102, App  
Sequence 393, App  
Sequence 597, App  
Sequence 468, App  
Sequence 53, Appl  
Sequence 93, Appl  
Sequence 53, Appl  
Sequence 108, App  
Sequence 169, App  
Sequence 179, App  
Sequence 286, App  
Sequence 424, App  
Sequence 436, App  
Sequence 274, App  
Sequence 169, App  
Sequence 179, App  
Sequence 286, App  
Sequence 424, App  
Sequence 436, App  
Sequence 89, Appl  
Sequence 233, App  
Sequence 234, App  
Sequence 57, Appl  
Sequence 39, Appl  
Sequence 193, App  
Sequence 27, Appl  
Sequence 77, Appl  
Sequence 217, App  
Sequence 33, Appl  
Sequence 18, Appl  
Sequence 15, Appl  
Sequence 26, Appl  
Sequence 69, Appl  
Sequence 85, Appl  
Sequence 25, Appl  
Sequence 405, App  
Sequence 9, Appli  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 34, Appl  
Sequence 29, Appl  
Sequence 2, Appli  
Sequence 181, App  
Sequence 1, Appli  
Sequence 34833, A  
Sequence 45132, A  
Sequence 32086, A  
Sequence 34082, A  
Sequence 153, App  
Sequence 138, App  
Sequence 26, Appl  
Sequence 35260, A  
Sequence 43517, A  
Sequence 53, Appl  
Sequence 4, Appli  
Sequence 17, Appl  
Sequence 550, App

89 4 23.5 19 15 US-10-225-567A-1354 Sequence 1354, Ap  
90 4 23.5 20 9 US-09-864-761-35404 Sequence 35404, A  
91 4 23.5 20 9 US-09-864-761-48956 Sequence 48956, A  
92 4 23.5 20 12 US-10-299-043-17 Sequence 17, Appl  
93 4 23.5 20 12 US-10-299-043-18 Sequence 18, Appl  
94 4 23.5 20 12 US-10-280-066-242 Sequence 242, App  
95 4 23.5 20 12 US-09-927-734C-11 Sequence 11, Appl  
96 4 23.5 20 15 US-10-194-985-25 Sequence 25, Appl  
97 3 17.6 3 15 US-10-233-885-5 Sequence 5, Appl  
98 3 17.6 3 15 US-10-231-581-5 Sequence 5, Appl  
99 3 17.6 4 10 US-09-808-832-208 Sequence 208, App  
100 3 17.6 4 12 US-10-084-388A-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-10-281-652-2  
; Sequence 2, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281.652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641.803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-2

Query Match 100.0%; Score 17; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred No. 3e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQLQVMPEQGD 17  
| | | | | | | | | | | | | | | | | |  
Db 1 LQTPQLQVMPEQGD 17

RESULT 2  
US-10-286-457-195  
; Sequence 195, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286.457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 195  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, ba  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-195

Query Match 35.3%; Score 6; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQP 6  
| | | | | |  
Db 2 LQTPQP 7

RESULT 3  
US-09-864-761-40147  
; Sequence 40147, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864.761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 40147  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC005343.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4

```

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
US-09-864-761-40147

```

```

Query Match 35.3%; Score 6; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 QPLLQV 10
Db 3 QPLLQV 8

```

```

RESULT 4
US-10-137-867-452
; Sequence 452, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 452
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-452

```

```

Query Match 29.4%; Score 5; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 QPLLQ 9
Db 7 QPLLQ 11

```

```

RESULT 5
US-10-168-758-15
; Sequence 15, Application US/10168758
; Publication No. US20030207812A1
; GENERAL INFORMATION:
; APPLICANT: Chapdelaine, Marc J
; APPLICANT: Katherine, Knappenberger
; APPLICANT: Steelman, Gary
; APPLICANT: Suchard, Suzanne
; APPLICANT: Sygowski, Linda
; TITLE OF INVENTION: CD45
; FILE REFERENCE: Z70624-1P US

```

```

; CURRENT APPLICATION NUMBER: US/10/168,758
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-168-758-15

```

```

Query Match 23.5%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 13 EPQG 16
Db 2 EPQG 5

```

```

RESULT 6
US-09-500-700-104
; Sequence 104, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT1160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-104

```

```

Query Match 23.5%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 PQPL 7
Db 1 PQPL 4

```

```

RESULT 7
US-09-822-270-12
; Sequence 12, Application US/09822270
; Patent No. US20020068697A1
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE

```

; APPLICANT: PLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA  
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS  
; FILE REFERENCE: 205060US0  
; CURRENT APPLICATION NUMBER: US/09/822,270  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-09-822-270-12

Query Match 23.5%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 LQTP 4  
|||  
Db 4 LQTP 7

RESULT 8  
US-10-342-371-12  
; Sequence 12, Application US/10342371  
; Publication No. US20030171289A1  
; GENERAL INFORMATION:  
; APPLICANT: TOURNAIRE, ROSELYNE  
; APPLICANT: DEMANGEL, CAROLINE  
; APPLICANT: DERBIN, CLAUDE  
; APPLICANT: PERRET, GERARD  
; APPLICANT: MAZIE, JEAN-CLAUDE  
; APPLICANT: PLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA  
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS  
; FILE REFERENCE: 205060US0  
; CURRENT APPLICATION NUMBER: US/10/342,371  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US/09/822,270  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-10-342-371-12

Query Match 23.5%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 1 LQTP 4  
|||  
Db 4 LQTP 7

RESULT 9  
US-09-894-018-76  
; Sequence 76, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:

; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Deniw  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligopeptide  
US-09-894-018-76

Query Match 23.5%; Score 4; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 4 PQPL 7  
|||  
Db 5 PQPL 8

RESULT 10  
US-10-089-549-17  
; Sequence 17, Application US/10089549  
; Publication No. US20030194762A1  
; GENERAL INFORMATION:  
; APPLICANT: KUBOTA, Michio  
; APPLICANT: TSUSAKI, Keiji  
; APPLICANT: HIGASHIYAMA, Takanobu  
; APPLICANT: FUKUDA, Shigeharu  
; APPLICANT: MIYAKE, Toshio  
; TITLE OF INVENTION: ALPHA-ISOMALTOSE-GLUCOSACCHARIDE-FORMING ENZYME, PROCESS AND I  
; TITLE OF INVENTION: SAME  
; FILE REFERENCE: KUBOTA=9  
; CURRENT APPLICATION NUMBER: US/10/089,549  
; CURRENT FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: JP 233364/2000  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: JP 234937/2000  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: PCT/JF01/06412  
; PRIOR FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Bacillus globisporus  
US-10-089-549-17

Query Match 23.5%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

Qy 14 PQGD 17  
|||  
Db 5 PQGD 8

RESULT 11  
 US-08-344-824-282  
 ; Sequence 282, Application US/08344824  
 ; Publication No. US20030152580A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SETTE, Alessandro  
 ; APPLICANT: SIDNEY, John  
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
 ; NUMBER OF SEQUENCES: 399  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: One Market Plaza, Steuart Street Tower, 20th  
 ; STREET: Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/344,824  
 ; FILING DATE: 23-NOV-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/278,634  
 ; FILING DATE: 21-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bastian, Kevin L.  
 ; REGISTRATION NUMBER: 34,774  
 ; REFERENCE/DOCKET NUMBER: 14137-80-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 543-9600  
 ; TELEFAX: (415) 543-5043  
 ; INFORMATION FOR SEQ ID NO: 282:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-344-824-282

Query Match 23.5%; Score 4; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 0; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 14 PQGD 17  
 Db 2 PQGD 5

RESULT 12  
 US-09-765-086-102  
 ; Sequence 102, Application US/09765086  
 ; Patent No. US20010046498A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; APPLICANT: Wadib, Arap  
 ; APPLICANT: Bredesen, Dale E.  
 ; APPLICANT: Ellerby, H. Michael  
 ; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With  
 ; TITLE OF INVENTION: Pro-Apoptotic Activity  
 ; FILE REFERENCE: P-LJ 3844  
 ; CURRENT APPLICATION NUMBER: US/09/765,086  
 ; CURRENT FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION NUMBER: US 09/489,582  
 ; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 235  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 102  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic peptide  
 ; US-09-765-086-102

Query Match 23.5%; Score 4; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 0; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 7 LLQV 10  
 Db 4 LLQV 7

RESULT 13  
 US-09-834-765-48  
 ; Sequence 48, Application US/09834765  
 ; Patent No. US20020055478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
 ; TITLE OF INVENTION: AND DETECTION OF CANCER  
 ; FILE REFERENCE: 129.6USU1  
 ; CURRENT APPLICATION NUMBER: US/09/834,765  
 ; CURRENT FILING DATE: 2001-09-21  
 ; PRIOR APPLICATION NUMBER: 60/197,647  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 770  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 48  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-834-765-48

Query Match 23.5%; Score 4; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 0; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 QY 4 PQPL 7  
 Db 4 PQPL 7

RESULT 14  
 US-09-834-765-130  
 ; Sequence 130, Application US/09834765  
 ; Patent No. US20020055478A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Pia M. Challita-Bid  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
 ; TITLE OF INVENTION: AND DETECTION OF CANCER  
 ; FILE REFERENCE: 129.6USU1  
 ; CURRENT APPLICATION NUMBER: US/09/834,765  
 ; CURRENT FILING DATE: 2001-09-21  
 ; PRIOR APPLICATION NUMBER: 60/197,647  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 770



; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 130  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-130

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|||  
Db 6 PQPL 9

RESULT 15  
US-09-834-765-356  
; Sequence 356, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 356  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-356

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|||  
Db 2 PQPL 5

RESULT 16  
US-09-834-765-462  
; Sequence 462, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 462  
; LENGTH: 9

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-462

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|||  
Db 6 PQPL 9

RESULT 17  
US-09-834-765-546  
; Sequence 546, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 546  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-546

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|||  
Db 6 PQPL 9

RESULT 18  
US-09-898-541-1  
; Sequence 1, Application US/09898541  
; Patent No. US20020072504A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Alan  
; Bartido, Shirley M.  
; Xu, Yiquing  
; Wang, Siqun  
; TITLE OF INVENTION: Method and Reagents for Genetic Immunization  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: PO Box 5270  
; CITY: Frisco  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80443-5270  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,541  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: MSK.P-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
DESCRIPTION: peptide  
HYPOTHETICAL: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: human  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
DB 4 QPLL 7

## RESULT 19

US-09-898-541-2  
Sequence 2, Application US/09898541  
Patent No. US20020072504A1

## GENERAL INFORMATION:

APPLICANT: Houghton, Alan  
Bartido, Shirley M.  
Xu, Yiquing  
Wang, Siqun

TITLE OF INVENTION: Method and Reagents for Genetic Immunization

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oppedahl & Larson

STREET: PO Box 5270

CITY: Frisco

STATE: CO

COUNTRY: USA

ZIP: 80443-5270

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS 5.0

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,541

FILING DATE: 02-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: MSK.P-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
DESCRIPTION: peptide  
HYPOTHETICAL: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: human  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-898-541-2

Query Match 23.5%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
DB 4 QPLL 7

## RESULT 20

US-09-984-056-56

Sequence 56, Application US/09984056  
Patent No. US20020120106A1

## GENERAL INFORMATION:

APPLICANT: BOGOCH, SAMUEL

TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICONS AND METHODS OF USE

FILE REFERENCE: 09425-46903

CURRENT APPLICATION NUMBER: US/09/984,056

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: 60/303,396

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: 60/278,761

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 09/146,755

PRIOR FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: 09/817,144

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 08/198,139

PRIOR FILING DATE: 1994-02-17

NUMBER OF SEQ ID NOS: 103

SOFTWARE: PatentIn 2.1

SEQ ID NO 56

LENGTH: 9

TYPE: FRT

ORGANISM: Human papillomavirus type 71

US-09-984-056-56

Query Match 23.5%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9  
DB 4 PLLQ 7

## RESULT 21

US-09-984-057-56

Sequence 56, Application US/09984057  
Patent No. US20020151677A1

## GENERAL INFORMATION:

APPLICANT: BOGOCH, SAMUEL

TITLE OF INVENTION: REPLICONS AND METHODS OF IDENTIFYING

REPLICIN-CONTAINING SEQUENCES

```
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
; US-09-984-057-56

Query Match 23.5%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PLLQ 9
 ||||
Db 4 PLLQ 7

RESULT 22
US-09-972-656-30
; Sequence 30, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-30

Query Match 23.5%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
 ||||
Db 4 LQTP 7

RESULT 23
US-10-375-992-102
; Sequence 102, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
```

```
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/375,992
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-375-992-102

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
 ||||
Db 4 LLQV 7

RESULT 24
US-10-105-232-56
; Sequence 56, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
; US-10-105-232-56

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 PLLQ 9
Db 4 PLLQ 7

RESULT 25
US-10-189-437-56
; Sequence 56, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus type 71
US-10-189-437-56

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
Db 4 PLLQ 7

RESULT 26
US-10-277-292-101
; Sequence 101, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-101

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
Db 4 PLLQ 7

RESULT 27
US-10-277-292-133
; Sequence 133, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-133

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 1 LLQV 4

RESULT 28
US-10-137-867-288
; Sequence 288, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
US-10-137-867-288

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 1 LLQV 4
```

```

; APPLICANT: Tamas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-288

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 6 LQTP 9

RESULT 29
US-10-280-340-101
; Sequence 101, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-101

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 6 LLQV 9

RESULT 30
US-10-280-340-133
; Sequence 133, Application US/10280340
; Publication No. US20030207835A1

```

```

; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-133

Query Match 23.5%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10
Db 1 LLQV 4

RESULT 31
US-10-264-374-102
; Sequence 102, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-264-374-102

Query Match 23.5%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 LLQV 10
 ||||
Db 4 LLQV 7

RESULT 32
US-08-344-824-393
; Sequence 393, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 393:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-393

Query Match 23.5%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
 ||||
Db 2 PQGD 5

RESULT 33
US-08-424-550B-597
; Sequence 597, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DANSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK

Query Match 23.5%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: ISA K. MUSAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 597:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-597

Query Match 23.5%; Score 4; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 1 LLQV 4

RESULT 34
US-09-834-765-468
; Sequence 468, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-468

Query Match 23.5%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 4 PQPL 7
 |||||
Db 7 PQPL 10

RESULT 35
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-908-322-53
Query Match 23.5%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 |||||
Db 1 PQPL 4

RESULT 36
US-09-867-852-93
; Sequence 93, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
```

```
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-28
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-93
Query Match 23.5%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
 |||||
Db 2 PLLQ 5

RESULT 37
US-09-783-931-53
; Sequence 53, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
```

```
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-783-931-53

Query Match 23.5%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
Db 1 PQPL 4

RESULT 38
US-09-573-822C-108
; Sequence 108, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG290 at 17-26 and may interact with Sequence
; OTHER INFORMATION: this patent.
US-09-573-822C-108

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
Db 4 PLLQ 7

RESULT 39
US-10-277-292-169
; Sequence 169, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-169

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 2 LLQV 5

RESULT 41
US-10-277-292-286
; Sequence 286, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
```



```
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 285
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-286

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 1 LLQV 4

RESULT 42
US-10-277-292-424
; Sequence 424, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 424
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-424

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 6 LLQV 9

RESULT 43
US-10-277-292-436
; Sequence 436, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-436

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 7 LLQV 10

RESULT 44
US-10-137-867-274
; Sequence 274, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuman, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
```

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 274
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-274

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 |||||
DB 6 PQPL 9

RESULT 45
US-10-280-340-169
; Sequence 169, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIAS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-169

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 |||||
DB 6 LLQV 9

RESULT 46
US-10-280-340-179
; Sequence 179, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIAS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-169

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 |||||
DB 6 LLQV 9

RESULT 46
US-10-280-340-179
; Sequence 179, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIAS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-286

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 |||||
DB 1 LLQV 4

RESULT 48
```

```
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-179

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 |||||
DB 2 LLQV 5

RESULT 47
US-10-280-340-286
; Sequence 286, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIAS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-286

Query Match 23.5%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 |||||
DB 1 LLQV 4

RESULT 48
```

US-10-280-340-424  
; Sequence 424, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-424

Query Match 23.5%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10  
|  
|  
|  
|  
Db 6 LLQV 9

RESULT 49  
US-10-280-340-436  
; Sequence 436, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 436  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-436

Query Match 23.5%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10  
|  
|  
|  
|  
Db 7 LLQV 10

RESULT 50  
US-10-185-815-89  
; Sequence 89, Application US/10185815  
; Publication No. US20030096354A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Corporation, plc  
; APPLICANT: O'Mahony, Daniel  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands  
; FILE REFERENCE: E1067-20093  
; CURRENT APPLICATION NUMBER: US/10/185,815  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/302,591  
; PRIOR FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 89  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Segment of CAPHI beta casein precursor  
US-10-185-815-89

Query Match 23.5%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|  
|  
|  
|  
Db 7 PQPL 10

RESULT 51  
US-09-829-855-233  
; Sequence 233, Application US/09829855  
; Patent No. US20020065609A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthew, Ashby N.  
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations  
; FILE REFERENCE: ASHBY-1  
; CURRENT APPLICATION NUMBER: US/09/829,855  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/196063  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/196258  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 233  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-1  
; NAME/KEY: MISC FEATURE  
; LOCATION: (8) ..(8)  
; OTHER INFORMATION: Unable to determine  
US-09-829-855-233

Query Match 23.5%; Score 4; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 QPLL 8  
|  
|  
|  
|  
|  
Db 3 QPLL 6

RESULT 52  
US-09-829-855-234  
; Sequence 234, Application US/09829855  
; Patent No. US20020065809A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthew, Ashby N.  
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations  
; FILE REFERENCE: ASHBY-1  
; CURRENT APPLICATION NUMBER: US/09/829,855  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/196063  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/196258  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Uncultured Acidobacterium Sub.Div-1  
US-09-829-855-234

Query Match 23.5%; Score 4; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 QPLL 8  
|  
|  
|  
|  
|  
Db 3 QPLL 6

RESULT 53  
US-10-076-047A-57  
; Sequence 57, Application US/10076047A  
; Publication No. US20030152935A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; FILE REFERENCE: 2543-1-026  
; CURRENT APPLICATION NUMBER: US/10/076,047A  
; CURRENT FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: GB 9919258.5  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: GB 0007754.5  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/03143  
; PRIOR FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 351  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-047A-57

Query Match 23.5%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 TPQP 6  
|  
|  
|  
|  
|

Query Match 23.5%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PLLQ 9  
|  
|  
|  
|  
|  
Db 4 PLLQ 7

RESULT 54  
US-09-281-717-39  
; Sequence 39, Application US/09281717  
; Patent No. US20020061539A1  
; GENERAL INFORMATION:  
; APPLICANT: Baxter, John D.  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun  
; APPLICANT: Fletterick, Robert J.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: West, Brian  
; APPLICANT: Yamamoto, Keith R.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: UCAL-253/02US  
; CURRENT APPLICATION NUMBER: US/09/281,717  
; CURRENT FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: US 60/079,956  
; EARLIER FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-281-717-39

Query Match 23.5%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PLLQ 9  
|  
|  
|  
|  
|  
Db 4 PLLQ 7

RESULT 55  
US-09-954-385-193  
; Sequence 193, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Winetzkzy, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
; FILE REFERENCE: Complexes  
; FILE REFERENCE: GC690  
; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 193  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-193

Query Match 23.5%; Score 4; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PLLQ 9  
|  
|  
|  
|  
|

Db 4 PLLQ 7

RESULT 56

US-09-992-238-27  
; Sequence 27, Application US/09992238  
; Publication No. US2003005444A1  
; GENERAL INFORMATION:  
; APPLICANT: BATTAGLINO, PETER  
; APPLICANT: FEDER, JOHN N  
; APPLICANT: MINTIER, GABE  
; APPLICANT: NELSON, THOMAS C  
; APPLICANT: RAMANATHAN, CHANDRA S  
; APPLICANT: WESTPHAL, RYAN  
; APPLICANT: CACACE, ANGELA  
; APPLICANT: BARBER, LAUREN  
; APPLICANT: HAWKEN, DONALD R  
; APPLICANT: KORNACKER, MICHAEL G  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP99MY8,  
; FILE REFERENCE: D0047NP  
; CURRENT APPLICATION NUMBER: US/09/992,238  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/317166  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/268581  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/248285  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized  
; OTHER INFORMATION: peptide  
US-09-992-238-27

Query Match 23.5%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10  
|  
|  
|  
|  
Db 6 LLQV 9

RESULT 57

US-09-992-238-77  
; Sequence 77, Application US/09992238  
; Publication No. US2003005444A1  
; GENERAL INFORMATION:  
; APPLICANT: BATTAGLINO, PETER  
; APPLICANT: FEDER, JOHN N  
; APPLICANT: MINTIER, GABE  
; APPLICANT: NELSON, THOMAS C  
; APPLICANT: RAMANATHAN, CHANDRA S  
; APPLICANT: WESTPHAL, RYAN  
; APPLICANT: CACACE, ANGELA  
; APPLICANT: BARBER, LAUREN  
; APPLICANT: HAWKEN, DONALD R  
; APPLICANT: KORNACKER, MICHAEL G  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP99MY8,  
; FILE REFERENCE: D0047NP  
; CURRENT APPLICATION NUMBER: US/09/992,238  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/317166  
; PRIOR FILING DATE: 2001-09-04

Query Match 23.5%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10  
|  
|  
|  
|  
Db 6 LLQV 9

; PRIOR APPLICATION NUMBER: 60/308285  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/268581  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/248285  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polypeptide  
US-09-992-238-77

Query Match 23.5%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LLQV 10  
|  
|  
|  
|  
Db 2 LLQV 5

RESULT 58

US-09-829-855-217  
; Sequence 217, Application US/09829855  
; Patent No. US20020065609A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthew, Ashby N.  
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations  
; FILE REFERENCE: ASHBY-1  
; CURRENT APPLICATION NUMBER: US/09/829,855  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/196063  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/196258  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 217  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Uncultured GNS bacteria BPC110  
US-09-829-855-217

Query Match 23.5%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8  
|  
|  
|  
|  
Db 3 QPLL 6

RESULT 59

US-10-271-078-33  
; Sequence 33, Application US/10271078  
; Publication No. US20030186267A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLC  
; FILE REFERENCE: D0157 NP  
; CURRENT APPLICATION NUMBER: US/10/271,078  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: U.S. 60/328,478  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 33  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-271-078-33

Query Match 23.5%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9  
|||  
Db 11 PLLQ 14

## RESULT 60

US-10-367-405-18  
; Sequence 18, Application US/10367405  
; Publication No. US20030215438A1

; GENERAL INFORMATION:  
; APPLICANT: Felix Hausch  
; APPLICANT: Gary Gray  
; APPLICANT: Lu Shan  
; APPLICANT: Chaitan Khosla  
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE  
; FILE REFERENCE: STAN-258US1  
; CURRENT APPLICATION NUMBER: US/10/367,405  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: 60/357,238  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: 60/380,761  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 60/392,782  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/422,933  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 60/428,033  
; PRIOR FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: 60/435,881  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-367-405-18

Query Match 23.5%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7  
|||  
Db 10 PQPL 13

## RESULT 61

US-10-256-865-15  
; Sequence 15, Application US/10256865  
; Publication No. US20030049672A1

; GENERAL INFORMATION:  
; APPLICANT: Kun Ping Lu  
; APPLICANT: Xiao Zhen Zhou  
; TITLE OF INVENTION: Methods and Compositions for Regulating  
; TITLE OF INVENTION: Protein-Protein Interactions  
; FILE REFERENCE: 1440.1034-000  
; CURRENT APPLICATION NUMBER: US/10/256,865  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/252,404  
; PRIOR FILING DATE: 1999-02-18  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: synthetic peptide  
US-10-256-865-15

Query Match 23.5%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|||  
Db 9 LQTP 12

## RESULT 62

US-10-120-604-26  
; Sequence 26, Application US/10120604  
; Publication No. US20030096347A1

; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECI  
; TITLE OF INVENTION: HGPBMY28 AND HGPBMY29, AND SPLICE VARIANTS THEREOF  
; FILE REFERENCE: D0143NP  
; CURRENT APPLICATION NUMBER: US/10/120,604  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,145  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,161  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/288,468  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 60/300,619  
; PRIOR FILING DATE: 2001-06-25  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-120-604-26

Query Match 23.5%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|||  
Db 9 LQTP 12

## RESULT 63

US-10-120-604-69  
; Sequence 69, Application US/10120604  
; Publication No. US20030096347A1

; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECI  
; TITLE OF INVENTION: HGPBMY28 AND HGPBMY29, AND SPLICE VARIANTS THEREOF  
; FILE REFERENCE: D0143NP  
; CURRENT APPLICATION NUMBER: US/10/120,604  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,145  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,161  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/288,468  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 60/300,619  
; PRIOR FILING DATE: 2001-06-25  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 69

; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-120-604-69

Query Match 23.5%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
Db 9 LQTP 12

## RESULT 64

US-10-120-604-85  
; Sequence 85, Application US/10120604  
; Publication No. US20030096347A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: D0143NP  
; CURRENT APPLICATION NUMBER: US/10/120,604  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,145  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/283,161  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/288,468  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 60/300,619  
; PRIOR FILING DATE: 2001-06-25  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 85  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-120-604-85

Query Match 23.5%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
Db 9 LQTP 12

## RESULT 65

US-10-294-891-25  
; Sequence 25, Application US/10294891  
; Publication No. US20030166569A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/294,891  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-294-891-25

Query Match 23.5%; Score 4; DB 12; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPOG 16  
Db 1 EPOG 4

## RESULT 66

US-10-161-791-405  
; Sequence 405, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 405:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-405

Query Match 23.5%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7  
Db 9 PQPL 12

## RESULT 67

US-10-360-836-9  
; Sequence 9, Application US/10360836  
; Publication No. US20030185854A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavala, Fidel

```

; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-9

Query Match 23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 12 LLQV 15

RESULT 68
US-10-360-836-10
; Sequence 10, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-10

Query Match 23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 7 LLQV 10

RESULT 69
US-10-360-836-11
; Sequence 11, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALIGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-11

Query Match 23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 7 LLQV 10

RESULT 70
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34

Query Match 23.5%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 ||||
Db 5 PQPL 8

RESULT 71
US-10-194-985-29
; Sequence 29, Application US/10194985
; Publication No. US20030105287A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Michael
; APPLICANT: Schneiderbauer, Michaela
; APPLICANT: Weidler, Sascha
; APPLICANT: Hallek, Michael
; APPLICANT: GSF Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Inhibition of the Proliferation of Cells of the
; TITLE OF INVENTION: Multiple Myeloma
; FILE REFERENCE: 080345-000100US
; CURRENT APPLICATION NUMBER: US/10/194,985
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: DE 19941897.7
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: US 09/625,225
; PRIOR FILING DATE: 2000-07-24

```

```

; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-11

Query Match 23.5%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 2 LLQV 5

RESULT 70
US-10-281-652-34
; Sequence 34, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34

Query Match 23.5%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
 ||||
Db 5 PQPL 8

RESULT 71
US-10-194-985-29
; Sequence 29, Application US/10194985
; Publication No. US20030105287A1
; GENERAL INFORMATION:
; APPLICANT: Schaeffer, Michael
; APPLICANT: Schneiderbauer, Michaela
; APPLICANT: Weidler, Sascha
; APPLICANT: Hallek, Michael
; APPLICANT: GSF Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Inhibition of the Proliferation of Cells of the
; TITLE OF INVENTION: Multiple Myeloma
; FILE REFERENCE: 080345-000100US
; CURRENT APPLICATION NUMBER: US/10/194,985
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: DE 19941897.7
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: US 09/625,225
; PRIOR FILING DATE: 2000-07-24

```



; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p5 peptide  
; OTHER INFORMATION: subfragment of Hck binding region of gp130  
US-10-194-985-29

Query Match 23.5%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLL 8  
Db 6 QPLL 9

RESULT 72  
US-10-299-043-2  
; Sequence 2, Application US/10299043  
; Publication No. US20030158115A1  
; GENERAL INFORMATION:  
; APPLICANT: TOBACK, F. GARY  
; APPLICANT: LIESKE, JOHN C.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
; TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO  
; TITLE OF INVENTION: KIDNEY CELLS  
; FILE REFERENCE: 21459/90606  
; CURRENT APPLICATION NUMBER: US/10/299,043  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US/09/537,226  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: 08/389,005  
; PRIOR FILING DATE: 1995-02-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-299-043-2

Query Match 23.5%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PQPL 7  
Db 10 PQPL 13

RESULT 73  
US-10-174-105A-181  
; Sequence 181, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,  
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 181  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated  
US-10-174-105A-181

Query Match 23.5%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4  
Db 11 LQTP 14

RESULT 74  
US-09-861-708-1  
; Sequence 1, Application US/09861708  
; Patent No. US20020098188A1  
; GENERAL INFORMATION:  
; APPLICANT: KAIBARA, Makoto  
; APPLICANT: IWATA, Hiroki  
; APPLICANT: TAKIO, Koji  
; APPLICANT: DOHMAE, Naoshi  
; TITLE OF INVENTION: Blood Coagulation Factor-Activating Protein and Antibody There  
; FILE REFERENCE: P21011  
; CURRENT APPLICATION NUMBER: US/09/861,708  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: JP 153096/2000  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: Unknown Amino Acid  
US-09-861-708-1

Query Match 23.5%; Score 4; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 PQGD 17  
Db 3 PQGD 6

RESULT 75  
US-09-864-761-34833  
; Sequence 34833, Application US/09864761  
; Patent No. US20020046763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aecomica-X-1

```

; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34833
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009473.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 30
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 31
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 49
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 29
US-09-864-761-34833
```

```

Query Match 23.5%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 6 PLLQ 9
Db 11 PLLQ 14
```

```

Search completed: November 25, 2003, 20:25:26
Job time : 35.8191 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 18.5372 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-2

Perfect score: 17

Sequence: 1 LQTPQLQWMPEQGD 17

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/protdata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/protdata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/protdata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/protdata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/protdata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/protdata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 17    | 100.0       | 17     | 4  | US-09-641-803-2   |
| 2          | 6     | 35.3        | 8      | 5  | PCT-US91-05177-19 |
| 3          | 5     | 29.4        | 7      | 1  | US-08-594-447-74  |
| 4          | 5     | 29.4        | 7      | 1  | US-08-541-964-73  |
| 5          | 5     | 29.4        | 7      | 2  | US-08-665-647-88  |
| 6          | 5     | 29.4        | 9      | 6  | 5204326-100       |
| 7          | 5     | 29.4        | 14     | 6  | 5204326-36        |
| 8          | 5     | 29.4        | 14     | 6  | 5204326-95        |
| 9          | 5     | 29.4        | 15     | 6  | 5204326-37        |
| 10         | 5     | 29.4        | 15     | 6  | 5204326-40        |
| 11         | 5     | 29.4        | 15     | 6  | 5204326-71        |
| 12         | 5     | 29.4        | 15     | 6  | 5204326-74        |
| 13         | 5     | 29.4        | 16     | 6  | 5204326-96        |
| 14         | 5     | 29.4        | 17     | 6  | 5204326-97        |
| 15         | 5     | 29.4        | 18     | 6  | 5204326-38        |
| 16         | 5     | 29.4        | 18     | 6  | 5204326-41        |
| 17         | 5     | 29.4        | 18     | 6  | 5204326-98        |
| 18         | 5     | 29.4        | 18     | 6  | 5204326-101       |
| 19         | 5     | 29.4        | 19     | 6  | 5204326-72        |
| 20         | 5     | 29.4        | 19     | 6  | 5204326-75        |
| 21         | 5     | 29.4        | 20     | 6  | 5204326-39        |
| 22         | 4     | 23.5        | 7      | 1  | US-08-594-447-75  |
| 23         | 4     | 23.5        | 7      | 1  | US-08-541-964-74  |
| 24         | 4     | 23.5        | 7      | 2  | US-08-666-473-40  |
| 25         | 4     | 23.5        | 7      | 2  | US-08-665-647-89  |
| 26         | 4     | 23.5        | 7      | 2  | US-09-160-126-3   |
| 27         | 4     | 23.5        | 7      | 4  | US-08-757-425B-62 |

|     |   |      |    |   |                     |                    |
|-----|---|------|----|---|---------------------|--------------------|
| 28  | 4 | 23.5 | 7  | 4 | US-08-757-425B-63   | Sequence 63, Appl  |
| 29  | 4 | 23.5 | 7  | 4 | US-09-822-270-12    | Sequence 12, Appl  |
| 30  | 4 | 23.5 | 8  | 2 | US-08-350-260A-362  | Sequence 362, App  |
| 31  | 4 | 23.5 | 8  | 2 | US-08-350-260A-452  | Sequence 452, App  |
| 32  | 4 | 23.5 | 8  | 2 | US-08-350-260A-453  | Sequence 453, App  |
| 33  | 4 | 23.5 | 8  | 2 | US-08-350-260A-458  | Sequence 458, App  |
| 34  | 4 | 23.5 | 8  | 2 | US-08-350-260A-460  | Sequence 460, App  |
| 35  | 4 | 23.5 | 8  | 2 | US-08-350-260A-515  | Sequence 515, App  |
| 36  | 4 | 23.5 | 8  | 2 | US-08-350-260A-520  | Sequence 520, App  |
| 37  | 4 | 23.5 | 8  | 4 | US-09-104-337A-362  | Sequence 362, App  |
| 38  | 4 | 23.5 | 8  | 4 | US-09-104-337A-452  | Sequence 452, App  |
| 39  | 4 | 23.5 | 8  | 4 | US-09-104-337A-453  | Sequence 453, App  |
| 40  | 4 | 23.5 | 8  | 4 | US-09-104-337A-458  | Sequence 458, App  |
| 41  | 4 | 23.5 | 8  | 4 | US-09-104-337A-460  | Sequence 460, App  |
| 42  | 4 | 23.5 | 8  | 4 | US-09-104-337A-515  | Sequence 515, App  |
| 43  | 4 | 23.5 | 8  | 4 | US-09-104-337A-520  | Sequence 520, App  |
| 44  | 4 | 23.5 | 9  | 1 | US-08-594-447-52    | Sequence 52, Appl  |
| 45  | 4 | 23.5 | 9  | 1 | US-08-541-964-51    | Sequence 51, Appl  |
| 46  | 4 | 23.5 | 9  | 2 | US-08-665-647-66    | Sequence 66, Appl  |
| 47  | 4 | 23.5 | 9  | 2 | US-08-350-260A-356  | Sequence 356, App  |
| 48  | 4 | 23.5 | 9  | 2 | US-08-350-260A-365  | Sequence 365, App  |
| 49  | 4 | 23.5 | 9  | 2 | US-08-350-260A-373  | Sequence 373, App  |
| 50  | 4 | 23.5 | 9  | 2 | US-08-318-856A-37   | Sequence 37, Appl  |
| 51  | 4 | 23.5 | 9  | 3 | US-08-159-339A-1062 | Sequence 1062, App |
| 52  | 4 | 23.5 | 9  | 3 | US-09-139-802-102   | Sequence 102, App  |
| 53  | 4 | 23.5 | 9  | 3 | US-09-230-199-1     | Sequence 1, Appl   |
| 54  | 4 | 23.5 | 9  | 3 | US-09-230-199-2     | Sequence 2, Appl   |
| 55  | 4 | 23.5 | 9  | 4 | US-08-737-109-5     | Sequence 5, Appl   |
| 56  | 4 | 23.5 | 9  | 4 | US-09-659-786-102   | Sequence 102, App  |
| 57  | 4 | 23.5 | 9  | 4 | US-09-104-337A-356  | Sequence 356, App  |
| 58  | 4 | 23.5 | 9  | 4 | US-09-104-337A-365  | Sequence 365, App  |
| 59  | 4 | 23.5 | 9  | 4 | US-09-104-337A-373  | Sequence 373, App  |
| 60  | 4 | 23.5 | 9  | 4 | US-08-926-914-102   | Sequence 102, App  |
| 61  | 4 | 23.5 | 10 | 2 | US-08-310-912A-91   | Sequence 91, Appl  |
| 62  | 4 | 23.5 | 10 | 3 | US-08-159-339A-971  | Sequence 971, App  |
| 63  | 4 | 23.5 | 10 | 3 | US-08-159-339A-1070 | Sequence 1070, App |
| 64  | 4 | 23.5 | 10 | 3 | US-08-841-089-93    | Sequence 93, Appl  |
| 65  | 4 | 23.5 | 10 | 3 | US-08-981-392-53    | Sequence 53, Appl  |
| 66  | 4 | 23.5 | 10 | 3 | US-09-301-085-93    | Sequence 93, Appl  |
| 67  | 4 | 23.5 | 10 | 4 | US-08-469-260A-597  | Sequence 597, App  |
| 68  | 4 | 23.5 | 10 | 4 | US-08-488-446-597   | Sequence 597, App  |
| 69  | 4 | 23.5 | 10 | 4 | US-08-467-344A-597  | Sequence 597, App  |
| 70  | 4 | 23.5 | 10 | 5 | PCT-US95-04570-93   | Sequence 93, Appl  |
| 71  | 4 | 23.5 | 10 | 5 | PCT-US95-04589-93   | Sequence 93, Appl  |
| 72  | 4 | 23.5 | 11 | 3 | US-09-183-846A-24   | Sequence 24, Appl  |
| 73  | 4 | 23.5 | 11 | 4 | US-08-339-214-56    | Sequence 56, Appl  |
| 74  | 4 | 23.5 | 12 | 6 | 5204326-35          | Patent No. 5204326 |
| 75  | 4 | 23.5 | 12 | 6 | 5204326-94          | Patent No. 5204326 |
| 76  | 4 | 23.5 | 13 | 3 | US-09-023-173-9     | Sequence 9, Appl   |
| 77  | 4 | 23.5 | 13 | 3 | US-09-023-339-7     | Sequence 7, Appl   |
| 78  | 4 | 23.5 | 14 | 2 | US-08-248-839C-31   | Sequence 31, Appl  |
| 79  | 4 | 23.5 | 14 | 3 | US-08-837-226-13    | Sequence 13, Appl  |
| 80  | 4 | 23.5 | 14 | 3 | US-09-252-404A-15   | Sequence 15, Appl  |
| 81  | 4 | 23.5 | 14 | 6 | 5204326-25          | Patent No. 5204326 |
| 82  | 4 | 23.5 | 14 | 6 | 5204326-83          | Patent No. 5204326 |
| 83  | 4 | 23.5 | 15 | 1 | US-08-477-877B-30   | Sequence 30, Appl  |
| 84  | 4 | 23.5 | 15 | 2 | US-08-472-281A-30   | Sequence 30, Appl  |
| 85  | 4 | 23.5 | 15 | 2 | US-08-477-989B-30   | Sequence 30, Appl  |
| 86  | 4 | 23.5 | 15 | 3 | US-08-602-999A-405  | Sequence 405, App  |
| 87  | 4 | 23.5 | 15 | 3 | US-09-500-124-405   | Sequence 405, App  |
| 88  | 4 | 23.5 | 15 | 4 | US-09-641-803-34    | Sequence 34, Appl  |
| 89  | 4 | 23.5 | 15 | 5 | PCT-US93-06751-40   | Sequence 40, Appl  |
| 90  | 4 | 23.5 | 15 | 5 | 5200320-34          | Patent No. 5200320 |
| 91  | 4 | 23.5 | 15 | 6 | 5204326-26          | Patent No. 5204326 |
| 92  | 4 | 23.5 | 15 | 6 | 5204326-29          | Patent No. 5204326 |
| 93  | 4 | 23.5 | 15 | 6 | 5204326-43          | Patent No. 5204326 |
| 94  | 4 | 23.5 | 15 | 6 | 5204326-58          | Patent No. 5204326 |
| 95  | 4 | 23.5 | 15 | 6 | 5204326-62          | Patent No. 5204326 |
| 96  | 4 | 23.5 | 15 | 6 | 5204326-65          | Patent No. 5204326 |
| 97  | 4 | 23.5 | 15 | 6 | 5204326-68          | Patent No. 5204326 |
| 98  | 4 | 23.5 | 15 | 6 | 5204326-84          | Patent No. 5204326 |
| 99  | 4 | 23.5 | 15 | 6 | 5204326-89          | Patent No. 5204326 |
| 100 | 4 | 23.5 | 16 | 3 | US-08-837-226-2     | Sequence 2, Appl   |

## ALIGNMENTS

RESULT 1  
US-09-641-803-2  
; Sequence 2, Application US/09641803  
; Patent No. 6508798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-2

Query Match 100.0%; Score 17; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQLQVMEPQGD 17  
| | | | | | | | | | | | | | | | | |  
DB 1 LQTPQLQVMEPQGD 17

RESULT 2  
PCT-US91-05177-19  
; Sequence 19, Application PC/TUS9105177  
; GENERAL INFORMATION:  
; APPLICANT: Berkner, Kathy L  
; TITLE OF INVENTION: GAMMA-CARBOXYLASE AND METHODS OF USE  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/05177  
; FILING DATE: 19910722  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/557,220  
; FILING DATE: 23-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 990008.544PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; TELEFAX: 206-682-6031

; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal  
PCT-US91-05177-19

Query Match 35.3%; Score 6; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPQPLL 8  
| | | | |  
DB 1 TPQPLL 6

RESULT 3  
US-08-594-447-74  
; Sequence 74, Application US/08594447  
; Patent No. 5776716  
; GENERAL INFORMATION:  
; APPLICANT: Ron, Dorit  
; APPLICANT: Napolitano, Eugene W.  
; APPLICANT: Voronova, Anna F.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH  
; BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES  
; THEREOF  
; TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES  
; THEREOF  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,447  
; FILING DATE: 31-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.24  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSH  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /label= PRK1-3  
US-08-594-447-74

Query Match 29.4%; Score 5; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 MEPOG 16  
| | | | |  
DB 1 MEPOG 5

ADDRESSER: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,647  
FILING DATE: 18-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFOERSWSH  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /label= PRK1-3  
US-08-665-647-88

Query Match 29.4%; Score 5; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEPQG 16  
| | | | |  
Db 1 MEPQG 5

RESULT 6  
5204326-100  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO  
; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO  
; METABOLISM IMPROVING AGENT  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO: 100;  
; LENGTH: 9  
5204326-100

Query Match 29.4%; Score 5; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
| | | | |  
Db 3 LQTPQ 7

RESULT 7  
5204326-36  
; Patent No. 5204326

US-08-541-964-73  
; Sequence 73, Application US/08541964  
; Patent No. 5783405  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; APPLICANT: Kauvar, Lawrence M.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS  
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,964  
; FILING DATE: 10-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.23  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /label= PRK1-3  
US-08-541-964-73

Query Match 29.4%; Score 5; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MEPQG 16  
| | | | |  
Db 1 MEPQG 5

RESULT 5  
US-08-665-647-88  
; Sequence 88, Application US/08665647  
; Patent No. 5935803  
; GENERAL INFORMATION:  
; APPLICANT: Dasquez, Nicki J.  
; APPLICANT: Ron, Dorit  
; APPLICANT: Voronova, Anna F.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:

; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:36:  
 ; LENGTH: 14  
 5204326-36

Query Match 29.4%; Score 5; DB 6; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 2 LQTPQ 6

## RESULT 8

5204326-95  
 ; Patent No. 5204326  
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:95:  
 ; LENGTH: 14  
 5204326-95

Query Match 29.4%; Score 5; DB 6; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 2 LQTPQ 6

## RESULT 9

5204326-37  
 ; Patent No. 5204326  
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:37:  
 ; LENGTH: 15  
 5204326-37

Query Match 29.4%; Score 5; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 3 LQTPQ 7

## RESULT 10

5204326-40  
 ; Patent No. 5204326  
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:40:  
 ; LENGTH: 15  
 5204326-40

Query Match 29.4%; Score 5; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 3 LQTPQ 7

## RESULT 11

5204326-71  
 ; Patent No. 5204326  
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:71:  
 ; LENGTH: 15  
 5204326-71

Query Match 29.4%; Score 5; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 3 LQTPQ 7

## RESULT 12

5204326-74  
 ; Patent No. 5204326  
 ; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIHITO;SHIMIZU, FUMIO  
 ; INAI, MASATOSHI;KINOSHITA, NAOsumi;NAKAMURA, SHIZUO;HIROHASHI,  
 ; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO  
 ; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
 ; METABOLISM IMPROVING AGENT  
 ; NUMBER OF SEQUENCES: 147  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/493,359  
 ; FILING DATE: 14-MAR-1990  
 ; SEQ ID NO:74:  
 ; LENGTH: 15  
 5204326-74

Query Match 29.4%; Score 5; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQ 5  
 |||||  
 Db 3 LQTPQ 7

```

Db 6 LQTPQ 10

RESULT 16
5204326-96
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:96:
; LENGTH: 16
5204326-96

Query Match 29.4%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 4 LQTPQ 8

RESULT 14
5204326-97
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:97:
; LENGTH: 17
5204326-97

Query Match 29.4%; Score 5; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 5 LQTPQ 9

RESULT 15
5204326-38
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:38:
; LENGTH: 18
5204326-38

Query Match 29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 5 LQTPQ 10

RESULT 17
5204326-98
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:98:
; LENGTH: 18
5204326-98

Query Match 29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 6 LQTPQ 10

RESULT 18
5204326-101
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:101:
; LENGTH: 18
5204326-101

Query Match 29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 6 LQTPQ 10

RESULT 18
5204326-101
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:101:
; LENGTH: 18
5204326-101

Query Match 29.4%; Score 5; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQ 5
 |||||
Db 6 LQTPQ 10
```

Query Match 29.4%; Score 5; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 41;



APPLICANT: Napolitano, Eugene W.  
TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS  
TITLE OF INVENTION: OF SIGNAL TRANSDUCTION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1889  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,964  
FILING DATE: 10-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.23  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFORSWSH  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /label= PRK2-3  
US-08-541-964-74

Query Match 23.5%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EPQG 16  
Db 2 EPQG 5

RESULT 24  
US-08-666-473-40  
Sequence 40, Application US/08666473  
Patent No. 5843713  
GENERAL INFORMATION:  
APPLICANT: YOSHIDA, Aruto  
APPLICANT: TAKEUCHI, Makoto  
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/666,473  
FILING DATE: 19-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP95/02238  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-22101  
FILING DATE: 09-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-269111  
FILING DATE: 01-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16887/837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-666-473-40

Query Match 23.5%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPOQ 6  
Db 4 TPOQ 7

RESULT 25  
US-08-665-647-89  
Sequence 89, Application US/08665647  
Patent No. 5935803  
GENERAL INFORMATION:  
APPLICANT: Dasquez, Nicki J.  
APPLICANT: Ron, Dorit  
APPLICANT: Voronova, Anna F.  
APPLICANT: Napolitano, Eugene W.  
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1889  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,647  
FILING DATE: 18-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168

Wed Nov 26 09:07:00 2003

TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 89:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..7  
; OTHER INFORMATION: /label= PRK2-3  
US-08-665-647-89

Query Match 23.5%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16  
|||  
Db 2 EPQG 5

RESULT 26  
US-09-160-126-3  
; Sequence 3, Application US/09160126  
; Patent No. 5962417  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Park, Hee-young  
; TITLE OF INVENTION: Methods of Modulating Melanin Synthesis  
; FILE REFERENCE: BU95-59A2  
; CURRENT APPLICATION NUMBER: US/09/160,126  
; CURRENT FILING DATE: 1998-09-24  
; EARLIER APPLICATION NUMBER: PCT/US97/04752  
; EARLIER FILING DATE: 1997-03-27  
; EARLIER APPLICATION NUMBER: 08/623,364  
; EARLIER FILING DATE: 1996-03-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-160-126-3

Query Match 23.5%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
|||  
Db 1 QPLL 4

RESULT 27  
US-08-757-425B-62  
; Sequence 62, Application US/08757425B  
; Patent No. 6506660  
; GENERAL INFORMATION:  
; APPLICANT: Fastrez, Jacques  
; TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity  
; FILE REFERENCE: 100390-09640  
; CURRENT APPLICATION NUMBER: US/08/757,425B  
; CURRENT FILING DATE: 1996-11-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mimotope

US-08-757-425B-62

Query Match 23.5%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17  
|||  
Db 2 PQGD 5

RESULT 28

US-08-757-425B-63  
; Sequence 63, Application US/08757425B  
; Patent No. 6506660  
; GENERAL INFORMATION:  
; APPLICANT: Fastrez, Jacques  
; TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity  
; FILE REFERENCE: 100390-09640  
; CURRENT APPLICATION NUMBER: US/08/757,425B  
; CURRENT FILING DATE: 1996-11-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 63  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mimotope  
US-08-757-425B-63

Query Match 23.5%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17  
|||  
Db 2 PQGD 5

RESULT 29

US-09-822-270-12  
; Sequence 12, Application US/09822270  
; Patent No. 6559126  
; GENERAL INFORMATION:  
; APPLICANT: TOURNAIRE, ROSELYNE  
; APPLICANT: DEMANGEL, CAROLINE  
; APPLICANT: DERBIN, CLAUDE  
; APPLICANT: PERRET, GERARD  
; APPLICANT: MAZIE, JEAN-CLAUDE  
; APPLICANT: PLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MI  
; FILE REFERENCE: 205060US0  
; CURRENT APPLICATION NUMBER: US/09/822,270  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-09-822-270-12

Query Match 23.5%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|||  
DB 4 LQTP 7

RESULT 30  
US-08-350-260A-362  
; Sequence 362, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 362:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-350-260A-362

Query Match

23.5%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|||  
DB 4 LQTP 7

RESULT 31  
US-08-350-260A-452  
; Sequence 452, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 452:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-350-260A-452

Query Match 23.5%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|  
|  
|  
|  
Db 4 LQTP 7

RESULT 32

US-08-350-260A-453

; Sequence 453, Application US/08350260A

; Patent No. 5962255

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; APPLICANT: Griffiths, Andrew David

; APPLICANT: Williams, Samuel Cameron

; APPLICANT: Waterhouse, Peter

; APPLICANT: Nissim, Ahuva

; APPLICANT: Johnson, Kevin Stuart

; APPLICANT: Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific

; NUMBER OF INVENTION: binding pairs

; NUMBER OF SEQUENCES: 602

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough

; STREET: Marshall, O'Toole, Gerstein, Murray &amp; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/350,260A

; FILING DATE: 05-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9110549.4

; FILING DATE: 15-MAY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB91/01134

; FILING DATE: 10-JUL-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/00883

; FILING DATE: 15-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB93/00605

; FILING DATE: 24-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/150,002

; FILING DATE: 31-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/307,619

; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Clough, David W

; REGISTRATION NUMBER: 36,107

; REFERENCE/DOCKET NUMBER: 28111/32372

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 453:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-350-260A-453

Query Match 23.5%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
|  
|  
|  
|  
Db 4 LQTP 7

RESULT 33

US-08-350-260A-458

; Sequence 458, Application US/08350260A

; Patent No. 5962255

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; APPLICANT: Griffiths, Andrew David

; APPLICANT: Williams, Samuel Cameron

; APPLICANT: Waterhouse, Peter

; APPLICANT: Nissim, Ahuva

; APPLICANT: Johnson, Kevin Stuart

; APPLICANT: Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific

; NUMBER OF INVENTION: binding pairs

; NUMBER OF SEQUENCES: 602

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough

; STREET: Marshall, O'Toole, Gerstein, Murray &amp; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/350,260A

; FILING DATE: 05-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9110549.4

; FILING DATE: 15-MAY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB91/01134

; FILING DATE: 10-JUL-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/00883

; FILING DATE: 15-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB93/00605

; FILING DATE: 24-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/150,002

; FILING DATE: 31-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/307,619

; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Clough, David W

; REGISTRATION NUMBER: 36,107

; REFERENCE/DOCKET NUMBER: 28111/32372

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

```
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-458

Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 34
US-08-350-260A-460
; Sequence 460, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107

; INFORMATION FOR SEQ ID NO: 459:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-459

Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 35
US-08-350-260A-515
; Sequence 515, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
```

Wed Nov 26 09:07:00 2003

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 515:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-515
;
Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 4 LQTP 7

RESULT 36
US-08-350-260A-520
; Sequence 520, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David W. Clough
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; NAME: Clough, David W
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 520:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-520
;
Query Match 23.5%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTP 4
Db 4 LQTP 7

RESULT 37
US-09-104-337A-362
; Sequence 362, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:

```

```
;
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-104-337A-362

Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 38
US-09-104-337A-452
; Sequence 452, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; INFORMATION FOR SEQ ID NO: 362:
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 452:
US-09-104-337A-452

Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
Db 4 LQTP 7

RESULT 39
US-09-104-337A-453
; Sequence 453, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 453:
```

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 453:
US-09-104-337A-453
Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
DB 4 LQTP 7

RESULT 40
US-09-104-337A-458
; Sequence 458, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 460:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 458:
US-09-104-337A-458
Query Match 23.5%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
DB 4 LQTP 7

RESULT 41
US-09-104-337A-460
; Sequence 460, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 460:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 460:

```



US-09-104-337A-460

Query Match 23.5%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQTP 4  
Db 4 LQTP 7

RESULT 42

US-09-104-337A-515  
; Sequence 515, Application US/09104337A  
; Patent No. 6492160

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul  
Griffiths, Andrew David  
Williams, Samuel Cameron  
Waterhouse, Peter  
Nissim, Ahuva  
Johnson, Kevin Stuart  
Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki

STREET: Marshall, Gerstein &amp; Borun

6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A

FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 515:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 515:

US-09-104-337A-515

Query Match

23.5%; Score 4; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQTP 4  
Db 4 LQTP 7

RESULT 43

US-09-104-337A-520

; Sequence 520, Application US/09104337A

; Patent No. 6492160

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul  
Griffiths, Andrew David  
Williams, Samuel Cameron  
Waterhouse, Peter  
Nissim, Ahuva  
Johnson, Kevin Stuart  
Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki

STREET: Marshall, Gerstein &amp; Borun

6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A

FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4

FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.

REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 520:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 520:

US-09-104-337A-520

Query Match

23.5%; Score 4; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4  
|  
|  
|  
|  
Db 4 LQTP 7

RESULT 44  
US-08-594-447-52  
; Sequence 52, Application US/08594447  
; Patent No. 5776716  
; GENERAL INFORMATION:  
; APPLICANT: Ron, Dorit  
; APPLICANT: Napolitano, Eugene W.  
; APPLICANT: Voronova, Anna F.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH  
; TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/541,964  
; FILING DATE: 10-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.23  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..9  
; OTHER INFORMATION: /label= theta-V3-2  
US-08-541-964-51

Query Match 23.5%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16  
|  
|  
|  
|  
Db 4 EPQG 7

RESULT 46  
US-08-665-647-66  
; Sequence 66, Application US/08665647  
; Patent No. 5935803  
; GENERAL INFORMATION:  
; APPLICANT: Dasquez, Nicki J.  
; APPLICANT: Ron, Dorit  
; APPLICANT: Voronova, Anna F.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

QY 1 LQTP 4  
|  
|  
|  
|  
Db 4 LQTP 7

RESULT 45  
US-08-541-964-51  
; Sequence 51, Application US/08541964  
; Patent No. 5783405  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; APPLICANT: Kauvar, Lawrence M.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS

Query Match 23.5%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16  
|  
|  
|  
|  
Db 4 EPQG 7

RESULT 45  
US-08-541-964-51  
; Sequence 51, Application US/08541964  
; Patent No. 5783405  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; APPLICANT: Kauvar, Lawrence M.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS

APPLICATION NUMBER: US/08/665,647  
FILING DATE: 18-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22550-20025.25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 822-0168  
TELEX: 90-4030 MRSNFORSHWSH  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..9  
OTHER INFORMATION: /label=theta-V3-2  
US-08-665-647-66

Query Match 23.5%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPOG 16  
||||  
Db 4 EPOG 7

## RESULT 47

US-08-350-260A-356  
Sequence 356, Application US/08350260A  
Patent No. 5962255  
GENERAL INFORMATION:  
APPLICANT: Winter, Gregory Paul  
APPLICANT: Griffiths, Andrew David  
APPLICANT: Williams, Samuel Cameron  
APPLICANT: Waterhouse, Peter  
APPLICANT: Nissim, Ahuva  
APPLICANT: Johnson, Kevin Stuart  
APPLICANT: Smith, Andrew John Hammond  
TITLE OF INVENTION: Methods for producing members of specific  
TITLE OF INVENTION: binding pairs  
NUMBER OF SEQUENCES: 602  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David W. Clough  
STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/350,260A  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01134

FILING DATE: 10-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00605  
FILING DATE: 24-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/150,002  
FILING DATE: 31-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/307,619  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32372  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 356:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-350-260A-356

Query Match 23.5%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4  
||||  
Db 4 LQTP 7

## RESULT 48

US-08-350-260A-365  
Sequence 365, Application US/08350260A  
Patent No. 5962255  
GENERAL INFORMATION:  
APPLICANT: Winter, Gregory Paul  
APPLICANT: Griffiths, Andrew David  
APPLICANT: Williams, Samuel Cameron  
APPLICANT: Waterhouse, Peter  
APPLICANT: Nissim, Ahuva  
APPLICANT: Johnson, Kevin Stuart  
APPLICANT: Smith, Andrew John Hammond  
TITLE OF INVENTION: Methods for producing members of specific  
TITLE OF INVENTION: binding pairs  
NUMBER OF SEQUENCES: 602  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David W. Clough  
STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/350,260A  
FILING DATE: 05-DEC-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9

;; FILING DATE: 24-MAR-1992  
;; PRIOR APPLICATION DATA: PCT/GB91/01134  
;; APPLICATION NUMBER: PCT/GB91/01134  
;; FILING DATE: 10-JUL-1991  
;; PRIOR APPLICATION DATA: PCT/GB92/00883  
;; APPLICATION NUMBER: PCT/GB92/00883  
;; FILING DATE: 15-MAY-1992  
;; PRIOR APPLICATION DATA: PCT/GB93/00605  
;; APPLICATION NUMBER: PCT/GB93/00605  
;; FILING DATE: 24-MAR-1993  
;; PRIOR APPLICATION DATA: US 08/150,002  
;; APPLICATION NUMBER: US 08/150,002  
;; FILING DATE: 31-MAR-1994  
;; PRIOR APPLICATION DATA: US 08/307,619  
;; APPLICATION NUMBER: US 08/307,619  
;; FILING DATE: 16-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clough, David W  
;; REGISTRATION NUMBER: 36,107  
;; REFERENCE/DOCKET NUMBER: 28111/32372  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312-474-6300  
;; INFORMATION FOR SEQ ID NO: 365:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-350-260A-365

Query Match 23.5%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4  
Db 4 LQTP 7

## RESULT 49

US-08-350-260A-373  
; Sequence 373, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Anuwa  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4

;; FILING DATE: 15-MAY-1991  
;; PRIOR APPLICATION DATA: GB 9206318.9  
;; APPLICATION NUMBER: GB 9206318.9  
;; FILING DATE: 24-MAR-1992  
;; PRIOR APPLICATION DATA: PCT/GB91/01134  
;; APPLICATION NUMBER: PCT/GB91/01134  
;; FILING DATE: 10-JUL-1991  
;; PRIOR APPLICATION DATA: PCT/GB92/00883  
;; APPLICATION NUMBER: PCT/GB92/00883  
;; FILING DATE: 15-MAY-1992  
;; PRIOR APPLICATION DATA: PCT/GB93/00605  
;; APPLICATION NUMBER: PCT/GB93/00605  
;; FILING DATE: 24-MAR-1993  
;; PRIOR APPLICATION DATA: US 08/150,002  
;; APPLICATION NUMBER: US 08/150,002  
;; FILING DATE: 31-MAR-1994  
;; PRIOR APPLICATION DATA: US 08/307,619  
;; APPLICATION NUMBER: US 08/307,619  
;; FILING DATE: 16-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clough, David W  
;; REGISTRATION NUMBER: 36,107  
;; REFERENCE/DOCKET NUMBER: 28111/32372  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312-474-6300  
;; INFORMATION FOR SEQ ID NO: 373:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-350-260A-373

Query Match 23.5%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQTP 4  
Db 4 LQTP 7

## RESULT 50

US-08-318-856A-37  
; Sequence 37, Application US/08318856A  
; Patent No. 5972351  
; GENERAL INFORMATION:  
; APPLICANT: Adrian V.S. Hill, et al.  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-  
; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE  
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1+  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,856A  
; FILING DATE: October 3, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 08 068.8  
; FILING DATE: April 3, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 17 704.7  
; FILING DATE: August 20, 1992

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-856A-37

Query Match 23.5%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4
 ||||
Db 5 LQTP 8

RESULT 51
US-08-159-339A-1062
; Sequence 1062, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1062:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-1062

Query Match 23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17
 ||||
Db 2 PQGD 5

RESULT 52
US-09-139-802-102
; Sequence 102, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-139-802-102

Query Match 23.5%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
 ||||
Db 4 LLQV 7

RESULT 53
US-09-230-199-1
; Sequence 1, Application US/09230199
; Patent No. 6294378
; GENERAL INFORMATION:
; APPLICANT: Houghton, Alan
; APPLICANT: Bartido, Shirley M.
; APPLICANT: Xu, Yiquing
; APPLICANT: Wang, Siqun
; TITLE OF INVENTION: Method and Reagents for Genetic
; TITLE OF INVENTION: Immunization
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
```

NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: MSK.P-012  
TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
DESCRIPTION: no  
HYPOTHETICAL: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: human  
ORGANISM: human  
US-09-230-199-1

Query Match 23.5%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
Db 4 QPLL 7

RESULT 54  
US-09-230-199-2  
Sequence 2, Application US/09230199  
Patent No. 6294378  
GENERAL INFORMATION:  
APPLICANT: Houghton, Alan  
APPLICANT: Bartigo, Shirley M.  
APPLICANT: Xu, Yiquing  
APPLICANT: Wang, Siqun  
TITLE OF INVENTION: Method and Reagents for Genetic  
TITLE OF INVENTION: Immunization  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson  
STREET: PO Box 5270  
CITY: Frisco  
STATE: CO  
COUNTRY: USA  
ZIP: 80443-5270  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/230,199  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/12675  
FILING DATE: 18-JUL-1997  
ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: MSK.P-012  
TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
DESCRIPTION: no  
HYPOTHETICAL: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: human  
ORGANISM: human  
US-09-230-199-2

Query Match 23.5%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
Db 4 QPLL 7

RESULT 55  
US-08-737-109-5  
Sequence 5, Application US/08737109  
Patent No. 6455688  
GENERAL INFORMATION:  
APPLICANT: SLABAS, Antoni Ryszard  
APPLICANT: ELBOROUGH, Kieran Michael  
APPLICANT: BRIGHT, Simon William Jonathan  
APPLICANT: FENTEM, Philip Anthony  
TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A  
TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/737,109  
FILING DATE: 21-Oct-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB94/00846  
FILING DATE: 02-MAY-1994  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Avena sativa  
US-08-737-109-5

Query Match 23.5%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EPQG 16  
      ||||  
Db 4 EPQG 7

## RESULT 56

US-09-659-786-102  
; Sequence 102, Application US/09659786  
; Patent No. 6491894  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: P-LJ 3203  
; CURRENT APPLICATION NUMBER: US/09/659,786  
; CURRENT FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 08/926,914  
; PRIOR FILING DATE: 1997-09-10  
; PRIOR APPLICATION NUMBER: 08/710,067  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-659-786-102

Query Match 23.5%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10  
      ||||  
Db 4 LLQV 7

## RESULT 57

US-09-104-337A-356  
; Sequence 356, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A  
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/350,260  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: GB 9110549.4  
FILING DATE: 15-MAY-1991  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
APPLICATION NUMBER: PCT/GB93/00605  
FILING DATE: 24-MAR-1993  
APPLICATION NUMBER: US 08/150,002  
FILING DATE: 31-MAR-1994  
APPLICATION NUMBER: US 08/307,619  
FILING DATE: 16-SEP-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.  
REGISTRATION NUMBER: 40,499  
REFERENCE/DOCKET NUMBER: 28111/32372A

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

## INFORMATION FOR SEQ ID NO: 356:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 356:

US-09-104-337A-356

## Query Match

23.5%; Score 4; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTP 4

Db 4 LQTP 7

## RESULT 58

US-09-104-337A-365  
; Sequence 365, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998  
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 365:
US-09-104-337A-365

```

```

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LQTP 4
 |||||
Db 4 LQTP 7

```

## RESULT 59

```

US-09-104-337A-373
; Sequence 373, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:

```

```

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4

```

```

; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-09-104-337A-373

```

```

Query Match 23.5%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LQTP 4
 |||||
Db 4 LQTP 7

```

## RESULT 60

```

US-08-926-914-102
; Sequence 102, Application US/08926914
; Patent No. 6576239
; GENERAL INFORMATION:

```

```

; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both

```



; MOLECULE TYPE: peptide  
US-08-926-914-102

Query Match 23.5%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10  
|||  
Db 4 LLQV 7

## RESULT 61

US-08-310-912A-93  
; Sequence 93, Application US/08310912A  
; Patent No. 5981730  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/310,912A  
; FILING DATE: September 22, 1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/227,360  
; FILING DATE: April 13, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lech, Karen F.  
; REGISTRATION NUMBER: 35,238  
; REFERENCE/DOCKET NUMBER: 00786/254001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254

; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-310-912A-93

Query Match 23.5%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9  
|||  
Db 2 PLLQ 5

## RESULT 62

US-08-159-339A-971  
; Sequence 971, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:

; INFORMATION FOR SEQ ID NO: 971:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-971

Query Match 23.5%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PQGD 17  
|||  
Db 6 PQGD 9

## RESULT 63

US-08-159-339A-1070  
; Sequence 1070, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 1070:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-159-339A-1070
;
; Query Match 23.5%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 2.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 14 PQGD 17
; Db 2 PQGD 5
;
; RESULT 64
; US-08-841-089-93
; Sequence 93, Application US/08841089
; Patent No. 6127607
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Skaskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
```

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,089
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-841-089-93
;
; Query Match 23.5%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 2.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 PLLQ 9
; Db 2 PLLQ 5
;
; RESULT 65
; US-08-981-392-53
; Sequence 53, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
```

```

; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-981-392-53

Query Match 23.5%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PQPL 7
Db 1 PQPL 4

RESULT 66
US-09-301-085-93
; Sequence 93, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-93

Query Match 23.5%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9
Db 2 PLLQ 5

RESULT 67
US-08-469-260A-597
; Sequence 597, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

; INFORMATION FOR SEQ ID NO: 597:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-597

Query Match 23.5%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLQV 10
Db 1 LLQV 4

RESULT 68
US-08-488-446-597
; Sequence 597, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,446  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; FILING DATE: US/08/424,550  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: FOREMSKI, PRISCILLA E.  
;; REGISTRATION NUMBER: 33,207  
;; REFERENCE/DOCKET NUMBER: 5527.PC.01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 708-937-6365  
;; TELEFAX: 708-938-2623  
;; INFORMATION FOR SEQ ID NO: 597:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-488-446-597

Query Match 23.5%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 LLQV 10  
|||  
Db 1 LLQV 4

RESULT 69  
US-08-467-344A-597  
; Sequence 597, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; TAMI J. PILOT-MATIAS  
; GEORGE J. DAWSON  
; GEORGE G. SCHLAUDER  
; SURESH M. DESAI  
; THOMAS P. LEARY  
; ANTHONY SCOTT MUERHOFF  
; JAMES C. ERKER  
; SHERI L. BUIJK  
; ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207

;; REFERENCE/DOCKET NUMBER: 5527.PC.01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 708-937-6365  
;; TELEFAX: 708-938-2623  
;; INFORMATION FOR SEQ ID NO: 597:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 597:  
US-08-467-344A-597

Query Match 23.5%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 LLQV 10  
|||  
Db 1 LLQV 4

RESULT 70  
PCT-US95-04570-93  
; Sequence 93, Application PC/TUS9504570  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04570  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,360  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/230001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-04570-93

Query Match 23.5%; Score 4; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 6 PLLQ 9  
|||  
Db 2 PLLQ 5

RESULT 71  
PCT-US95-04589-93  
; Sequence 93, Application PC/TUS9504589  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-liang  
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 201  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04589  
; FILING DATE:

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,360  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/230001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-04589-93

Query Match 23.5%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PLLQ 9  
|||  
Db 2 PLLQ 5

RESULT 72  
US-09-183-846A-24  
; Sequence 24, Application US/09183846A  
; Patent No. 6255046  
; GENERAL INFORMATION:  
; APPLICANT: Richard J. Bucala et al.

; TITLE OF INVENTION: Inducible Phosphofructokinase and the Warberg Effect  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVIS WRIGHT TREMAINE  
; STREET: 1501 Fourth Avenue, 2600 Century Square  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: 98101

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/183,846A  
; FILING DATE: 10/30/98  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oster, Jeffrey B.  
; REGISTRATION NUMBER: 32,585  
; REFERENCE/DOCKET NUMBER: 0902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206 628 7711  
; TELEFAX: 206 628 7699  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: polypeptide  
; US-09-183-846A-24

Query Match 23.5%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPLL 8  
|||  
Db 2 QPLL 5

RESULT 73  
US-08-339-214-56  
; Sequence 56, Application US/08339214  
; Patent No. 6348334  
; GENERAL INFORMATION:  
; APPLICANT: Negata, Shigikazu  
; APPLICANT: Suda, Takashi  
; APPLICANT: Takahashi, Tomoniro  
; APPLICANT: Nakamura, No. 6348334io  
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/339,214  
; FILING DATE: 10-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr., Gerald M.

; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-139P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..11  
; OTHER INFORMATION: /label= peptide  
; OTHER INFORMATION: /note= "peptide 1"  
US-08-339-214-56

Query Match 23.5%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VMME 13  
|||  
Db 2 VMME 5

RESULT 74  
5204326-35  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO  
; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO: 35:  
; LENGTH: 12  
5204326-35

Query Match 23.5%; Score 4; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTPQ 5  
|||  
Db 1 QTPQ 4

RESULT 75  
5204326-94  
; Patent No. 5204326  
; APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIHITO; SHIMIZU, FUMIO  
; INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROHASHI,  
; MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO  
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
; METABOLISM IMPROVING AGENT  
; NUMBER OF SEQUENCES: 147  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/493,359  
; FILING DATE: 14-MAR-1990  
; SEQ ID NO: 94:  
; LENGTH: 12  
5204326-94

Query Match 23.5%; Score 4; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QTPQ 5  
|||  
Db 1 QTPQ 4

Search completed: November 25, 2003, 20:15:57  
Job time : 19.5372 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 : Search time 16.5638 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-3  
Perfect score: 18  
Sequence: 1 DQPPDVKKPLQPFQVQS 18

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: PIR 76.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 5     | 27.8        | 9      | 2     | S66419      |
| 2          | 5     | 27.8        | 15     | 2     | S20410      |
| 3          | 4     | 22.2        | 15     | 2     | A60221      |
| 4          | 4     | 22.2        | 17     | 2     | B44873      |
| 5          | 4     | 22.2        | 19     | 2     | S59485      |
| 6          | 4     | 22.2        | 19     | 2     | S59486      |
| 7          | 4     | 22.2        | 20     | 2     | S11416      |
| 8          | 3     | 16.7        | 6      | 2     | PC4392      |
| 9          | 3     | 16.7        | 7      | 2     | S71299      |
| 10         | 3     | 16.7        | 7      | 2     | S68004      |
| 11         | 3     | 16.7        | 7      | 2     | PT0283      |
| 12         | 3     | 16.7        | 8      | 2     | PT0030      |
| 13         | 3     | 16.7        | 8      | 2     | I48935      |
| 14         | 3     | 16.7        | 9      | 2     | G58502      |
| 15         | 3     | 16.7        | 9      | 2     | A61620      |
| 16         | 3     | 16.7        | 10     | 1     | RHAQ1       |
| 17         | 3     | 16.7        | 10     | 2     | A32543      |
| 18         | 3     | 16.7        | 10     | 2     | C35389      |
| 19         | 3     | 16.7        | 10     | 2     | A60476      |
| 20         | 3     | 16.7        | 10     | 2     | A61007      |
| 21         | 3     | 16.7        | 10     | 2     | B61218      |
| 22         | 3     | 16.7        | 10     | 2     | C54226      |
| 23         | 3     | 16.7        | 10     | 2     | PA0116      |
| 24         | 3     | 16.7        | 10     | 2     | PS0220      |
| 25         | 3     | 16.7        | 11     | 2     | YHRT        |
| 26         | 3     | 16.7        | 11     | 2     | YHHT        |
| 27         | 3     | 16.7        | 11     | 2     | YHBO        |
| 28         | 3     | 16.7        | 11     | 2     | YHAE        |
| 29         | 3     | 16.7        | 11     | 2     | YHJFY       |

|     |   |      |    |   |        |                     |
|-----|---|------|----|---|--------|---------------------|
| 30  | 3 | 16.7 | 11 | 2 | PC2254 | cytochrome P450 3A  |
| 31  | 3 | 16.7 | 12 | 2 | S10059 | tachykinin - Afric  |
| 32  | 3 | 16.7 | 12 | 2 | S07436 | tachykinin - Afric  |
| 33  | 3 | 16.7 | 12 | 2 | C64030 | hypothetical prote  |
| 34  | 3 | 16.7 | 12 | 2 | T46794 | hypothetical prote  |
| 35  | 3 | 16.7 | 12 | 2 | A35585 | cytokinin-binding   |
| 36  | 3 | 16.7 | 12 | 2 | S21152 | tryptophyllin-rela  |
| 37  | 3 | 16.7 | 13 | 2 | A05174 | tryptophyllin-13    |
| 38  | 3 | 16.7 | 13 | 2 | PT0331 | Ig heavy chain CRD  |
| 39  | 3 | 16.7 | 13 | 2 | G61458 | Ig lambda chain V-  |
| 40  | 3 | 16.7 | 13 | 2 | A39836 | aggrscan - bovine   |
| 41  | 3 | 16.7 | 14 | 2 | I39753 | nitrogenase (EC 1.  |
| 42  | 3 | 16.7 | 14 | 2 | PS0371 | hypothetical prote  |
| 43  | 3 | 16.7 | 14 | 2 | I49514 | Bl44 protein A - m  |
| 44  | 3 | 16.7 | 15 | 2 | PA0003 | nucleoside-diphosp  |
| 45  | 3 | 16.7 | 15 | 2 | I58116 | Dp116 - human       |
| 46  | 3 | 16.7 | 15 | 2 | S29207 | avenin gamma-4 - o  |
| 47  | 3 | 16.7 | 15 | 2 | PQ0681 | photosystem I 19.0  |
| 48  | 3 | 16.7 | 15 | 2 | B39109 | hypothetical 1.5K   |
| 49  | 3 | 16.7 | 15 | 2 | S24138 | alkaline proteinas  |
| 50  | 3 | 16.7 | 15 | 2 | S39012 | proteinase - therm  |
| 51  | 3 | 16.7 | 15 | 2 | S21238 | hydrogensulfite re  |
| 52  | 3 | 16.7 | 15 | 2 | E56819 | PS I complex subun  |
| 53  | 3 | 16.7 | 15 | 2 | A56891 | gamma 1 gliadin -   |
| 54  | 3 | 16.7 | 15 | 2 | B56891 | gamma 2 gliadin -   |
| 55  | 3 | 16.7 | 15 | 2 | PA0053 | protein QP200006 -  |
| 56  | 3 | 16.7 | 15 | 2 | PA0051 | protein QP200016 -  |
| 57  | 3 | 16.7 | 15 | 2 | PA0088 | protein QP200051 -  |
| 58  | 3 | 16.7 | 15 | 2 | PA0071 | superoxide dismuta  |
| 59  | 3 | 16.7 | 15 | 2 | JN0263 | antigen (clone pV1  |
| 60  | 3 | 16.7 | 15 | 2 | PC1313 | small granule S6 c  |
| 61  | 3 | 16.7 | 15 | 2 | F57789 | galbladder stone    |
| 62  | 3 | 16.7 | 15 | 4 | I38032 | hypothetical MNI/T  |
| 63  | 3 | 16.7 | 16 | 1 | A49761 | locustapyrokinin -  |
| 64  | 3 | 16.7 | 16 | 2 | D58501 | 26K kidney and gal  |
| 65  | 3 | 16.7 | 16 | 2 | D45193 | zinc finger protei  |
| 66  | 3 | 16.7 | 16 | 2 | D83865 | hypothetical prote  |
| 67  | 3 | 16.7 | 17 | 2 | S66198 | alcohol dehydrogen  |
| 68  | 3 | 16.7 | 17 | 2 | PN0587 | tyrosine 3-monooxy  |
| 69  | 3 | 16.7 | 17 | 2 | S50901 | chlorophyll a/b-b1  |
| 70  | 3 | 16.7 | 17 | 2 | S66364 | sodium-translocati  |
| 71  | 3 | 16.7 | 17 | 2 | A42920 | fatty acid ethyl e  |
| 72  | 3 | 16.7 | 17 | 2 | S10786 | enamelin, 26K - bo  |
| 73  | 3 | 16.7 | 17 | 2 | PD0005 | very-high-density   |
| 74  | 3 | 16.7 | 17 | 4 | I51887 | hypothetical EMSR1  |
| 75  | 3 | 16.7 | 18 | 2 | PN0149 | beta-gliadine 13 -  |
| 76  | 3 | 16.7 | 18 | 2 | S52125 | gamma2-gliadin P25  |
| 77  | 3 | 16.7 | 18 | 2 | S29166 | guinaldine oxidore  |
| 78  | 3 | 16.7 | 18 | 2 | S10452 | hypothetical prote  |
| 79  | 3 | 16.7 | 18 | 2 | B57789 | kidney stone matri  |
| 80  | 3 | 16.7 | 18 | 2 | S26664 | microtubule-associ  |
| 81  | 3 | 16.7 | 19 | 1 | EW5MAN | anconvenin - Strept |
| 82  | 3 | 16.7 | 19 | 2 | I49422 | L-lactate dehydrog  |
| 83  | 3 | 16.7 | 19 | 2 | PS0186 | superoxide dismuta  |
| 84  | 3 | 16.7 | 19 | 2 | C56049 | superoxide dismuta  |
| 85  | 3 | 16.7 | 19 | 2 | PA0012 | superoxide dismuta  |
| 86  | 3 | 16.7 | 19 | 2 | PC1251 | tesin II - rat (f   |
| 87  | 3 | 16.7 | 19 | 2 | C21182 | 4K prothoracicotro  |
| 88  | 3 | 16.7 | 19 | 2 | A37968 | neural surface pro  |
| 89  | 3 | 16.7 | 20 | 2 | S21176 | testosterone beta   |
| 90  | 3 | 16.7 | 20 | 2 | S65135 | xanthine dehydroge  |
| 91  | 3 | 16.7 | 20 | 2 | S36842 | acylaminoacyl-pept  |
| 92  | 3 | 16.7 | 20 | 2 | A60100 | fimbrial antigen C  |
| 93  | 3 | 16.7 | 20 | 2 | PS0028 | flagellar motor sw  |
| 94  | 3 | 16.7 | 20 | 2 | S33867 | quinaldic acid 4-o  |
| 95  | 3 | 16.7 | 20 | 2 | B39089 | hydrogenase (EC 1.  |
| 96  | 3 | 16.7 | 20 | 2 | D25507 | proteinase inhibit  |
| 97  | 3 | 16.7 | 20 | 2 | A61276 | superoxide dismuta  |
| 98  | 3 | 16.7 | 20 | 2 | A41439 | acid ribonuclease   |
| 99  | 3 | 16.7 | 20 | 2 | A60897 | class I histocompa  |
| 100 | 3 | 16.7 | 20 | 2 | A60802 | 25K acrosomal auto  |

## ALIGNMENTS

## RESULT 1

S66419  
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)  
C:Species: Spinacia oleracea (spinach)  
C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997  
C:Accession: S66419  
R:kuwabara, T.  
FBS Lett. 371, 195-198, 1995  
A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spi  
A:Reference number: S66419, MUID:95402209; PMID:7672127  
A:Accession: S66419  
A:Molecule type: protein  
A:Residues: 1-9 <KOW>

Query Match 27.8%; Score 5; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8  
|||  
DB 5 PDVEK 9

## RESULT 2

S20410  
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
N:Alternate names: LHCI protein kinase  
C:Species: chloroplast Spinacia oleracea (spinach)  
C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C:Accession: S20410  
R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.  
FBS Lett. 298, 33-35, 1992  
A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyto  
A:Reference number: S20410; MUID:92183823; PMID:1544419  
A:Accession: S20410  
A:Molecule type: protein  
A:Residues: 1-15 <GAL>  
C:Genetics:  
A:Genome: chloroplast  
C:Function:  
A:Description: is responsible for the regulation of energy distribution between photosys  
A:Note: does not exhibit redox-controlled activation  
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match 27.8%; Score 5; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8  
|||  
DB 5 PDVEK 9

## RESULT 3

A60221  
apolipoprotein A-I - common carp (fragment)  
C:Species: Cyprinus carpio (common carp)  
C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993  
C:Accession: A60221  
R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.  
J. Neurochem. 55, 1237-1243, 1990  
A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg  
A:Reference number: A60221; MUID:90376100; PMID:2118944  
A:Accession: A60221  
A:Molecule type: protein  
A:Residues: 1-15 <HAR>  
A:Note: protein from plasma and from optic nerve yielded the same sequence  
C:Keywords: lipid binding; lipoprotein

Query Match 22.2%; Score 4; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPP 4  
|||  
DB 1 DQPP 4

## RESULT 4

B44873  
caldesmon - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Mar-2000  
C:Accession: B44873  
R:Kebe, M.; Hornick, T.  
Arch. Biochem. Biophys. 288, 538-542, 1991  
A:Title: Determination of the phosphorylation sites of smooth muscle caldesmon by pro  
A:Reference number: A44873; MUID:91378498; PMID:1898046  
A:Accession: B44873  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <IKE>  
A:Experimental source: skeletal myosin  
A:Note: sequence extracted from NCBI backbone (NCBIP:63202)  
C:Superfamily: caldesmon

Query Match 22.2%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9  
|||  
DB 8 VEKP 11

## RESULT 5

S59485  
hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)  
C:Species: Phaseolus vulgaris (kidney bean)  
C:Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Dec-1998  
C:Accession: S59485; S59484; S59483  
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A:Title: Specificity in the immobilisation of cell wall proteins in response to diffe  
A:Reference number: S59481; MUID:96011753; PMID:7548825  
A:Accession: S59485  
A:Molecule type: protein  
A:Residues: 1-19 <WOJ>  
A:Note: hydroxyproline-rich cell wall glycoprotein, 42K  
A:Accession: S59484  
A:Molecule type: protein  
A:Residues: 1-15 <WOW>  
A:Note: hydroxyproline-rich cell wall glycoprotein, 84K  
A:Accession: S59483  
A:Molecule type: protein  
A:Residues: 1-14 <WOF>  
A:Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component  
C:Superfamily: proline-rich protein 3  
C:Keywords: glycoprotein; hydroxyproline  
F:6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 22.2%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9  
|||  
DB 7 VEKP 10

## RESULT 6

S59486  
cell wall protein, 22K - kidney bean (fragment)



C;Species: Phaseolus vulgaris (kidney bean)  
 C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C;Accession: S59486  
 R;Wojtaszek, P.; Trzethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
 A;Reference number: S59481; MUID:96011753; PMID:7548825  
 A;Accession: S59486  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <WOJ>

Query Match 22.2%; Score 4; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5  
 DB 3 QPPD 6

RESULT 7  
 S11416  
 ribosomal protein L6, cytosolic [validated] - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jul-2000  
 C;Accession: S11416  
 R;Wittmann-Liebold, B.; Geissler, A.W.; Lin, A.; Wool, I.G.  
 J. Supramol. Struct. 12, 425-433, 1979  
 A;Title: Sequence of the amino-terminal region of rat liver ribosomal proteins S4, S6, S  
 A;Reference number: S11413; MUID:80252792; PMID:398910  
 A;Accession: S11416  
 A;Molecule type: protein  
 A;Residues: 1-20 <WIT>  
 A;Note: the protein is designated as ribosomal protein L6  
 C;Keywords: protein biosynthesis; ribosome

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXPD 10  
 DB 6 EXPD 9

RESULT 8  
 PC4392  
 whey glycoprotein WGP-88 - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 10-Nov-1997 #sequence\_revision 10-Nov-1997 #text\_change 07-May-1999  
 C;Accession: PC4392  
 R;Hwangbo, S.; Azuma, N.; Kurisaki, J.; Kanno, C.  
 Biosci. Biotechnol. Biochem. 61, 1568-1574, 1997  
 A;Title: Purification and characterization of novel whey glycoprotein WGP-88 which binds  
 A;Reference number: PC4392; MUID:97480944; PMID:9339560  
 A;Accession: PC4392  
 A;Molecule type: protein  
 A;Residues: 1-6 <HWA>  
 A;Experimental source: milk  
 C;Comment: This protein binds to the monoclonal antibody to PAS-4 glycoprotein.

Query Match 16.7%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQ 17  
 DB 4 QVQ 6

RESULT 9  
 S71299

C;Species: Paramaecium tetraurelia (fragment)  
 C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
 C;Accession: S71299  
 R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
 Eur. J. Biochem. 238, 121-128, 1996  
 A;Title: Characterization of centrin genes in Paramaecium.  
 A;Reference number: S71298; MUID:96248429; PMID:8665928  
 A;Accession: S71299  
 A;Molecule type: protein  
 A;Residues: 1-7 <MAD>  
 A;Experimental source: strain d4-2  
 A;Genetic code: SGCS

Query Match 16.7%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4  
 DB 2 QPP 4

RESULT 10  
 S68004  
 hucolin, 75K chain - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C;Accession: S68004  
 R;Edgar, P.F.  
 PERS Lett. 375, 159-161, 1995  
 A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structu  
 A;Reference number: S68004; MUID:96087107; PMID:7498469  
 A;Accession: S68004  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <EDG>

Query Match 16.7%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQ 12  
 DB 5 DLQ 7

RESULT 11  
 PT0283  
 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0283  
 R;Yamada, M.; Massman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 175, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0283  
 A;Molecule type: DNA  
 A;Residues: 1-7 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4  
 DB 5 QPP 7

## RESULT 12

PT0030  
 inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
 N;Alternate names: inulase  
 C;Species: Aspergillus ficuum  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
 C;Accession: PT0030  
 R;Etalalibi, M.; Baratti, J.C.  
 Agric. Biol. Chem. 54, 61-68, 1990  
 A;Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.  
 A;Reference number: PT0030; MUID:90344234; PMID:1369526  
 A;Accession: PT0030  
 A;Molecule type: protein  
 A;Residues: 1-8 <ET>  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQP 3  
 |||  
 Db 4 DQP 6

## RESULT 13

I48935  
 apolipoprotein A-II - western wild mouse (fragment)  
 C;Species: Mus spretus (western wild mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C;Accession: I48935  
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maerzaki, Y.; Nadeau, J.H.  
 Mamm. Genome 5, 349-355, 1994  
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A;Reference number: I48934; MUID:94319082; PMID:8043949  
 A;Accession: I48935  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-8 <RS>  
 A;Cross-references: EMBL:U05692; NID:g497011; PIDN:AAB60463.1; PID:g642827

Query Match 16.7%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKP 9  
 |||  
 Db 1 EKP 3

## RESULT 14

G58502  
 kidney and bladder stone protein - unidentified bacterium (fragment)  
 C;Species: unidentified bacterium  
 C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
 C;Accession: G58502  
 R;Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, October 1996  
 A;Description: The proteins of kidney and gallbladder stones.  
 A;Reference number: A58501  
 A;Accession: G58502  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <BIN>  
 A;Experimental source: human kidney stone, bladder stone  
 A;Note: a secondary sequence AAKENPKD was also found

Query Match 16.7%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6  
 |||

Db 3 PDV 5

## RESULT 15

A61620  
 locustamyotropin III - migratory locust  
 C;Species: Locusta migratoria (migratory locust)  
 C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jul-1997  
 C;Accession: A61620  
 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.  
 Insect Biochem. Mol. Biol. 22, 447-452, 1992  
 A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two  
 A;Reference number: A61620  
 A;Accession: A61620  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <SCH>  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14  
 |||  
 Db 3 QPF 5

## RESULT 16

RHA01  
 gonadoliberin I - American alligator  
 N;Alternate names: gonadotropin-releasing hormone I  
 C;Species: Alligator mississippiensis (American alligator)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C;Accession: A60066  
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swan  
 Regul. Pept. 33, 105-116, 1991  
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains  
 A;Reference number: A60066; MUID:91352338; PMID:1882082  
 A;Accession: A60066  
 A;Molecule type: protein  
 A;Residues: 1-10 <LOV>  
 C;Superfamily: gonadoliberin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13  
 |||  
 Db 7 LQP 9

## RESULT 17

A32543  
 cardioexcitatory neuropeptide - desert locust  
 C;Species: Schistocerca gregaria (desert locust)  
 C;Date: 20-Dec-1989 #sequence\_revision 20-Dec-1989 #text\_change 18-Aug-2000  
 C;Accession: A32543  
 R;Robb, S.; Packman, L.C.; Evans, P.D.  
 Biochem. Biophys. Res. Commun. 160, 850-856, 1989  
 A;Title: Isolation, primary structure and bioactivity of Schistocerca gregaria, a FMRF-ar  
 A;Reference number: A32543; MUID:89246543; PMID:2719702  
 A;Accession: A32543  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <ROB>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide

F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDV 6  
|||  
Db 1 PDV 3

#### RESULT 18

C35389  
urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)  
C;Species: Morganella morganii  
C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993  
C;Accession: C35389  
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
J. Bacteriol. 172, 3073-3080, 1990  
A;Title: Morganella morganii urease: purification, characterization, and isolation of gene  
A;Reference number: A35389; MUID:90264298; PMID:2345135  
A;Accession: C35389  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <HUA>  
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8  
|||  
Db 8 VEK 10

#### RESULT 19

A60476  
S-layer protein - Bacillus thuringiensis (fragment)  
C;Species: Bacillus thuringiensis  
C;Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 12-Mar-1993  
C;Accession: A60476  
R;Luckevich, M.D.; Beveridge, T.J.  
J. Bacteriol. 171, 6656-6667, 1989  
A;Title: Characterization of a dynamic S layer on Bacillus thuringiensis.  
A;Reference number: A60476; MUID:90078111; PMID:2592346  
A;Accession: A60476  
A;Molecule type: protein  
A;Residues: 1-10 <LUC>  
C;Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDV 6  
|||  
Db 6 PDV 8

#### RESULT 20

A61007  
hementin (EC 3.4.-.-) - Amazon leech (fragment)  
C;Species: Haementeria ghilianii (Amazon leech)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C;Accession: A61007  
R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.  
J. Chromatogr. 502, 359-369, 1990  
A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from  
A;Reference number: A61007; MUID:90256973; PMID:2187898  
A;Accession: A61007  
A;Molecule type: protein  
A;Residues: 1-10 <SWA>

C;Keywords: anticoagulant; hydrolase; saliva

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11  
|||  
Db 8 PDL 10

#### RESULT 21

B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C;Species: Haynaldia villosa, Dasypyrum villosum  
C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: B61218  
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Hayn.  
A;Reference number: A61218; MUID:91315394; PMID:1859356  
A;Accession: B61218  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SHE>  
C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13  
|||  
Db 8 LQP 10

#### RESULT 22

C54226  
light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)  
C;Species: Chromatium purpuratum  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
C;Accession: C54226  
R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.  
Biochemistry 33, 2178-2184, 1994  
A;Title: Purification and characterization of the peripheral antenna of the purple-su  
A;Reference number: A54226; MUID:94162224; PMID:8117674  
A;Accession: C54226  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <KER>  
C;Keywords: antenna complex; light-harvesting polypeptide

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VQS 18  
|||  
Db 8 VQS 10

#### RESULT 23

PA0116  
ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 03-Jun-2002  
C;Accession: PA0116  
R;Kamo, M.; Tsugita, A.  
submitted to JIFID, March 1995  
A;Reference number: PA0114  
A;Accession: PA0116  
A;Molecule type: protein  
A;Residues: 1-10 <KAM>



A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900  
 A;Accession: A93900  
 A;Molecule type: protein  
 A;Residues: 1-11 <SCH>  
 R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 A;Contents: annotation; synthesis  
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head  
 n mammalian intestine and hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4  
 ||||  
 Db 1 QPP 3

# RESULT 29

YHJPHY

morphogenetic neuropeptide - Hydra attenuata  
 N;Alternate names: head activator  
 C;Species: Hydra attenuata  
 C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C;Accession: B93900; A01427  
 R;Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A;Reference number: A93900  
 A;Accession: B93900  
 A;Molecule type: protein  
 A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 A;Contents: annotation; synthesis  
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head  
 n mammalian intestine and hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4  
 ||||  
 Db 1 QPP 3

# RESULT 30

PC2254

Cytochrome P450 3A - savannah baboon (fragment)  
 C;Species: Papio hamadryas doguera (savannah baboon)  
 C;Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 19-May-2000  
 C;Accession: PC2254  
 R;Ohmori, S.; Kudo, S.; Nakasa, H.; Horie, T.; Kitada, M.  
 Biol. Pharm. Bull. 17, 1584-1588, 1994  
 A;Title: Purification and characterization of cytochrome P450 3A enzyme from hepatic mid  
 A;Reference number: PC2254; MUID:95253110; PMID:7735199  
 A;Accession: PC2254  
 A;Molecule type: protein

A;Residues: 1-11 <OHM>  
 A;Experimental source: liver

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11  
 ||||  
 Db 5 PDL 7

# RESULT 31

S10059

tachykinin - African tree frog (Kassina maculata)  
 N;Alternate names: hylambates-kassinin  
 C;Species: Kassina maculata  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Sep-2000  
 C;Accession: S10059  
 R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.  
 Biomed. Res. 2, 613-617, 1981  
 A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, i  
 A;Reference number: S07436  
 A;Accession: S10059  
 A;Molecule type: protein  
 A;Residues: 1-12 <YAS>

A;Experimental source: skin  
 A;Note: the source is designated as Hylambates maculatus  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10  
 ||||  
 Db 4 KPD 6

# RESULT 32

S07436

tachykinin - African tree frog (Kassina maculata)  
 N;Alternate names: hylambatin  
 C;Species: Kassina maculata  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Sep-2000  
 C;Accession: S07436  
 R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.  
 Biomed. Res. 2, 613-617, 1981  
 A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, i  
 A;Reference number: S07436  
 A;Accession: S07436  
 A;Molecule type: protein  
 A;Residues: 1-12 <YAS>

A;Experimental source: skin  
 A;Note: the source is designated as Hylambates maculatus  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5  
 ||||  
 Db 2 PPD 4

# RESULT 33

C64030

hypothetical protein H11451 - Haemophilus influenzae (strain Rd KW20)

```

C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997
C;Accession: C64030
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64030
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <TIGR>
A;Cross-references: GB:U32823; GB:L42023; NID:G1574281; PID:G1574296; TIGR:HI1451

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
Db 9 PPD 11

RESULT 34
T46794
hypothetical protein [imported] - Haloarcula marismortui (fragment)
C;Species: Haloarcula marismortui
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T46794
R;Arndt, E. 267, 193-198, 1990
FEBS Lett. 267, 193-198, 1990
A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and
A;Reference number: S10731; MUID:90336772; PMID:2143141
A;Accession: T46794
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-12 <ARN>
A;Cross-references: EMBL:X55311; NID:G43610; PIDN:CAA39015.1; PID:G43611

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQ 12
Db 7 DLQ 9

RESULT 35
A35585
cytokinin-binding factor 1 - durum wheat
C;Species: Triticum durum (durum wheat)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C;Accession: A35585
R;Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.; Fox
Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988
A;Title: Characterization of a benzyladenine binding-site peptide isolated from a wheat
by mass spectrometry.
A;Reference number: A35585; MUID:88320357; PMID:3413067
A;Accession: A35585
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <BRI>

Query Match 16.7%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
Db 3 LQP 5

RESULT 36
S21152
tryptophyllin-related peptide - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S21152
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspaner, G.; Kreil,
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of
A;Reference number: S21152; MUID:923339502; PMID:1633846
A;Accession: S21152
A;Molecule type: protein
A;Residues: 1-13 <MIG>
A;Experimental source: skin
C;Superfamily: unassigned animal peptides

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EXP 9
Db 2 EXP 4

RESULT 37
A05174
tryptophyllin-13 - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C;Accession: A05174
R;Montecucchi, P.C.; Gozzini, L.; Erspaner, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A;Reference number: A05174
A;Accession: A05174
A;Molecule type: protein
A;Residues: 1-13 <MON>
C;Superfamily: unassigned animal peptides
C;Keywords: pyroglutamic acid; skin
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EXP 9
Db 2 EXP 4

RESULT 38
PT0331
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0331
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0331
A;Molecule type: DNA
A;Residues: 1-13 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15

```

```

Db 11 PFQ 13

RESULT 39
Ig lambda chain V-II region (AZI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: G61458; P10159
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein
A:Reference number: A61458; MUID:90039128; PMID:2478651
C:Accession: G61458
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein
C:Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
 |||
Db 6 QPP 8

RESULT 40
A39836
aggreccan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 24-Jun-1993
C:Accession: A39836
R:Sandy, J.D.; Neame, P.J.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8683-8685, 1991
A:Title: Catabolism of aggrecan in cartilage explants. Identification of a major cleavage site
A:Reference number: A39836; MUID:91224956; PMID:2026585
C:Accession: A39836
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <SAN>

Query Match 16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
 |||
Db 10 KPD 12

RESULT 41
I39753
nitrogenase (EC 1.18.6.1) - Azospirillum brasilense (fragment)
N:Alternate names: dinitrogenase reductase
C:Species: Azospirillum brasilense
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jan-2001
C:Accession: I39753
R:Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A:Title: Cloning, sequencing, mutagenesis, and functional characterization of draT and draX genes
A:Reference number: I39751; MUID:92250433; PMID:1577701
C:Accession: I39753
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M87319; NID:gl42411; PIDN:AAA22182.1; PID:gl42414
C:Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Db 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
 |||
Db 8 EXP 10

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 42
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhial, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning
A:Reference number: JS0694; MUID:92201692; PMID:1551590
C:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:Cross-references: GB:M86238; NID:gl54574; PIDN:AAA27351.1; PID:g552030

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
 |||
Db 12 LQP 14

RESULT 43
I49514
B144 protein A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49514
R:Tauge, I.; Shen, F.
Immunogenetics 26, 378-380, 1987
A:Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex whi
A:Reference number: I49514; MUID:88031493; PMID:3117682
C:Accession: I49514
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M18187; NID:gl92097; PIDN:AAA37272.1; PID:gl92098

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQ 12
 |||
Db 3 DLQ 5

RESULT 44
PA0003
nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996
C:Accession: PA0003
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Taugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0003
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: leaf and callus
C:Superfamily: nucleoside-diphosphate kinase
C:Keywords: phosphotransferase

```

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPD 10  
|||  
Db 11 KPD 13

## RESULT 45

I58116  
Dp116 - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I58116  
R;Byers, T.J.; Lidov, H.G.; Kunkel, L.M.  
Nature Genet. 4, 77-81, 1993  
A;Title: An alternative dystrophin transcript specific to peripheral nerve.  
A;Reference number: I58116; MUID:93291881; PMID:8513330  
A;Accession: I58116  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-15 <RES>  
A;Cross-references: GB:S62617; NID:G386224; PIDN:AA827159.1; PID:G386225  
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQ 12  
|||  
Db 11 DLQ 13

## RESULT 46

S29207  
avenin gamma-4 - oat (fragment)  
N;Alternate names: CIP-1; coeliac immunoreactive protein 1  
C;Species: Avena sativa (oat)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C;Accession: S29207  
R;Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.  
FEBS Lett. 310, 37-40, 1992  
A;Title: Identification of the three major coeliac immunoreactive proteins and one alpha  
A;Reference number: S29207; MUID:92405739; PMID:1526282  
A;Accession: S29207  
A;Molecule type: protein  
A;Residues: 1-15 <ROC>  
A;Experimental source: endosperm  
C;Superfamily: gliadin  
C;Keywords: prolamin; seed

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14  
|||  
Db 13 QPF 15

## RESULT 47

PQ0681  
photosystem I 19.0K D1 chain - common tobacco (fragment)  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C;Accession: PQ0681  
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.  
Plant Physiol. 102, 1259-1267, 1993  
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a  
A;Reference number: PQ0681; MUID:94105345; PMID:8278548  
A;Accession: PQ0681

A;Molecule type: protein  
A;Residues: 1-15 <OBO>  
C;Superfamily: photosystem I chain II  
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEX 8  
|||  
Db 2 VEX 4

## RESULT 48

B39109  
hypothetical 1.5K protein - hepatitis C virus  
N;Alternate names: hypothetical protein 2  
C;Species: hepatitis C virus  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C;Accession: B39109; JQ1585  
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Teka  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identific  
A;Reference number: A39109; MUID:91156678; PMID:1705704  
A;Accession: B39109  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-15 <HAN>  
A;Cross-references: GB:M58406  
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992  
A;Title: Cloning and sequencing of the structural region and expression of putative c  
A;Reference number: JQ1584; MUID:92300349; PMID:1318944  
A;Accession: JQ1585  
A;Molecule type: genomic RNA  
A;Residues: 1-15 <KUM>  
A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
|||  
Db 5 QPP 7

## RESULT 49

S24138  
alkaline proteinase (EC 3.4.21.-) - Thermus sp. (strain Rt41A) (fragment)  
C;Species: Thermus sp.  
A;Variety: strain Rt41A  
C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C;Accession: S24138  
R;Peek, K.; Daniel, R.M.; Monk, C.; Parker, L.; Coolbear, T.  
Eur. J. Biochem. 207, 1035-1044, 1992  
A;Title: Purification and characterization of a thermostable proteinase isolated from  
A;Reference number: S24138; MUID:92362605; PMID:1499549  
A;Accession: S24138  
A;Molecule type: protein  
A;Residues: 1-15 <PEE>  
A;Experimental source: strain Rt41a  
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VQS 18  
|||  
Db 2 VQS 4



RESULT 50  
 S39012  
 proteinase - Thermus sp.  
 C:Species: Thermus sp.  
 C>Date: 18-Feb-1994 #sequence\_revision 19-Apr-1996 #text\_change 07-May-1999  
 C:Accession: S39012  
 R:Freeman, S.A.; Peek, K.; Prescott, M.; Daniel, R.  
 Biochem. J. 295, 463-469, 1993  
 A:Title: Characterization of a chelator-resistant proteinase from *Thermus* strain Rt4A2.  
 A:Reference number: S39012; MUID:94058984; PMID:8240244  
 A:Accession: S39012  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <FRE>  
 A>Note: 13-Ala was also found

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VQS 18  
 |||  
 Db 2 VQS 4

RESULT 51  
 S21238  
 hydrogensulfite reductase (EC 1.8.99.3) beta chain - *Desulfovibrio vulgaris* (fragment)  
 N:Alternate names: bisulfite reductase; desulfofuscidin; desulfurubidin; desulfoviridin;  
 C:Species: *Desulfovibrio vulgaris*  
 C>Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C:Accession: S21238  
 R:Pierik, A.J.; Duyvis, M.G.; van Helvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.  
 Eur. J. Biochem. 205, 111-115, 1992  
 A:Title: The third subunit of desulfoviridin-type dissimilatory sulfite reductases.  
 A:Reference number: S21197; MUID:92209491; PMID:1555572  
 A:Accession: S21238  
 A:Molecule type: protein  
 A:Residues: 1-15 <PIE>  
 A:Experimental source: strain Hildenborough  
 C:Genetics:  
 A:Gene: dsbB  
 C:Complex: heterohexamer; two alpha, two beta and two gamma chains  
 C:Function:  
 A:Description: catalyzes the six-electron reduction of sulfite to sulfide  
 A:Pathway: the terminal oxidase in the sulfate-reduction pathway  
 C:Keywords: heterohexamer; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9  
 |||  
 Db 10 EXP 12

RESULT 52  
 E56819  
 PS I complex subunit 8 - cucumber (fragment)  
 C:Species: *Cucumis sativus* (cucumber)  
 C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C:Accession: E56819  
 R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.  
 Biochim. Biophys. Acta 1059, 141-148, 1991  
 A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te  
 A:Reference number: A56819; MUID:91355209; PMID:1883835  
 A:Accession: E56819  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <IWA>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FQV 16  
 |||  
 Db 8 FQV 10

RESULT 53  
 A56891  
 gamma 1 gliadin - wheat (fragment)  
 C:Species: *Triticum sp.* (wheat)  
 C>Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 08-Dec-1995  
 C:Accession: A56891  
 R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.  
 Clin. Chim. Acta 207, 227-237, 1992  
 A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.  
 A:Reference number: A56891; MUID:93009000; PMID:1395028  
 A:Contents: Kadett  
 A:Accession: A56891  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <SJO>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:119387)

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQ 17  
 |||  
 Db 9 QVQ 11

RESULT 54  
 B56891  
 gamma 2 gliadin - wheat (fragment)  
 C:Species: *Triticum sp.* (wheat)  
 C>Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 08-Dec-1995  
 C:Accession: B56891  
 R:Sjostrom, H.; Friis, S.U.; Noren, O.; Anthonsen, D.  
 Clin. Chim. Acta 207, 227-237, 1992  
 A:Title: Purification and characterisation of antigenic gliadins in coeliac disease.  
 A:Reference number: A56891; MUID:93009000; PMID:1395028  
 A:Contents: Kadett  
 A:Accession: B56891  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <SJO>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:119388)

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQ 17  
 |||  
 Db 9 QVQ 11

RESULT 55  
 PA0053  
 protein QF200006 - fungus (*Fusarium sporotrichioides*) (fragment)  
 C:Species: *Fusarium sporotrichioides*  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0053  
 R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotr*  
 A:Reference number: PA0051  
 A:Accession: PA0053

A;Molecule type: protein  
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9  
|||  
Db 4 EXP 6

#### RESULT 56

PA0051

protein QF200016 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0051

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JPIID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0051

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEX 8  
|||  
Db 2 VEX 4

#### RESULT 57

PA0088

protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0088

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JPIID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0088

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10  
|||  
Db 2 KPD 4

#### RESULT 58

PA0071

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0071

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JPIID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0071

A;Molecule type: protein

A;Residues: 1-15 <CHO>

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Keywords: metalloprotein; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11  
|||  
Db 5 PDL 7

#### RESULT 59

JN0263

antigen (clone PV12) - Plasmodium vivax (fragment)

C;Species: Plasmodium vivax

C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 09-Sep-1997

C;Accession: JN0263; S21344

R;Ray, P.; Sharma, Y.D.

Biochem. Biophys. Res. Commun. 184, 668-672, 1992

A;Title: Molecular cloning and serological characterization of a new Plasmodium vivax

A;Reference number: JN0263; PMID:92246949; PMID:1575740

A;Accession: JN0263

A;Molecule type: DNA

A;Residues: 1-15 <RAY>

A;Cross-references: GB:X53681; NID:G10084; PID:G10085

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQP 3  
|||  
Db 1 DQP 3

#### RESULT 60

PC1313

small granule S6 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)

C;Species: Tachyplesus tridentatus

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C;Accession: PC1313

R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.

J. Biochem. 114, 307-316, 1993

A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)

A;Reference number: PC1309; PMID:94110249; PMID:8282718

A;Accession: PC1313

A;Molecule type: protein

A;Residues: 1-15 <SHI>

C;Comment: This protein contributes to a self-defense system against invaders.

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9  
|||  
Db 1 EXP 3

#### RESULT 61

F57789

gallbladder stone matrix protein 2, 41K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 03-May-1996

C;Accession: F57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: F57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BIN>

A;Note: 9-Phe was also found

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred.No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 KPD 10  
Db 4 KPD 6  
  
RESULT 62  
I38032  
hypothetical MN1/TEL mutant fusion protein type I - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
C;Accession: I38032  
R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.  
Oncogene 10, 1511-1519, 1995  
A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion  
A;Reference number: I38031; MUID:95249265; PMID:7731705  
A;Accession: I38032  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-15 <BUI>  
A;Cross-references: EMBL:X85025; NID:9971467; PIDN:CAA59398.1; PID:9971468  
C;Comment: This sequence is the chimeric product of a translocation mutation.  
C;Genetics:  
A;Gene: MN1/ETV6; MN1/TEL  
A;Map position: 22q11/12p13  
C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred.No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 LQP 13  
Db 9 LQP 11

RESULT 63  
A49761  
locustapyrokinin - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 08-Dec-1995  
C;Accession: A49761  
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.  
Gen. Comp. Endocrinol. 81, 97-104, 1991  
A;Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide  
A;Reference number: A49761; MUID:91224474; PMID:2026322  
A;Accession: A49761  
A;Molecule type: protein  
A;Residues: 1-16 <SCH>  
C;Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut as  
C;Superfamily: pyrokinin  
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental  
F;16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 QPF 14  
Db 10 QPF 12

RESULT 64  
D58501  
26K kidney and gallbladder stone protein - unidentified bacterium (fragment)  
C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C;Accession: D58501  
R;Binette, J.P.; Binette, M.B.  
Submitted to the Protein Sequence Database, October 1996  
A;Description: The proteins of kidney and gallbladder stones.  
A;Reference number: A58501  
A;Accession: D58501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BIN>  
A;Experimental source: human kidney and gallbladder stones

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 KPD 10  
Db 4 KPD 6

RESULT 65  
D45193  
zinc finger protein ZNF60 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 01-Jan-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C;Accession: D45193  
R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.  
Genomics 13, 999-1007, 1992  
A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile  
A;Reference number: A43284; MUID:92372070; PMID:1505991  
A;Accession: D45193  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <LIC>  
A;Cross-references: GB:M88369; NID:9340475; PIDN:AAA61327.1; PID:9340476  
A;Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBIP:111664)

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 EXP 9  
Db 5 EXP 7

RESULT 66  
D83865  
hypothetical protein BH1724 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: D83865  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H.  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: D83865  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <STO>  
A;Cross-references: GB:AP001512; GB:BA000004; NID:910174030; PIDN:BA05443.1; GSPDB:G  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH1724

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PDV 6  
Db 10 PDV 12

```

RESULT 67
S66198
alcohol dehydrogenase (EC 1.1.1.1) class III - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 14-Feb-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C;Accession: S66198
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
zyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66198
A;Molecule type: protein
A;Residues: 1-17 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVE 7
 |||
Db 15 DVE 17

RESULT 68
PN0587
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)
N;Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PN0587
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PN0575; MUID:93371398; PMID:7689834
A;Accession: PN0587
A;Molecule type: genomic RNA
A;Residues: 1-17 <ICH>
A;Cross-references: GB:L14801
A;Experimental source: kidney
C;Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosy
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
 |||
Db 15 LQP 17

RESULT 69
S50901
chlorophyll a/b-binding protein Lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: cnlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys

```

```

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
 |||
Db 4 LQP 6

RESULT 70
S66364
sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) gamma-1 chain - Vib
C;Species: Vibrio alginolyticus
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C;Accession: S66364
R;Beattie, P.; Tan, K.; Bourne, R.M.; Leach, D.; Rich, P.R.; Ward, F.B.
FEBS Lett. 356, 333-338, 1994
A;Title: Cloning and sequencing of four structural genes for the Na(+)-translocating
A;Reference number: S51013; MUID:95104445; PMID:7805867
A;Accession: S66364
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BEA>
C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QVQ 17
 |||
Db 15 QVQ 17

RESULT 71
A42920
fatty acid ethyl ester synthase-II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A42920
R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.
J. Biol. Chem. 267, 13217-13221, 1992
A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from
A;Reference number: A42920; MUID:92317032; PMID:1618826
A;Accession: A42920
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-17 <BOR>
A;Experimental source: myocardium
A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
 |||
Db 3 PPD 5

RESULT 72
S10786
enamelin, 26K - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10786
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10786
A;Molecule type: protein

```

A;Residues: 1-17 <STR>  
C;Keywords: enamel; phosphoprotein

Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4  
|||  
Db 3 QPP 5

## RESULT 73

PD0005 very-high-density lipoprotein - sand crayfish (fragment)

N;Alternate names: VMDL

C;Species: Ibacus ciliatus (sand crayfish)

C;Date: 13-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 07-May-1999

C;Accession: PD0005

R;Komatsu, M.; Ando, S.

Biosci. Biotechnol. Biochem. 62, 459-463, 1998

A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand ch

A;Reference number: PD0005; MUID:98233268; PMID:9571775

A;Accession: PD0005

A;Molecule type: protein

A;Residues: 1-17 <KOW>

C;Comment: This protein plays an important role in the defense process of crustacea, it a

Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13  
|||  
Db 1 LQP 3

## RESULT 74

I51887

hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000

C;Accession: I51887

R;Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; Mc

Am. J. Pathol. 143, 1294-1300, 1993

A;Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripher

A;Reference number: I51887; MUID:94056652; PMID:8238248

A;Accession: I51887

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-17 <DOW>

A;Cross-references: GB:S66911; NID:G440935; PIDN:AAB28655.1; PID:G440936

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: EWSR1/FLI1; EWS/FLI-1

A;Map position: 22q12/11q24

C;Keywords: fusion protein

Query Match 16.7%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11  
|||  
Db 10 PDL 12

## RESULT 75

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.  
Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0149

A;Molecule type: protein

A;Residues: 1-18 <ODI>

A;Experimental source: strain K-202

C;Superfamily: gliadin

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13  
|||  
Db 8 LQP 10

Search completed: November 25, 2003, 18:28:15

Job time : 18.5638 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 8.71277 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-3  
Perfect score: 18  
Sequence: 1 DQPPDVEKPLQPFQVQS 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description         |
|------------|-------|-------------|--------|-------------|---------------------|
| 1          | 3     | 16.7        | 7      | UF04_MOUSE  | P38642 mus musculus |
| 2          | 3     | 16.7        | 9      | LMT3_LOCOMI | P41489 locusta mig  |
| 3          | 3     | 16.7        | 10     | FARP_PANRE  | P82660 panagrellus  |
| 4          | 3     | 16.7        | 10     | FARP_LOCOMI | P38553 locusta mig  |
| 5          | 3     | 16.7        | 10     | GONI_ALLMI  | P37041 alligator m  |
| 6          | 3     | 16.7        | 10     | SLAP_BACTG  | F49325 bacillus th  |
| 7          | 3     | 16.7        | 10     | UPA2_HUMAN  | P30088 homo sapien  |
| 8          | 3     | 16.7        | 10     | URE3_MORMO  | P17339 morganella   |
| 9          | 3     | 16.7        | 11     | MORN_HUMAN  | P01163 homo sapien  |
| 10         | 3     | 16.7        | 12     | HS9A_RAT    | P82995 rattus norv  |
| 11         | 3     | 16.7        | 12     | TKN1_KASMA  | P08613 kassina mac  |
| 12         | 3     | 16.7        | 12     | TKN2_KASMA  | P08614 kassina mac  |
| 13         | 3     | 16.7        | 13     | E121_LITRU  | P82097 littoria rub |
| 14         | 3     | 16.7        | 13     | E122_LITRU  | P82098 littoria rub |
| 15         | 3     | 16.7        | 13     | IDHP_RAT    | P56574 rattus norv  |
| 16         | 3     | 16.7        | 13     | PEDI_HYDAT  | P80578 hydra atten  |
| 17         | 3     | 16.7        | 13     | SODM_CANFA  | P54712 canis famil  |
| 18         | 3     | 16.7        | 13     | TY13_PHYRO  | P04096 phyllomedus  |
| 19         | 3     | 16.7        | 14     | MARI_ALTPS  | P29399 alteromonas  |
| 20         | 3     | 16.7        | 15     | HS11_PINPS  | P81083 pinus pinas  |
| 21         | 3     | 16.7        | 15     | MK1_PALPR   | P80408 palomena pr  |
| 22         | 3     | 16.7        | 15     | MK2A_PALPR  | P80409 palomena pr  |
| 23         | 3     | 16.7        | 15     | ONC1_ONCMY  | P83287 oncorhynch   |
| 24         | 3     | 16.7        | 15     | PSAO_CUCSA  | F42052 cucumis sat  |
| 25         | 3     | 16.7        | 15     | VORA_METTM  | P80907 methanobact  |
| 26         | 3     | 16.7        | 16     | LPK1_LOCOMI | P20404 locusta mig  |
| 27         | 3     | 16.7        | 16     | MK2B_PALPR  | P80410 palomena pr  |
| 28         | 3     | 16.7        | 16     | MK3_PALPR   | P80411 palomena pr  |
| 29         | 3     | 16.7        | 16     | MMFX_SOLTU  | P80501 solanum tub  |
| 30         | 3     | 16.7        | 18     | SODM_MYCHA  | P80582 mycobacteri  |
| 31         | 3     | 16.7        | 18     | UC21_MAIZE  | P80627 zea mays (m  |
| 32         | 3     | 16.7        | 19     | LANC_STRSQ  | P38655 streptomyc   |
| 33         | 3     | 16.7        | 20     | ACPH_BOVIN  | P80227 bos taurus   |

|     |   |      |    |   |             |
|-----|---|------|----|---|-------------|
| 34  | 3 | 16.7 | 20 | 1 | BULB_NARPS  |
| 35  | 3 | 16.7 | 20 | 1 | CHP_THICU   |
| 36  | 3 | 16.7 | 20 | 1 | CP35_PAFSP  |
| 37  | 3 | 16.7 | 20 | 1 | DER6_DERPT  |
| 38  | 3 | 16.7 | 20 | 1 | SODM_HORVU  |
| 39  | 3 | 16.7 | 20 | 1 | TRYL_STREX  |
| 40  | 4 | 11.1 | 5  | 1 | TUFT_HUMAN  |
| 41  | 4 | 11.1 | 5  | 1 | SUGA_ACHDO  |
| 42  | 2 | 11.1 | 6  | 1 | ACPH_RABIT  |
| 43  | 2 | 11.1 | 6  | 1 | OVN_DEPDE   |
| 44  | 2 | 11.1 | 7  | 1 | TRPI_PSEPU  |
| 45  | 2 | 11.1 | 7  | 1 | FAR1_HELTI  |
| 46  | 2 | 11.1 | 7  | 1 | FAR4_PANRE  |
| 47  | 2 | 11.1 | 7  | 1 | FARB_CALVO  |
| 48  | 2 | 11.1 | 7  | 1 | LANC_CARUI  |
| 49  | 2 | 11.1 | 7  | 1 | PPH2_LYCES  |
| 50  | 2 | 11.1 | 7  | 1 | TPFY_PACDA  |
| 51  | 2 | 11.1 | 7  | 1 | UH11_RAT    |
| 52  | 2 | 11.1 | 7  | 1 | UN06_PINPS  |
| 53  | 2 | 11.1 | 8  | 1 | ACT_CARMA   |
| 54  | 2 | 11.1 | 8  | 1 | AKHG_GRYBI  |
| 55  | 2 | 11.1 | 8  | 1 | AKH_LIBAU   |
| 56  | 2 | 11.1 | 8  | 1 | AKH_MEML    |
| 57  | 2 | 11.1 | 8  | 1 | ALL2_CARMA  |
| 58  | 2 | 11.1 | 8  | 1 | ALL5_CALVO  |
| 59  | 2 | 11.1 | 8  | 1 | ANG2_BOTJA  |
| 60  | 2 | 11.1 | 8  | 1 | HTPI_PERAM  |
| 61  | 2 | 11.1 | 8  | 1 | LCK3_LEUMA  |
| 62  | 2 | 11.1 | 8  | 1 | LCK6_LEUMA  |
| 63  | 2 | 11.1 | 8  | 1 | NPB_BOVIN   |
| 64  | 2 | 11.1 | 8  | 1 | PLP_BRANA   |
| 65  | 2 | 11.1 | 8  | 1 | PPK2_PERAM  |
| 66  | 2 | 11.1 | 8  | 1 | PPK3_PERAM  |
| 67  | 2 | 11.1 | 8  | 1 | UC26_MAIZE  |
| 68  | 2 | 11.1 | 8  | 1 | UH09_RAT    |
| 69  | 2 | 11.1 | 8  | 1 | UPA1_HUMAN  |
| 70  | 2 | 11.1 | 9  | 1 | AL10_CARMA  |
| 71  | 2 | 11.1 | 9  | 1 | CCAP_CARMA  |
| 72  | 2 | 11.1 | 9  | 1 | COW_CONVE   |
| 73  | 2 | 11.1 | 9  | 1 | COXE_THOEB  |
| 74  | 2 | 11.1 | 9  | 1 | FAR3_PENMO  |
| 75  | 2 | 11.1 | 9  | 1 | FAR4_CALVO  |
| 76  | 2 | 11.1 | 9  | 1 | FAR4_PENMO  |
| 77  | 2 | 11.1 | 9  | 1 | FARS_ASCSU  |
| 78  | 2 | 11.1 | 9  | 1 | FRF1_SARBU  |
| 79  | 2 | 11.1 | 9  | 1 | HUTU_KLEAE  |
| 80  | 2 | 11.1 | 9  | 1 | KNL3_BOMVA  |
| 81  | 2 | 11.1 | 9  | 1 | LMIP_LOCOMI |
| 82  | 2 | 11.1 | 9  | 1 | OXYT_BUPRE  |
| 83  | 2 | 11.1 | 9  | 1 | PPH1_LYCES  |
| 84  | 2 | 11.1 | 9  | 1 | PTSP_BOMMO  |
| 85  | 2 | 11.1 | 9  | 1 | RT33_BOVIN  |
| 86  | 2 | 11.1 | 9  | 1 | UHA2_HUMAN  |
| 87  | 2 | 11.1 | 9  | 1 | ULAE_HUMAN  |
| 88  | 2 | 11.1 | 9  | 1 | ULAH_HUMAN  |
| 89  | 2 | 11.1 | 9  | 1 | UPA6_HUMAN  |
| 90  | 2 | 11.1 | 9  | 1 | YBFR_AZOVI  |
| 91  | 2 | 11.1 | 10 | 1 | AH3_PRUSE   |
| 92  | 2 | 11.1 | 10 | 1 | AKHG_LOCOMI |
| 93  | 2 | 11.1 | 10 | 1 | ANG1_BOTJA  |
| 94  | 2 | 11.1 | 10 | 1 | ANGT_BOVIN  |
| 95  | 2 | 11.1 | 10 | 1 | ANGT_CHICK  |
| 96  | 2 | 11.1 | 10 | 1 | APE_CAGPI   |
| 97  | 2 | 11.1 | 10 | 1 | BPF2_BOTIN  |
| 98  | 2 | 11.1 | 10 | 1 | BPF2_BOTJA  |
| 99  | 2 | 11.1 | 10 | 1 | BPP8_BOTIN  |
| 100 | 2 | 11.1 | 10 | 1 | BPP_VIPAS   |

ALIGNMENTS

RESULT 1

```

UF04 MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
Db 3 PPD 5

RESULT 2
LMT3 LOCMI
ID LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR: A61620; A61620.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9
FT SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
Db 3 QPF 5

```

```

RESULT 3
FAR6 PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF6 (NGAPQFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OC NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RX Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
peptides (FARPs) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
Db 5 QPF 7

RESULT 4
FARP LOCMI
ID FARP_LOCMI STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistoflrfamide (PVDHFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Veelaert D., Amelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PVDHFLRFamide
RT (Schistoflrfamide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct."
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria."
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.

```





```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson B.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR: C35389; C35389.
KW Hydrolase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
Db 8 VEK 10

RESULT 9
MORN HUMAN
ID MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A. elegantissima, and H. attenuata;
RX Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Bitt C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.

```

```

CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR: A01427; YHRT.
DR PIR: A93900; YHXA.
DR PIR: B01427; YHUU.
DR PIR: B93900; YHJPHY.
DR PIR: C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4
Db 1 QPP 3

RESULT 10
HS9A RAT STANDARD; PRT; 12 AA.
ID HS9A RAT
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasma 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro: IPR001404; Hsp90.
DR PROSITE: PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQP 3
Db 8 DQP 10

RESULT 11
TKN1 KASMA
ID TKN1 KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)

```

DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hylambates kassinin ((Glu2,Pro1)kassinin).  
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
OC Kassina.  
OX NCBI\_TaxID=8414;  
RN [1]\_TaxID=8414;  
RN SEQUENCE.  
RP TISSUE=Skin secretion;  
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
RT "New tachykinins, Glu2, Pro1-kassinin (hylambates-kassinin) and  
RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
RT maculatus.", 2:613-617(1981).  
RL Biomed. Res. 2:613-617(1981).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; S10059; S10059.  
DR InterPro; IPR003580; Protachykinin.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 12 12  
FT SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;  
SQ  
Query Match 16.7%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 KPD 10  
Db 4 KPD 6  
RESULT 12  
TXN2\_KASMA STANDARD; PRT; 12 AA.  
ID TXN2\_KASMA  
AC F08614;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hylambatin.  
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
OC Kassina.  
OX NCBI\_TaxID=8414;  
RN [1]\_TaxID=8414;  
RN SEQUENCE.  
RP TISSUE=Skin secretion;  
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
RT "New tachykinins, Glu2, Pro1-kassinin (hylambates-kassinin) and  
RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
RT maculatus.", 2:613-617(1981).  
RL Biomed. Res. 2:613-617(1981).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; S07436; S07436.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 12 12  
FT SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;  
SQ  
Query Match 16.7%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPD 5  
Db 2 PPD 4  
RESULT 13  
E121\_LITRU STANDARD; PRT; 13 AA.  
ID E121\_LITRU  
AC P82097;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.",  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 13 13  
FT SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;  
SQ  
Query Match 16.7%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PDV 6  
Db 10 PDV 12  
RESULT 14  
E122\_LITRU STANDARD; PRT; 13 AA.  
ID E122\_LITRU  
AC P82098;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 2.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.",  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.  
 FT MOD RES 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1538 MW; C1808EF33B357322 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred.No.1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 PDV 6  
 DB 10 PDV 12  
  
 RESULT 15  
 IDHP RAT STANDARD; PRT; 13 AA.  
 AC P56574;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)  
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) (ICD-M) (Fragment).  
 GN IDH2  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;  
 RL Submitted P.R.;  
 RL Submitter (SEP-1998) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2) + NADPH.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.  
 DR InterPro; IPR001804; IsoDH.  
 DR PROSITE; PS00470; IDH, IMPDH, PARTIAL.  
 KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle; Mitochondrion.  
 KW Mitochondrion.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1526 MW; 5F81031723B02C3 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred.No.1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 VEK 8  
 DB 7 VEK 9  
  
 RESULT 16  
 PEDI HYDAT STANDARD; PRT; 13 AA.  
 AC P80578;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE Pedin.  
 DE Hydra attenuata (Hydra) (Hydra vulgaris).  
 OS Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Anthomedusae;  
 OC Hydridae; Hydra.  
 ON NCBI\_TaxID=6087;

```

DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]_
RN SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 7 EXP 9
Db 2 EXP 4

RESULT 19
MARI_ALTRSP STANDARD; PRT; 14 AA.
AC P2939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 (Marinostatin C-1; Marinostatin D).
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]_
RN SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kanei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14 MARINOSTATIN C-2.
FT PEPTIDE 3 14 MARINOSTATIN C-1.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
SQ SEQUENCE 14 AA; 1644 MW; 6B7CEFP92EF32E44 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 12 QPF 14
Db 1 QPF 3

RESULT 20
HSII_PINPS STANDARD; PRT; 15 AA.
AC P81083;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

```

---

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable class I heat shock protein (water stress responsive protein
DE 3) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]_
RN SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]_
RN SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
RN [3]_
RN REVISION TO 1.
RA Frigerio J.-M.;
RL Submitted (SEP-2001) to the SWISS-PROT data bank.
CC -!- SUBUNIT: FORMS OLIGOMERIC STRUCTURES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N144) IS: 6.1. ITS MW IS: 17 kDa.
CC -!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
CC FAMILY.
CC -!- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS
CC TO CLASS I.
DR InterPro; IPR002068; Hsp20.
DR PROSITE; PS01031; HSP20; PARTIAL.
KW Heat shock; Multigene family.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 13 PFQ 15
Db 12 PFQ 14

RESULT 21
MK1_PALPR STANDARD; PRT; 15 AA.
AC P80408;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metainikowin I.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]_
RN SEQUENCE.
RA TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect

```

```

RT Palomena prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin." ;
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
CC Antibiotic; Insect immunity.
KW QW SEQUENCE 15 AA; 1838 MW; 214078663CE46299 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 22
MK2A_PALPR STANDARD; PRT; 15 AA.
ID MK2A_PALPR
AC P80409;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metanikowin IIA.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidae; Pentatomidae;
OC Palomena
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S.; Cociancich S.; Briand J.-P.; Hetru C.; Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomena prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin." ;
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -!- INDUCTION: By bacterial infection.
CC Antibiotic; Insect immunity.
KW QW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 23
ONC1_ONCMY STANDARD; PRT; 15 AA.
ID ONC1_ONCMY
AC P83287;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oncorhynchin 1 (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RA Fernandes J.M.O.; Smith V.J.; Kemp G.D.;
RT "Purification and N-terminal sequencing of a 3 kDa antibacterial

```

```

RT peptide from skin secretions of rainbow trout." ;
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium P.citreus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003795; F:antimicrobial peptide activity; NAS.
DR GO; GO:0006805; P: xenobiotic metabolism; NAS.
KW Antibiotic.
FT UNSURE 4 4 OR G.
FT UNSURE 9 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVE 7
DB 9 DVE 11

RESULT 24
PSAO_CUCSA STANDARD; PRT; 15 AA.
ID PSAO_CUCSA
AC F42052;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa
DE protein) (Fragment).
GN PSAM.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE.
RC TISSUE=Cotyledon;
RX MEDLINE=9135209; PubMed=1883835;
RA Iwasaki Y.; Ishikawa H.; Hibino T.; Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing." ;
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.
DR PIR; E56819; E56819.
KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FOV 16
DB 8 FOV 10

RESULT 25
VORA_METTM STANDARD; PRT; 15 AA.
ID VORA_METTM
AC P80907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ketosovalerate oxidoreductase subunit VORA (EC 1.-.-.-) (VOR) (2-
DE oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-
DE ferredoxin oxidoreductase alpha subunit) (Fragment).
GN VORA.

```

```

OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133) .
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature
of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531C5A28F CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 7 KPD 9

RESULT 26
LPK1_LOGMI
ID LPK1_LOGMI STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=91224474; PubMed=20263322;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1827 MW; A178BDC0A0FDD6 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
DB 10 QPF 12

RESULT 27
MK2B_PALPR
ID MK2B_PALPR STANDARD; PRT; 16 AA.
AC P80410;
DT 01-NOV-1995 (Rel. 32, Created)

```

```

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metelnikowin IIB.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 28
MK3_PALPR
ID MK3_PALPR STANDARD; PRT; 16 AA.
AC P80411;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metelnikowin III.
OS Palomena prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Palomena.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
BACTERIA.
CC -!- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 3 KPD 5

RESULT 29
MMPX_SOLTU
ID MMPX_SOLTU STANDARD; PRT; 16 AA.
AC P80501;

```

```

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE
RC TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Krutt V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW Mitochondrion.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
 |||
DB 9 VEK 11

RESULT 30
SODM MYCHA
ID _SODM_MYCHA STANDARD; PRT; 18 AA.
AC P80582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1) (Fragment).
GN SODA OR SOD.
OS Mycobacterium habana.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1784;
RN [1]
RP SEQUENCE.
RC STRAIN=TMC 5135;
RX MEDLINE=96262709; PubMed=8704977;
RA Bist D., Mehrotra J., Dhindsa M.S., Singh N.B., Sinha S.;
RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the
vaccine candidate Mycobacterium habana is superoxide dismutase.";
RL Microbiology 142:1375-1383(1996).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1883 MW; A4161A3DAC93F710 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
 |||

```

```

Db 6 PDL 8

RESULT 31
UC21 MAIZE
ID _UC21_MAIZE STANDARD; PRT; 18 AA.
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
 (Fragment).
DE Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
DR Maize-2DPAGE; P80627; COLEOPTILE.
DR MaizeDB; 123953; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
 |||
DB 15 VEK 17

RESULT 32
LANC STRSQ
ID _LANC_STRSQ STANDARD; PRT; 19 AA.
AC P38655;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lanthibiotic ancovenin.
OS Streptomyces sp. (strain A647P-2).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
RT "The structure of ancovenin, a new peptide inhibitor of angiotensin I
 converting enzyme.";
RL Tetrahedron Lett. 26:665-668(1985).
CC -!- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
 thr, and Ser into dehydrated AA and the formation of thioether
 bonds with cysteine or the formation of dialkylamine bonds with
 lysine. This is followed by membrane translocation and cleavage of
 the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
DR PIR; A61284; ESWMAN.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18
 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14
 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11
 Beta-methylanthionine (Cys-Thr).

```

```

FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VQS 18
DB 2 VQS 4

RESULT 33
ACPH_BOVIN
ID ACPH_BOVIN STANDARD; PRT; 20 AA.
AC P80227;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Lens;
RX MEDLINE=93387316; PubMed=8375399;
RA Sharma K.K., Ortworth B.J.;
RT "Bovine lens acylpeptide hydrolase. Purification and characterization
of a tetrameric enzyme resistant to urea denaturation and proteolytic
inactivation."
RL Eur. J. Biochem. 216:631-637(1993).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
+ peptide.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; S36842; S36842.
DR InterPro; IPR002471; Prol endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2325 MW; B9D028BA8378F624 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 1 KPD 3

RESULT 34
BULB_NARPS
ID BULB_NARPS STANDARD; PRT; 20 AA.
AC P80554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Bulb protein (Fragment).
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.

```

```

OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 2 PDV 4

RESULT 35
CHP_THICU
ID CHP_THICU STANDARD; PRT; 20 AA.
AC P80486;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemoheterotroph-specific protein (fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOHETEROTROPHICALLY.
FT NON_TER 20 20
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2167 MW; E5BAEC1BA3238A0A CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPD 10
DB 17 KPD 19

RESULT 36
CP35_PAPSP
ID CP35_PAPSP STANDARD; PRT; 20 AA.
AC P80056;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYP11A5) (P450 FA) (6-beta-
testosterone hydroxylase) (Fragment).
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boullenc X., Fabre G., Maurel P., Bonfils C.;
RL "Purification of two cytochrome P450 isozymes related to CYP2A and
CYP3A gene families from monkey (baboon, Papio papio) liver
microsomes. Cross reactivity with human forms."
RL Eur. J. Biochem. 204:641-648 (1992).

```



```

CC -!- FUNCTION: 6-BETA-TESTOSTERONE HYDROXYLASE.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro: IPR001128; Cytochrome P450.
DR PROSITE: PS00086; CYTOCHROME P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT NON_TER 20
FT SEQUENCE 20 AA; 2226 MW; 3FEF8B6E2BC0F36 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 5 PDL 7

RESULT 37
DER6_DERPT STANDARD; PRT; 20 AA.
AC P49277;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mite allergen Der P 6 [EC 3.4.21.-] (Der P VI) (DP5) (Fragment).
GN DERP6.
OS Dermatophagoides pteronyssinus (House-dust mite).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
CC Acariformes; Sarcophormes; Astigmata; Psoroptidia; Analgoidea;
CC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP SEQUENCE.
RX MEDLINE=93327207; PubMed=8334537;
RA Yasueda H., Mita H., Akiyama K., Shida T., Ando T., Sugiyama S.,
RA Yamakawa H.;
RT "Allergens from Dermatophagoides mites with chymotryptic activity.";
RL Clin. Exp. Allergy 23:384-390(1993).
CC -!- CATALYTIC ACTIVITY: Specificity similar to chymotrypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR MEROPS: S01.187; -.
DR InterPro: IPR001254; Ser. protease Try.
DR PROSITE: PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease; Allergen.
FT UNSURE 1
FT UNSURE 6
FT UNSURE 10
FT UNSURE 11
FT UNSURE 17
FT UNSURE 17
FT NON_TER 20
FT SEQUENCE 20 AA; 2082 MW; 26D5F39E06639983 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15
Db 13 PFQ 15

RESULT 38
SODM_HORVU STANDARD; PRT; 20 AA.
ID _SODM_HORVU
AC P28524;

```

```

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial [EC 1.15.1.1] (Fragment).
GN SODA.
OS Hordeum vulgare (Barley).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
CC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. CM 72; TISSUE=Root;
RA Hurkman W.J., Tao H.P., Tanaka C.K.;
RT "Germin-like polypeptides increase in barley roots during salt
RT stress.";
RL Plant Physiol. 97:366-374(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON_TER 20
FT SEQUENCE 20 AA; 2152 MW; 7F7CAE8DFF1C9657 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 7 PDL 9

RESULT 39
TRYL_STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease [EC 3.4.21.-] (Fragment).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX MEDLINE=95291424; PubMed=7773379;
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13.";
RL Microbiology 141:1017-1025(1995).
CC -!- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
DR MEROPS: S01.101; -.
DR InterPro: IPR001254; Ser. protease Try.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
FT SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFQ 15  
Db 13 PFQ 15

## RESULT 40

TUFT HUMAN  
ID TUFT\_HUMAN STANDARD; PRT; 4 AA.  
AC P01858;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phagocytosis-stimulating peptide (Tuftsin).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72187087; PubMed=4112769;  
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;  
RT "The characteristics, isolation and synthesis of the phagocytosis  
stimulating peptide tuftsin.";  
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).  
RN [2]

## IMMUNOGLOBULIN CLASS.

RX MEDLINE=68091045; PubMed=4169272;  
RA Fidalgo B.V., Najjar V.A.;  
RT "The physiological role of the lymphoid system. VI. The stimulatory  
effect of leucophilic gamma globulin (leucokinin) on the phagocytic  
activity of human polymorphonuclear leucocyte.";  
RL Biochemistry 6:3386-3392(1967).  
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE  
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE  
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.  
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC  
ACTIVITY OF NEUTROPHILS.

CC PIR: A02147; A02147.  
DR MW: 191150; -.

DR GO: G0:0003823; F:antigen binding activity; NAS.  
DR GO: G0:0006909; P:phagocytosis; NAS.

DR GO: G0:0006909; P:phagocytosis; NAS.  
SQ SEQUENCE 4 AA; 501 MW; 74176321C000000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KP 9  
Db 2 KP 3

## RESULT 41

SUGA ACHDO  
ID SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P19991;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Subesophagical ganglion pentapeptide.  
OS Acheta domesticus (House cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Acheta.  
OX NCBI\_TaxID=6997;  
RN [1]  
RP SEQUENCE.  
RA Wicker C.;  
RT "Isolation and structure of a peptide isolated from the  
subesophagical ganglion of Acheta domesticus (orthoptera).";  
RL Comp. Biochem. Physiol. 88C:185-187(1987).

CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
CC GANGLIA.  
DR PIR: JS0319; JS0319.  
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14  
Db 4 PF 5

## RESULT 42

ACPH RABIT  
ID ACPH\_RABIT STANDARD; PRT; 6 AA.  
AC P25154;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)  
DE (APH) (Acylaminoacyl-peptidase) (Fragment).  
GN APEH.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.

PC TISSUE=Muscle;  
RX MEDLINE=92222120; PubMed=1807161;  
RA Krishna R.G., Chin C.C.Q., Wold F.;

RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
unblocking with N-acylaminoacyl-peptide hydrolase.";  
RL Anal. Biochem. 199:45-50(1991).

CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
+ peptide.

CC -!- SUBUNIT: Homotetramer.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.

DR PIR: A49792; A49792.

DR MEROPS: S09.004; -.

DR InterPro: IPR002471; Prol endopep\_ser.

DR PROSITE: PS00708; PRO\_ENDOPEP\_SER; PARTIAL.

KW Hydrolase; Acetylation.

FT MOD\_RES: 1 1 ACETYLATION.

FT NON\_TER: 1 6

SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QV 16  
Db 4 QV 5

## RESULT 43

OVN LEPDE  
ID OVN\_LEPDE STANDARD; PRT; 6 AA.  
AC P42585;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Oviductal motility stimulating peptide (Leb-OVM).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
 OC Chrysomelini; Leptinotarsa.  
 OX NCBI\_TaxID=7539;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=91271080; PubMed=2052497;  
 RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,  
 RA Proost P., Torrekens S., de Loof A.;  
 RT "Isolation, identification and synthesis of novel oviductal motility  
 RT stimulating head peptide in the Colorado potato beetle, *Leptinotarsa*  
 RT decemlineata.";  
 RL Peptides 12:31-36 (1991).  
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
 CC OVIDUCT.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 8 KP 9  
 DB 4 KP 5  
 RESULT 44  
 ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TrpBA operon transcriptional activator (fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPG1 C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas*  
 RT putida.";  
 RL Biochimie 71:521-531 (1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING  
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC ENBL; X13299; CAA31660.1; .  
 DR InterPro; IPR000847; HTH\_LysR.  
 DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 10 DL 11  
 DB 4 DL 5  
 RESULT 45  
 ID FARL\_HELTI STANDARD; PRT; 7 AA.  
 AC P41871;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide GDPFIRF-amide.  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Planorbidae; Helisoma.  
 OX NCBI\_TaxID=27815;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*  
 RT trivolvis".  
 RL Peptides 15:31-36 (1994).  
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
 CC THE KIDNEY, MANTLE AND SKIN.  
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 13 PF 14  
 DB 3 PF 4  
 RESULT 46  
 ID FAR4\_PANRE STANDARD; PRT; 7 AA.  
 AC P41875;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95232026; PubMed=7716079;  
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,  
 RA Thim L., Kubiak T.M., Martin R.A., Geary T.G.;  
 RT "Isolation and preliminary biological characterization of  
 RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living  
 RT nematode, *Panagrellus redivivus*.";  
 RL Peptides 16:87-93 (1995).  
 CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT  
 CC MUSCLE TENSION INCREASE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.

SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9  
DB 1 KP 2

RESULT 47

ID FARB CALVO STANDARD; PRT; 7 AA.

AC P41866;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE CalliFMRamide 11.

OS Calliphora vomitoria (Blue blowfly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Calliphoridae; Calliphora.

OX NCBI\_TaxID=27454;

RN [1]

RP SEQUENCE.

RC TISSUE=Thoracic ganglion;

RX MEDLINE=92196111; PubMed=1549595;

RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
Rehfeld J.F., Thorpe A.;

RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
neuropeptides (designated calliFMRamides) from the blowfly  
Calliphora vomitoria.;

RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.

CC PIR: B44787; B44787.

DR Neuropeptide; Amidation.

KW MOD\_RES 7

FT SEQUENCE 7 AA; 926 MW; 69D40699C444AB700 CRC64;

SQ SEQUENCE 7 AA; 926 MW; 69D40699C444AB700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PD 5  
DB 1 PD 2

RESULT 48

ID LANC CARUI STANDARD; PRT; 7 AA.

AC P36960;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lantibiotic carnoicin UI49 (Fragment).

OS Carnobacterium sp. (strain UI49).

OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;

OC Carnobacterium

OX NCBI\_TaxID=35782;

RN [1]

RP SEQUENCE.

RX MEDLINE=92321768; PubMed=1622206;

RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
Nes I.F.;

RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.;"

RL Appl. Environ. Microbiol. 58:1417-1422(1992).

CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
ACTIVE ON GRAM-POSITIVE BACTERIA.

KW Antibiotic; Bacteriocin; Lantibiotic.

FT NON TER 7 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3  
DB 5 QP 6

RESULT 49

ID PP2 LYCES STANDARD; PRT; 7 AA.

AC P83379;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridaceae; lamiids; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4081;

RN [1]

RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
GLYCOSYLATION.

RC STRAIN=cv. Moneymaker; TISSUE=Seed;

RX MEDLINE=22361242; PubMed=12473124;

RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;

RT "Purification and characterization of two secreted purple acid  
phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
esculentum) cell cultures.;"

RT Eur. J. Biochem. 269:6278-6286(2002).

CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
alcohol + phosphate.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- PTM: Glycosylated.

CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of  
purple acid phosphatase.

KW Hydrolase; Glycoprotein.

FT NON\_TER 1 1  
FT NON\_TER 7 7

SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DL 11  
DB 6 DL 7

RESULT 50

ID TPFY PACDA STANDARD; PRT; 7 AA.

AC P83455;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE TrypToPhyllin-1 (pdt-1).

OS Pachymedusa dancicolor (Giant mexican leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;

OC Phyllomedusinae; Pachymedusa.

OX NCBI\_TaxID=75988;

RN [1]

RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
PRO-7.

KW TISSUE=Skin secretion;

```

RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dancicolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
Db 2 PP 3

RESULT 51
UH11_RAT
ID UH11_RAT STANDARD; PRT; 7 AA.
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- PROTEIN IS: 8.5, ITS MW IS: 42 KDa.
FT UNSURE 2 2 OR A.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 QS 18
Db 1 QS 2

RESULT 52
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.

```

```

RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14
Db 6 PF 7

RESULT 53
ACT_CARMA
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 34, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 kDa.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin-like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAEB3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DV 6
Db 3 DV 4

RESULT 54
AKHG_GRYBI
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
RP SEQUENCE.

```

```

Qy 15 QV 16
Db ||
 1 QV 2

RESULT 55
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
NCBI_TaxID=6966;
[1]
SEQUENCE, AND SYNTHESIS.
RC TISSUE=Cordora cardiaca;
RX MEDLINE=903559055; Pubmed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

```

12/

SEQUENCE.

SPECIES=P.marginata; TISSUE=Corpora cardiaca;  
MEDLINE=92265187; PubMed=1586453;  
Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;  
"Primary structures of neuropeptides isolated from the corpora  
cardiaca of various cetonid beetle species determined by  
pulsed-liquid phase sequencing and tandem fast atom bombardment mass  
spectrometry.";  
Biol. Chem. Hoppe-Seyler 373:133-142 (1992).  
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
GLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RFCH FAMILY.  
PIR; A58641; A58641.  
PIR; S15422; S15422.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 PD 5  
||  
6 PD 7

## RESULT 57

AL12\_CARMA STANDARD; PRT; 8 AA.  
 ID \_ALL2\_CARMA  
 AC P81815;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 12.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 SEQUENCE.  
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Multigene family.  
 SQ SEQUENCE 8 AA; 915 MW; 672879CDBC569AB7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PD 5  
 Db 1 PD 2

## RESULT 58

ALL5\_CALVO STANDARD; PRT; 8 AA.  
 ID \_ALL5\_CALVO  
 AC P41841;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 SEQUENCE.  
 RP MEDLINE=93211980; PubMed=8460157;  
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Callatostatins: neuropeptides from the blowfly *Calliphora vomitoria*  
 RT with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 [2]  
 RN CHARACTERIZATION, AND HYDROXYLATION.  
 RP TISSUE=Head;  
 RX MEDLINE=94342269; PubMed=8063725;  
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
 RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
 RT a novel neuropeptide from the blowfly *Calliphora vomitoria*.";  
 RL J. Biol. Chem. 269:21059-21066(1994).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

## DR

PIR; E47393; E47393.  
 KW Neuropeptide; Amidation; Hydroxylation.  
 FT MOD RES 3 3 HYDROXYLATION (20%).  
 FT MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4  
 Db 2 PP 3

## RESULT 59

ANG2\_BOTJA STANDARD; PRT; 8 AA.  
 ID \_ANG2\_BOTJA  
 AC Q10582;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide II (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 SEQUENCE.  
 RP TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dallie Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake *Bothrops jararaca*.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PF 14  
 Db 7 PF 8

## RESULT 60

HTF1\_PERAM STANDARD; PRT; 8 AA.  
 ID \_HTF1\_PERAM  
 AC P04548;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)  
 DE (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).  
 OS Periplaneta americana (American cockroach),  
 OS Leptinotarsa decemlineata (Colorado potato beetle), and  
 OS Blattella orientalis (Oriental cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978; 7539, 6976;  
 RN [1]  
 SEQUENCE.  
 RP SPECIES=P.americana;  
 RX MEDLINE=85046530; PubMed=6548628;  
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,

RA Rinehart K.L. Jr.;  
 RT "Structures of two cockroach neuropeptides assigned by fast atom  
 RT bombardment mass spectrometry.";  
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=P. americana;  
 RX MEDLINE=84298179; PubMed=6591205;  
 RA Scarborough R.M.; PubMed=2576128;  
 RA Gaede G., Kellner R.;  
 RA "The metabolic neuropeptides of the corpus cardiaca from the potato  
 RT beetle and the American cockroach are identical.";  
 RT Peptides 10:1287-1289(1989).  
 RL [4]  
 RN SEQUENCE.  
 RP SPECIES=B. orientalis; TISSUE=Corpora cardiaca;  
 RC MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RA "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 RT atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A44960; A49823; A49823; A49823;  
 DR PIR; S08995; S08995;  
 DR InterPro; IPR002047; AKH;  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 QV 16  
 DB 1 QV 2

RESULT 61  
 LCK3\_LEUMA  
 ID LCK3\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin III (L-III).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 CC Blaberidae; Leucophaea.  
 CC NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides  
 RT from Leucophaea maderae: members of a new family of  
 RT Cephalomyotropins.";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DQ 2  
 DB 1 DQ 2

RESULT 62  
 LCK6\_LEUMA  
 ID LCK6\_LEUMA STANDARD; PRT; 8 AA.  
 AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucokinin VI (L-VI).  
 OS Leucophaea maderae (Madeira cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 CC Blaberidae; Leucophaea.  
 CC NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RA MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 RT myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 89C:27-30(1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
 CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.  
 DR PIR; JS0316; JS0316.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B51E9D5A5A6 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 QS 18  
 DB 1 QS 2

RESULT 63  
 NPB\_BOVIN  
 ID NPB\_BOVIN STANDARD; PRT; 8 AA.  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropeptide B.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;



```

RN NCBI_TaxID=6978;
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
KW PIR; B24749; B24749.
DR Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 4 QP 5

RESULT 64
PLP_BRANA
ID_PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planca 208:588-598(1999).
CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.
CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHERS.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DV 6
DB 3 DV 4

RESULT 65
PPK2_PERAM
ID_PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.

```

```

OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=983; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR Interpro; IPR001484; Pyrokinin.
KW PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 2 PP 3

RESULT 66
PPK3_PERAM
ID_PPK3_PERAM STANDARD; PRT; 8 AA.
AC P82618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-3 (Pea-PK-3) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

```

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PF 14  
Db 3 PF 4

RESULT 67  
UC26 MAIZE STANDARD; PRT; 8 AA.  
AC P80632;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Tourret P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program."  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.  
DR Maize-2DPAGE; P80632; COLEOPTILE.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2  
Db 5 DQ 6

RESULT 68  
UH09 RAT STANDARD; PRT; 8 AA.  
AC P56575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 QS 18  
Db 5 QS 6

RESULT 69  
UPAL HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
DR SWISS-2DPAGE; P30087; HUMAN.  
FT NON\_TER 1  
FT NON\_TER 8  
FT UNSURE 8  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQ 2  
Db 1 DQ 2

RESULT 70  
AL10 CARMA STANDARD; PRT; 9 AA.  
AC P81813;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 10.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas."  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD\_RES 9  
FT AMIDATION.  
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 3 QP 4

RESULT 71
CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
SEQUENCE.
RC SPECIES=M.sexta;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9
FT SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PF 14
DB 1 PF 2

RESULT 72
COW_COWVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
snail Conus ventricosus.";
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD RES 5 5
FT MOD RES 9 9
FT SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9
DB 6 KP 7

RESULT 73
COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3

Db 3 QP 4

## RESULT 74

FAR3 PENMO STANDARD; PRT; 9 AA.  
AC P83318;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP3 (AQPSMRLEF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]

## SEQUENCE, AND MASS SPECTROMETRY.

RP TISSUE=Eyestalk;  
RC MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,  
RA Chaivithangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 9 AMIDATION.

SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3

Db 2 QP 3

## RESULT 75

FAR4 CALVO STANDARD; PRT; 9 AA.  
AC P41859;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRamide 4.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]

## SEQUENCE.

RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
neuropeptides (designated calliFMRamides) from the blowfly  
Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; D41978; D41978.

KW Neuropeptide; Amidation.  
FT MOD RES 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KP 9

Db 1 KP 2

Search completed: November 25, 2003, 18:17:23

Job time : 9.71277 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 43.3723 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18

Sequence: 1 DQPPDVEXPDLPQFQVQS 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 5     | 27.8        | 15     | 8     | Q972K8      |
| 2          | 4     | 22.2        | 11     | 2     | Q9S618      |
| 3          | 4     | 22.2        | 11     | 6     | Q8HYM4      |
| 4          | 4     | 22.2        | 13     | 2     | Q9R3R6      |
| 5          | 4     | 22.2        | 15     | 12    | Q86174      |
| 6          | 4     | 22.2        | 17     | 6     | Q9LB06      |
| 7          | 4     | 22.2        | 17     | 6     | Q9TRW1      |
| 8          | 4     | 22.2        | 17     | 12    | Q919B0      |
| 9          | 4     | 22.2        | 18     | 2     | Q9X3E9      |
| 10         | 4     | 22.2        | 18     | 2     | Q67971      |
| 11         | 4     | 22.2        | 18     | 2     | Q9R4E0      |
| 12         | 4     | 22.2        | 18     | 6     | P82674      |
| 13         | 4     | 22.2        | 18     | 10    | Q9S8G8      |
| 14         | 4     | 22.2        | 18     | 12    | Q919D5      |
| 15         | 4     | 22.2        | 18     | 12    | Q919B3      |
| 16         | 4     | 22.2        | 18     | 12    | Q919B5      |

|    |   |      |    |    |        |
|----|---|------|----|----|--------|
| 17 | 4 | 22.2 | 18 | 12 | Q919B7 |
| 18 | 4 | 22.2 | 18 | 12 | Q919C5 |
| 19 | 4 | 22.2 | 18 | 12 | Q919D1 |
| 20 | 4 | 22.2 | 18 | 12 | Q919D3 |
| 21 | 4 | 22.2 | 18 | 12 | Q919B9 |
| 22 | 4 | 22.2 | 18 | 12 | Q919A8 |
| 23 | 4 | 22.2 | 18 | 12 | Q919C7 |
| 24 | 4 | 22.2 | 18 | 12 | Q919C9 |
| 25 | 4 | 22.2 | 18 | 13 | Q13167 |
| 26 | 4 | 22.2 | 19 | 2  | Q9R7I3 |
| 27 | 4 | 22.2 | 19 | 10 | Q9S8G9 |
| 28 | 4 | 22.2 | 20 | 2  | Q67964 |
| 29 | 4 | 22.2 | 20 | 2  | Q9X3M3 |
| 30 | 4 | 22.2 | 20 | 2  | Q67966 |
| 31 | 4 | 22.2 | 20 | 2  | Q9R4L9 |
| 32 | 4 | 22.2 | 20 | 10 | Q9S8H0 |
| 33 | 4 | 22.2 | 20 | 11 | Q91X54 |
| 34 | 3 | 16.7 | 8  | 6  | Q95M23 |
| 35 | 3 | 16.7 | 8  | 11 | Q62528 |
| 36 | 3 | 16.7 | 9  | 2  | Q9EZ14 |
| 37 | 3 | 16.7 | 9  | 2  | Q9R735 |
| 38 | 3 | 16.7 | 9  | 4  | Q9UCS8 |
| 39 | 3 | 16.7 | 9  | 4  | Q16605 |
| 40 | 3 | 16.7 | 9  | 10 | Q9FX10 |
| 41 | 3 | 16.7 | 9  | 10 | P82429 |
| 42 | 3 | 16.7 | 9  | 13 | Q8AYL5 |
| 43 | 3 | 16.7 | 9  | 13 | Q8AUM7 |
| 44 | 3 | 16.7 | 9  | 16 | Q935G1 |
| 45 | 3 | 16.7 | 10 | 2  | Q9XBH3 |
| 46 | 3 | 16.7 | 10 | 8  | Q8SHA8 |
| 47 | 3 | 16.7 | 10 | 13 | Q9PRY8 |
| 48 | 3 | 16.7 | 11 | 2  | Q47606 |
| 49 | 3 | 16.7 | 11 | 2  | Q47604 |
| 50 | 3 | 16.7 | 11 | 7  | Q19718 |
| 51 | 3 | 16.7 | 11 | 10 | Q8RV30 |
| 52 | 3 | 16.7 | 11 | 13 | Q8UUP1 |
| 53 | 3 | 16.7 | 12 | 4  | Q9UC37 |
| 54 | 3 | 16.7 | 12 | 4  | Q8IVH0 |
| 55 | 3 | 16.7 | 12 | 8  | P92457 |
| 56 | 3 | 16.7 | 12 | 10 | P82328 |
| 57 | 3 | 16.7 | 12 | 12 | Q88577 |
| 58 | 3 | 16.7 | 12 | 12 | Q88578 |
| 59 | 3 | 16.7 | 12 | 12 | Q88579 |
| 60 | 3 | 16.7 | 12 | 12 | Q88575 |
| 61 | 3 | 16.7 | 12 | 12 | Q88580 |
| 62 | 3 | 16.7 | 12 | 12 | Q88582 |
| 63 | 3 | 16.7 | 12 | 12 | Q88581 |
| 64 | 3 | 16.7 | 12 | 12 | Q88576 |
| 65 | 3 | 16.7 | 13 | 11 | Q88176 |
| 66 | 3 | 16.7 | 13 | 11 | Q8CJ33 |
| 67 | 3 | 16.7 | 13 | 12 | Q67604 |
| 68 | 3 | 16.7 | 13 | 13 | Q8JJ32 |
| 69 | 3 | 16.7 | 14 | 2  | Q55326 |
| 70 | 3 | 16.7 | 14 | 2  | Q43905 |
| 71 | 3 | 16.7 | 14 | 2  | P81715 |
| 72 | 3 | 16.7 | 14 | 3  | P90342 |
| 73 | 3 | 16.7 | 14 | 3  | Q8U1G2 |
| 74 | 3 | 16.7 | 14 | 4  | Q9P2A2 |
| 75 | 3 | 16.7 | 14 | 4  | Q96Q50 |
| 76 | 3 | 16.7 | 14 | 4  | Q16045 |
| 77 | 3 | 16.7 | 15 | 11 | Q9Z1H4 |
| 78 | 3 | 16.7 | 15 | 2  | Q9R531 |
| 79 | 3 | 16.7 | 15 | 3  | Q9UR63 |
| 80 | 3 | 16.7 | 15 | 3  | Q9URCS |
| 81 | 3 | 16.7 | 15 | 4  | Q08947 |
| 82 | 3 | 16.7 | 15 | 4  | Q9UCV1 |
| 83 | 3 | 16.7 | 15 | 5  | Q26159 |
| 84 | 3 | 16.7 | 15 | 5  | Q9TWQ2 |
| 85 | 3 | 16.7 | 15 | 8  | Q9T2H9 |
| 86 | 3 | 16.7 | 15 | 10 | Q9AT15 |
| 87 | 3 | 16.7 | 15 | 10 | Q9S8N8 |
| 88 | 3 | 16.7 | 15 | 10 | Q9S8V2 |
| 89 | 3 | 16.7 | 15 | 10 | Q9S8V3 |

|        |             |
|--------|-------------|
| Q919B7 | human papil |
| Q919C5 | human papil |
| Q919D1 | human papil |
| Q919D3 | human papil |
| Q919B9 | human papil |
| Q919A8 | human papil |
| Q919C7 | human papil |
| Q919C9 | human papil |
| Q13167 | xiphias gla |
| Q9R7I3 | prochloroco |
| Q9S8G9 | psophocarpu |
| Q67964 | prochloroco |
| Q9X3M3 | prochloroco |
| Q67966 | prochloroco |
| Q9R4L9 | streptomyc  |
| Q9S8H0 | psophocarpu |
| Q91X54 | mus musculu |
| Q95M23 | sus scrofa  |
| Q62528 | mus spratus |
| Q9EZ14 | sodalis glo |
| Q9R735 | streptomyc  |
| Q9UCS8 | homo sapien |
| Q16605 | homo sapien |
| Q9FX10 | lilium long |
| P82429 | nicotiana t |
| Q8AYL5 | carassius a |
| Q8AUM7 | salmonella  |
| Q9XBH3 | bacillus ce |
| Q8SHA8 | rhampoleon  |
| Q9PRY8 | triakis scy |
| Q47606 | escherichia |
| Q47604 | escherichia |
| Q19718 | homo sapien |
| Q8RV30 | zea mays (m |
| Q8UUP1 | xenopus lae |
| Q9UC37 | homo sapien |
| Q8IVH0 | homo sapien |
| P92457 | ephedra sp. |
| P82328 | pisum sativ |
| Q88577 | theiler's e |
| Q88578 | theiler's e |
| Q88579 | theiler's e |
| Q88575 | theiler's e |
| Q88580 | theiler's e |
| Q88582 | theiler's e |
| Q88581 | theiler's e |
| Q88576 | theiler's e |
| Q88176 | mus musculu |
| Q8CJ33 | mus musculu |
| Q67604 | squash leaf |
| Q8JJ32 | ficedula al |
| Q55326 | synecococc  |
| Q43905 | azospirillu |
| P81715 | streptomyc  |
| P90342 | saccharomyc |
| Q8U1G2 | ashbya goss |
| Q9P2A2 | homo sapien |
| Q96Q50 | homo sapien |
| Q16045 | homo sapien |
| Q9Z1H4 | mus musculu |
| Q9R531 | thermus. ch |
| Q9UR63 | emericeia   |
| Q9URCS | saccharomyc |
| Q08947 | homo sapien |
| Q9UCV1 | homo sapien |
| Q26159 | plasmodium  |
| Q9TWQ2 | tachypleus  |
| Q9T2H9 | nicotiana s |
| Q9AT15 | lycopersico |
| Q9S8N8 | hordeum vul |
| Q9S8V2 | triticum ae |
| Q9S8V3 | triticum ae |

90 Q08936 nicotiana t  
 91 Q9quy3 rattus sp.  
 92 Q9r4l3 mycobacteri  
 93 Q9r596 micrococcus  
 94 Q9ur86 candida par  
 95 Q9uc65 homo sapien  
 96 Q9ud41 homo sapien  
 97 Q9twn7 toxoplasma  
 98 Q9tr97 oryctolagus  
 99 Q33429 anas platyr  
 100 Q9t2r0 solanum tub

## ALIGNMENTS

RESULT 1  
 Q9T2K8 PRELIMINARY; PRT; 15 AA.  
 AC Q9T2K8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE LHCII kinase, 64 kDa kinase (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92183823; PubMed=1544419;  
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;  
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with  
 the cytochrome complex.";  
 RL FEBS Lett. 298:33-35(1992).  
 FT NON\_TER 1  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 27.8%; Score 5; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVEK 8  
 Db 5 PDVEK 9

RESULT 2  
 Q9S618 PRELIMINARY; PRT; 11 AA.  
 AC Q9S618;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Cytochrome b6/f complex subunit IV (fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream.";  
 RL Limnol. Oceanog. 43:1615-1630(1998).  
 DR EMBL; AF070132; AAD20740.1; -.  
 FT NON\_TER 11  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 KPDL 11  
 Db 6 KPDL 9

RESULT 3  
 Q8HYM4 PRELIMINARY; PRT; 11 AA.  
 AC Q8HYM4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Coagulation factor IX (fragment).  
 GN F9.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;  
 RT "Characterization of 8 feline Type I Markers.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF459805; AAO15586.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 11  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1169 MW; 9C8E7EFCA05B02CA CRC64;

Query Match 22.2%; Score 4; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVE 7  
 Db 3 PDVE 6

RESULT 4  
 Q9R3R6 PRELIMINARY; PRT; 13 AA.  
 AC Q9R3R6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Cytochrome b6/f complex subunit IV (fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream.";  
 RL Limnol. Oceanog. 43:1615-1630(1998).  
 DR EMBL; AF070222; AAD23275.1; -.  
 DR EMBL; AF070221; AAD23273.1; -.  
 FT NON\_TER 13  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1522 MW; 4CDE4CC38013B763 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 6 KPDL 9

```

RESULT 5
Q66174
ID Q66174 PRELIMINARY; PRT; 15 AA.
AC Q66174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (Fragment).
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Sidell S.;
RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
RL Nucleic Acids Res. 17:6387-6387(1989).
DR EMBL; X15654; CAA33680.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 8 DVEK 11

RESULT 6
Q9LB06
ID Q9LB06 PRELIMINARY; PRT; 17 AA.
AC Q9LB06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]_
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RL sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070156; AAD23193.2; -.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1904 MW; CCEB69C5A202E54F CRC64;

Query Match 22.2%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 2 KPDL 5

RESULT 7
Q9TRW1
ID Q9TRW1 PRELIMINARY; PRT; 17 AA.
AC Q9TRW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CALDESMON-PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
RT by protein kinase C.";
RL Arch. Biochem. Biophys. 288:538-542(1991).
DR InterPro; IPR006018; Caldesmon_LSP.
DR Pfam; PF02029; Caldesmon; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1889 MW; 77EACD3EB02F95F6 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
Db 8 VEKP 11

RESULT 8
Q919B0
ID Q919B0 PRELIMINARY; PRT; 17 AA.
AC Q919B0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16GCC14;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404705; AAL01367.1; -.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1998 MW; 4471DB6BF776889B CRC64;

Query Match 22.2%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 9
Q9X3E9
ID Q9X3E9 PRELIMINARY; PRT; 18 AA.
AC Q9X3E9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b6/f complex subunit IV (fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.

```

```
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL: AF070147; AAD20766.1; -.
FT NON_TER 18
FT SEQUENCE 18 AA; 2029 MW; EBF8A4E54FDCDE56 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db [1]
6 KPDL 9

RESULT 10
O67971 PRELIMINARY; PRT; 18 AA.
ID O67971
AC O67971;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE B6/f complex subunit IV (Fragment).
GN PTD.
OS Synechococcus sp. (strain WH8103).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=29410;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WH8103;
RX MEDLINE=98123172; PubMed=9452521;
RT "Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
RT "Rapid diversification of marine picophytoplankton with dissimilar
RT light-harvesting structures inferred from sequences of Prochlorococcus
RT and Synechococcus (Cyanobacteria).";
RL J. Mol. Evol. 46:188-201(1998).
DR EMBL: AF001492; AAC05631.1; -.
FT NON_TER 18
FT SEQUENCE 18 AA; 2098 MW; C205CA0BB21CDE4C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db [1]
6 KPDL 9

RESULT 11
Q9R4E0 PRELIMINARY; PRT; 18 AA.
ID Q9R4E0
AC Q9R4E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dipeptidyl aminopeptidase type I (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=96200096; PubMed=8631703;
RA Ogasawara W., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
RA Morikawa Y.;
RT "A novel dipeptidyl aminopeptidase from Pseudomonas sp. strain WO24.";
RL J. Bacteriol. 178:1283-1288(1996).
```

```
SQ SEQUENCE 18 AA; 1813 MW; 369B0388C394A737 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPDV 6
Db [1]
5 PPDV 8

RESULT 12
P82674 PRELIMINARY; PRT; 18 AA.
ID P82674
AC P82674;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=LIVER;
RA Koc E.C.; Burkhardt W., Blackburn K., Moseley A., Koc H.,
RA Spremulli L.L.;
RT "Identification of four proteins from the small subunit of the
RT mammalian mitochondrial ribosome using a proteomics approach.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -|- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.
CC -|- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR000851; Ribosomal S5.
DR PROSITE: PS00585; RIBOSOMAL S5; PARTIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_CONS 8
FT UNSURE 17 17 OR I.
FT NON_TER 18
FT SEQUENCE 18 AA; 2127 MW; 199BC913E7E25FAF CRC64;

Query Match 22.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db [1]
15 PDLQ 18

RESULT 13
Q9S8G8 PRELIMINARY; PRT; 18 AA.
ID Q9S8G8
AC Q9S8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells.";
```



RL Plant Cell Physiol. 36:441-446(1995).  
SQ SEQUENCE 18 AA; 2252 MW; 4FD7D1DA18B5D94A CRC64;

Query Match 22.2%; Score 4; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9  
DB 11 VEKP 14  
|||||

RESULT 14  
Q919D5 PRELIMINARY; PRT; 18 AA.  
ID Q919D5  
AC Q919D5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404692; AAL01341.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 15  
Q919B3 PRELIMINARY; PRT; 18 AA.  
ID Q919B3  
AC Q919B3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404703; AAL01360.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 16  
Q919B5 PRELIMINARY; PRT; 18 AA.  
ID Q919B5  
AC Q919B5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC11;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404702; AAL01362.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 17  
Q919B7 PRELIMINARY; PRT; 18 AA.  
ID Q919B7  
AC Q919B7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC10;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404701; AAL01360.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 18  
Q919C5 PRELIMINARY; PRT; 18 AA.  
ID Q919C5  
AC Q919C5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404703; AAL01362.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 19  
Q919C5 PRELIMINARY; PRT; 18 AA.  
ID Q919C5  
AC Q919C5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404703; AAL01362.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 20  
Q919C5 PRELIMINARY; PRT; 18 AA.  
ID Q919C5  
AC Q919C5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404703; AAL01362.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 14 DLQP 17  
|||||

RESULT 21  
Q919C5 PRELIMINARY; PRT; 18 AA.  
ID Q919C5  
AC Q919C5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16E6CC12;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF404703; AAL01362.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches

```

ID Q919C5 PRELIMINARY; PRT; 18 AA.
AC Q919C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404697; AAL01352.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17

RESULT 19
Q919D1 ID Q919D1 PRELIMINARY; PRT; 18 AA.
AC Q919D1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404694; AAL01346.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17

RESULT 20
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.

```

```

OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17

RESULT 21
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC9;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON TER 18
FT SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 14 DLQP 17

RESULT 22
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC15;

```

```
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 23
Q919C7
ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC5;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404696; AAL01350.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 24
Q919C9
ID Q919C9 PRELIMINARY; PRT; 18 AA.
AC Q919C9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC4;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404695; AAL01348.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;
```

```
Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 14 DLQP 17

RESULT 25
O13167
ID O13167 PRELIMINARY; PRT; 18 AA.
AC O13167;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein S7 (Fragment).
OS Xiphias gladius (Swordfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Xiphiidae; Xiphias.
OX NCBI_TaxID=8245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Chow S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=J26B;
RA Chow S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95521; AAB58281.1; -.
DR EMBL; U89244; AAB58379.1; -.
DR EMBL; U95515; AAB58275.1; -.
DR EMBL; U95516; AAB58276.1; -.
DR EMBL; U95517; AAB58277.1; -.
DR EMBL; U95518; AAB58278.1; -.
DR EMBL; U95519; AAB58279.1; -.
DR EMBL; U95520; AAB58280.1; -.
KW Ribosomal protein.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1978 MW; E716F226CC5BBB15 CRC64;

Query Match 22.2%; Score 4; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKPD 10
Db 14 EKPD 17

RESULT 26
Q9R7I3
ID Q9R7I3 PRELIMINARY; PRT; 19 AA.
AC Q9R7I3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE B6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=12119;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MIT9107;
RX MEDLINE=98123172; PubMed=9452521;
RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
```

RT "Rapid diversification of marine picophytoplankton with dissimilar  
 RT light-harvesting structures inferred from sequences of Prochlorococcus  
 RL and Synchococcus (Cyanobacteria).";  
 RL J. Mol. Evol. 46:188-201(1998).  
 DR EMBL; AF001490; AAC05627.1; -.  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2113 MW; 1FEA1A34E54FDCDE CRC64;

Query Match 22.2%; Score 4; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 6 KPDL 9

## RESULT 27

Q9S8G9 ID Q9S8G9 PRELIMINARY; PRT; 19 AA.  
 AC Q9S8G9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS Psophocarpus tetragonolobus (Goa bean) (asparagus bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OC NCBI\_TaxID=3891;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=95277008; PubMed=7757337;  
 RA Esaka M., Hayakawa H.;  
 RT "Specific secretion of proline-rich proteins by salt-adapted winged  
 RT bean cells";  
 RL Plant Cell Physiol. 36:441-446(1995).  
 SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 22.2%; Score 4; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VKXP 9  
 Db 7 VKXP 10

## RESULT 28

O67964 ID O67964 PRELIMINARY; PRT; 20 AA.  
 AC O67964;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE B6/f complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus sp. (strain CCMP 1378 / MED4).  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OC NCBI\_TaxID=59919;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CCMP1378;  
 RX MEDLINE=98123172; PubMed=9452521;  
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;  
 RT "Rapid diversification of marine picophytoplankton with dissimilar  
 RT light-harvesting structures inferred from sequences of Prochlorococcus  
 RL and Synchococcus (Cyanobacteria).";  
 RL J. Mol. Evol. 46:188-201(1998).  
 DR EMBL; AF001488; AAC05623.1; -.  
 FT NON\_TER 20

SQ SEQUENCE 20 AA; 2241 MW; C46FEA1A34E54FDC CRC64;  
 Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 6 KPDL 9

## RESULT 29

O9X3M3 ID O9X3M3 PRELIMINARY; PRT; 20 AA.  
 AC O9X3M3;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE Cytochrome b6/f complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OC NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream";  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070219; AAC03270.1; -.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2264 MW; C46FEA1A23D55F9C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 6 KPDL 9

## RESULT 30

O67966 ID O67966 PRELIMINARY; PRT; 20 AA.  
 AC O67966;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE B6/f complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus marinus.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OC NCBI\_TaxID=1219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NATL2;  
 RX MEDLINE=98123172; PubMed=9452521;  
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;  
 RT "Rapid diversification of marine picophytoplankton with dissimilar  
 RT light-harvesting structures inferred from sequences of Prochlorococcus  
 RL and Synchococcus (Cyanobacteria).";  
 RL J. Mol. Evol. 46:188-201(1998).  
 DR EMBL; AF001489; AAC05625.1; -.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2259 MW; C17BECCE134E54FDC CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 6 KPDL 9

```

QY 8 KPDL 11
DB ||||
 6 KPDL 9

RESULT 31
Q9R4L9
ID Q9R4L9 PRELIMINARY; PRT; 20 AA.
AC Q9R4L9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE P6 protein (Fragment).
OS Streptomyces tendae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1932;
RN [1]
RP SEQUENCE.
RA MEDLINE=95302967; PubMed=7783626;
RX Mohrle V., Roos U., Bormann C.;
RT "Identification of cellular proteins involved in nikkomycin production
RT in Streptomyces tendae Tu901.";
RL Mol. Microbiol. 15:561-571 (1995).
SQ SEQUENCE 20 AA; 2229 MW; D3E7BD4689D594FD CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPFQ 15
DB ||||
 13 QPFQ 16

RESULT 32
Q9S8H0
ID Q9S8H0 PRELIMINARY; PRT; 20 AA.
AC Q9S8H0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpaceae.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells.";
RL Plant Cell Physiol. 36:441-446 (1995).
SQ SEQUENCE 20 AA; 2246 MW; AEE9ED45C4F0F877 CRC64;

Query Match 22.2%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
DB ||||
 7 VEKP 10

RESULT 33
Q91X54
ID Q91X54 PRELIMINARY; PRT; 20 AA.
AC Q91X54;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

QY 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Unknown (Protein for IMAGE:4195625) (Fragment).
CN 1700020C11RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012242; AAH12242.1; -
DR MGD; MGI:1916686; 1700020C11RIK.
FT NON TER 1
SQ SEQUENCE 20 AA; 2278 MW; 4A7143DBC4DF384C CRC64;

Query Match 22.2%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
DB ||||
 14 VEKP 17

RESULT 34
Q95M23
ID Q95M23 PRELIMINARY; PRT; 8 AA.
AC Q95M23;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pietrain;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -.
KW Hydrolase.
FT NON TER 1
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
DB ||||
 2 VEK 4

RESULT 35
Q62528
ID Q62528 PRELIMINARY; PRT; 8 AA.
AC Q62528;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE Apolipoprotein A-II (APO-AII) (Fragment).
GN APOA2.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA KO M.S., Wang X., Horton J.H., Takahashi N., Maezaki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
RL Mamm. Genome 5:349-355(1994).
CC -1- FUNCTION: MAY STABILIZE HDL (HIGH DENSITY LIPOPROTEIN) STRUCTURE
CC BY ITS ASSOCIATION WITH LIPIDS, AND AFFECT THE HDL METABOLISM.
DR EMBL; U05692; AAB60463.1; -.
DR MGD; MGI:88050; APOA2.
KW Plasma; Lipid transport; HDL.
FT NON_TER 1
SQ SEQUENCE 8 AA; 827 MW; 223DDDD72DC7633B CRC64;

Query Match 16.7%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 1 EXP 3

RESULT 36
ID Q9EZ14 PRELIMINARY; PRT; 9 AA.
AC Q9EZ14;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Spas (Fragment).
GN SPAS.
OS Sodalis glossinidius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=21117132; PubMed=11172045;
RA Dale C., Young S.A., Haydon D.T., Welburn S.C.;
RT "The insect endosymbiont Sodalis glossinidius utilizes a type III
RT secretion system for cell invasion.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1883-1888(2001).
DR EMBL; AF306650; AAG48607.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1035 MW; 818E633B01A33455 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 6 EXP 8

RESULT 37
ID Q9R735 PRELIMINARY; PRT; 9 AA.
AC Q9R735;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FkA protein (Fragment).
GN FkA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FKBP-binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene.";
RL EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84282.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db 4 EXP 6

RESULT 38
ID Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=32075698; PubMed=1742316;
RA Einholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Blochim. Biophys. Acta 1086:255-260(1991).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPD 5
Db 7 PPD 9

RESULT 39
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes

```

RT products of different but overlapping substrate specificities.";  
 RL J. Biol. Chem. 263:12797-12800(1988).  
 DR EMBL; M21867; AAA52617.1; -;  
 DR EMBL; M21866; AAA35938.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;  
 Query Match 16.7%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 EXP 9  
 Db ||||  
 3 EXP 5  
 RESULT 40  
 Q9FXL0 PRELIMINARY; PRT; 9 AA.  
 AC Q9FXL0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE LIM8 protein (Fragment).  
 GN LIM8.  
 OS Lilium longiflorum (Trumpet lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
 OX NCBI\_TaxID=4690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Hinomoto;  
 RA Uesuji H., Takase H., Hiratsuka K.;  
 RT "Lilium longiflorum LIM8 gene, promoter region and partial sequence.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050987; BAB17856.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;  
 Query Match 16.7%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 VQS 18  
 Db ||||  
 3 VQS 5  
 RESULT 41  
 P82429 PRELIMINARY; PRT; 9 AA.  
 AC P82429;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 44 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 9

SQ SEQUENCE 9 AA; 986 MW; C22CCADGCG77776 CRC64;  
 Query Match 16.7%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QPP 4  
 Db ||||  
 2 QPP 4  
 RESULT 42  
 Q8AYL5 PRELIMINARY; PRT; 9 AA.  
 AC Q8AYL5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome P450 aromatase (Fragment).  
 GN CYP19A.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
 RT "Promoter characteristics of two CYP19 genes differentially expressed  
 RT in the brain and ovary of teleost fish.";  
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
 DR EMBL; AF324897; AAN32618.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;  
 Query Match 16.7%; Score 3; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 LQP 13  
 Db ||||  
 6 LQP 8  
 RESULT 43  
 Q8AUM7 PRELIMINARY; PRT; 9 AA.  
 AC Q8AUM7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome P450 aromatase (Fragment).  
 GN CYP19A.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
 RT "Promoter characteristics of two CYP19 genes differentially expressed  
 RT in the brain and ovary of teleost fish.";  
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
 DR EMBL; AF324895; AAN32616.1; -;  
 DR EMBL; AF324896; AAN32617.1; -;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;  
 Query Match 16.7%; Score 3; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 11 LQP 13 Best Local Similarity 100.0%; Pred.No. 8.5e+03; Gaps 0;
Db 6 LQP 8 Matches 3; Conservative 0; Mismatches 0; Indels 0;
 |||
 6 VEK 8
 ||||
 8 VEK 10

RESULT 44
Q935G1 PRELIMINARY; PRT; 9 AA.
ID Q935G1 AC Q935G1 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Putative membrane protein (Fragment).
GN HCM1.OIC. OS Salmonella typhi.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella. NCBI_TaxID=601;
OX [1] RN SEQUENCE FROM N.A.
RP STRAIN=CT18; RC MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mangall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K.P., Chillingworth T., Connorson F., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whithead S., Barrrell B.G.; RA "Complete genome sequence of a multiple drug resistant Salmonella RT enterica serovar Typhimurium CT18."; RL Nature 413:848-852(2001); DR EMBL: AL513383; CAD09867.1; - KW Plasmid; Complete proteome. FT NON_TER 3 9 SQ SEQUENCE 9 AA; 904 MW; 5FDCD77776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db 5 QPP 7
 |||
 2 QPP 4
 ||||
 5 QPP 7

RESULT 45
Q9XBH3 PRELIMINARY; PRT; 10 AA.
ID Q9XBH3 AC Q9XBH3 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE Cell-like protein (fragment). GN CELF. OG Bacillus cereus. OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1396;
RN [1] RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987; RX MEDLINE=99231848; PubMed=10217496; RA Ostad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.; RT "Genome organisation is not conserved between Bacillus cereus and Bacillus subtilis." Microbiology 145:621-631(1999).
RL EMBL: AJ000394; CAB40625.1; - FT NON_TER 1 1 SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;

```



```

RESULT 48
Q47606
ID Q47606 PRELIMINARY; PRT; 11 AA.
AC Q47606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63622; AAA24562.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
Db 3 VEK 5

RESULT 49
Q47604
ID Q47604 PRELIMINARY; PRT; 11 AA.
AC Q47604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Rease protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63621; AAA24560.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
Db 4 PDL 6

RESULT 50
O19718
ID O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

```

---

```

DE MHC class II antigen (Fragment).
CN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merzlyan P., Degar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzler J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).
DR EMBL; M15074; AAA59810.1; -.
FT NON TER 1
SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B76D7 CRC64;

Query Match 16.7%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LQP 13
Db 4 LQP 6

RESULT 51
Q8RV30
ID Q8RV30 PRELIMINARY; PRT; 11 AA.
AC Q8RV30;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Methionine adenosyltransferase 1-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "GNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486085; AAL85893.1; -.
DR EMBL; AF486086; AAL85894.1; -.
DR EMBL; AF486087; AAL85895.1; -.
DR EMBL; AF486088; AAL85896.1; -.
DR EMBL; AF486089; AAL85897.1; -.
DR EMBL; AF486090; AAL85898.1; -.
DR EMBL; AF486091; AAL85899.1; -.
DR EMBL; AF486092; AAL85900.1; -.
DR EMBL; AF486093; AAL85901.1; -.
DR EMBL; AF486094; AAL85902.1; -.
DR EMBL; AF486095; AAL85903.1; -.
DR EMBL; AF486096; AAL85904.1; -.
DR EMBL; AF486097; AAL85905.1; -.
DR EMBL; AF486098; AAL85906.1; -.
DR EMBL; AF486099; AAL85907.1; -.
DR EMBL; AF486100; AAL85908.1; -.
DR EMBL; AF486101; AAL85909.1; -.
DR EMBL; AF486102; AAL85910.1; -.
DR EMBL; AF486104; AAL85911.1; -.
DR EMBL; AF486105; AAL85912.1; -.
DR EMBL; AF486106; AAL85913.1; -.
DR EMBL; AF486107; AAL85914.1; -.
DR EMBL; AF486108; AAL85915.1; -.
DR EMBL; AF486109; AAL85916.1; -.
DR EMBL; AF486110; AAL85917.1; -.

```

```

DR EMBL; AF486111; AAL85918.1; -.
DR EMBL; AF486112; AAL85919.1; -.
DR EMBL; AF486113; AAL85920.1; -.
DR EMBL; AF486114; AAL85921.1; -.
DR EMBL; AF486115; AAL85922.1; -.
DR EMBL; AF486116; AAL85923.1; -.
DR EMBL; AF486117; AAL85924.1; -.
DR EMBL; AF486118; AAL85925.1; -.
KW Transferase. 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1183 MW; 448D42ED3B05B337 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db |||
7 EXP 9

RESULT 52
Q8UUP1 PRELIMINARY; PRT; 11 AA.
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis";
RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
Db |||
9 QPP 11

RESULT 53
Q9UC37 PRELIMINARY; PRT; 12 AA.
AC Q9UC37;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Alpha B crystallin fragment 5 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

```

```

RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1268 MW; D37BD529CCCB1B2CD CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
Db |||
2 EXP 4

RESULT 54
Q8IVH0 PRELIMINARY; PRT; 12 AA.
AC Q8IVH0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Truncated PAX6 protein (Fragment).
GN PAX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Neethirajan G., Krishnadas S.R., Vijayalakshmi P., Sundaresan P.;
RT "Mutation analysis in Human PAX6 gene of Aniridia.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548390; AAN86817.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1511 MW; 9E169541A67B51F1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
Db |||
8 PDV 10

RESULT 55
P92457 PRELIMINARY; PRT; 12 AA.
AC P92457;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chloroplast subunit of light-independent protochlorophyllide reductase (Fragment).
GN CHLB GENE.
OS Euphorbia sp.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnetales; Gnecopsida; Ephedrales; Ephedraceae;
OC Ephedra.
OX NCBI_TaxID=41991;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263785; PubMed=9108142;
RA Karpinska B., Karpinski S., Hallgren J.E.;
RT "The chlB gene encoding a subunit of light-independent protochlorophyllide reductase is edited in chloroplast of conifers.";
RL Curr. Genet. 31:343-347(1997).
DR EMBL; X98573; CAA67182.1; -.

```

KW Chloroplast. 1 1  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1441 MW; 164C1B7CC2276724 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 DLQ 12  
DB 2 DLQ 4  
RESULT 56  
P82328 PRELIMINARY; PRT; 12 AA.  
AC P82328;  
DT 01-JUN-2000 (TREMELrel. 14, Created)  
DT 01-JUN-2000 (TREMELrel. 14, Last sequence update)  
DT 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
targeting analysis of luminal and peripheral thylakoid proteins.";  
RL Plant Cell 12:319-341(2000).  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
KW Chloroplast; Thylakoid membrane.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1264 MW; 96691CBG663B1B01 CRC64;  
Query Match 16.7%; Score 3; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 EXP 9  
DB 7 EXP 9  
RESULT 57  
Q88577 PRELIMINARY; PRT; 12 AA.  
AC Q88577;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TO(4);  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80887; AAA73158.1; -.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80885; AAA73156.1; -.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
Query Match 16.7%; Score 3; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PDV 6  
DB 8 PDV 10  
RESULT 58  
Q88578 PRELIMINARY; PRT; 12 AA.  
AC Q88578;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TO(B15);  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80886; AAA73157.1; -.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
Query Match 16.7%; Score 3; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PDV 6  
DB 8 PDV 10  
RESULT 59  
Q88579 PRELIMINARY; PRT; 12 AA.  
AC Q88579;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds  
(Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VL;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80887; AAA73158.1; -.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

```

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 60
Q88575 PRELIMINARY; PRT; 12 AA.
AC Q88575;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80883; AAA73154.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 61
Q88580 PRELIMINARY; PRT; 12 AA.
AC Q8580;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vilyuisk;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80888; AAA73159.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDV 6

```

```

DB 8 PDV 10

RESULT 62
Q88582 PRELIMINARY; PRT; 12 AA.
AC Q8582;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO(Vale);
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80890; AAA73161.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 63
Q88581 PRELIMINARY; PRT; 12 AA.
AC Q8581;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WW;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80889; AAA73160.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 64

```

```

Q88576
ID Q88576 PRELIMINARY; PRT; 12 AA.
AC Q88576;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHG;
RX MEDLINE=32194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80884; AAA73155.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6
DB 8 PDV 10

RESULT 65
ID Q88176 PRELIMINARY; PRT; 13 AA.
AC Q88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-C; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RT of a muscle-specific exon in the mouse NCAM gene."
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13
DB 7 LQP 9

RESULT 66
ID Q8CJ33 PRELIMINARY; PRT; 13 AA.
AC Q8CJ33;

```

```

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myoneurin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-C; TISSUE=Kidney;
RX MEDLINE=20334280; PubMed=10873615;
RA Alliel P.M., Seddigi N., Goudou D., Cifuentes-Diaz C., Romero N.,
RA Velasco E., Rieger F., Perin J.P.;
RT "Myoneurin, a novel member of the BTR/POZ-zinc finger family highly
RT expressed in human muscle."
RL Biochem. Biophys. Res. Commun. 273:385-391(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-C; TISSUE=Kidney;
RA Bitoun M., Perin J.P., Seddigi N., Goudou D., Camuzat A., Mattei M.G.,
RA Rieger F., Alliel P.M.;
RT "The human and mouse myoneurin genes: Genomic organization, splice
RT variants, chromosomal mapping and flanking genes."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530454; AAN28707.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1445 MW; 9CB68B708CA1597E CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
DB 1 EXP 3

RESULT 67
ID Q67604 PRELIMINARY; PRT; 13 AA.
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BCL1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;
RT "Diversity among geminiviruses associated with vegetables from Valle
RT del Fuerte, Sinaloa, Mexico."
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L27273; AAA47820.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPP 4
DB 7 QPP 9

RESULT 68

```

Q8JUJ32  
ID Q8JUJ32 PRELIMINARY; PRT; 13 AA.  
AC Q8JUJ32;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 37LRP/d40 (Fragment).  
OS Ficedula albicollis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OX NCBI\_TaxID=59894;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=B8;  
RX MEDLINE=21918460; PubMed=11918793;  
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;  
RT "Single-nucleotide polymorphism characterization in species with  
RT limited available sequence information: high nucleotide diversity  
RT revealed in the avian genome";  
RL Mol. Ecol. 11:603-612(2002).  
DR EMBL; AF454232; AAM22911.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;  
  
Query Match 16.7%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 PDL 11  
Db 3 PDL 5  
  
RESULT 69  
Q55326 PRELIMINARY; PRT; 14 AA.  
ID Q55326;  
AC Q55326;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Putative ORF1 (Fragment)  
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32049;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=PR6;  
RX MEDLINE=92201692; PubMed=1551590;  
RA Rhie E., Stireswalt V.L., Gasparich G.E., Bryant D.A.;  
RT "The psac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa:  
RT cloning and sequence analysis";  
RL Gene 112:123-128(1992).  
DR EMBL; M86238; AAA27351.1; -.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 LQP 13  
Db 12 LQP 14  
  
RESULT 70  
Q43905 PRELIMINARY; PRT; 14 AA.  
ID Q43905;  
AC Q43905;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Dinitrogenase reductase (Fragment).  
OS Azospirillum brasilense.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Rhodospirillaceae; Azospirillum.  
OX NCBI\_TaxID=192;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sp7;  
RX MEDLINE=92250433; PubMed=1577701;  
RA Zhang Y., Burris R.H., Roberts G.P.;  
RT "Cloning, sequencing, mutagenesis, and functional characterization of  
RT drat and drag genes from Azospirillum brasilense.";  
RL J. Bacteriol. 174:3364-3369(1992).  
DR EMBL; M87319; AAA22182.1; -.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1485 MW; DOF9B16263390219 CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 EXP 9  
Db 8 EXP 10  
  
RESULT 71  
P81715 PRELIMINARY; PRT; 14 AA.  
ID P81715;  
AC P81715;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).  
OS Streptomyces exfoliatus (Streptomyces hydrogenans).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1905;  
RN [1]  
RC SEQUENCE.  
RX STRAIN=SMF13;  
RX PubMed=9531495;  
RA Kim I.S., Kim Y.B., Lee K.J.;  
RT "Characterization of the leupeptin-inactivating enzyme from  
RT Streptomyces exfoliatus SMF13 which produces leupeptin.";  
RL Biochem. J. 331:539-545(1998).  
CC -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN  
CC OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.  
CC -!- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-  
CC LEUCINE, LEUCINE AND ARGININAL.  
CC -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1  
CC SITE.  
CC -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE  
CC INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
KW Hydrolase; Metalloprotease.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PPD 5  
Db 4 PPD 6  
  
RESULT 72  
P90342 PRELIMINARY; PRT; 14 AA.  
ID P90342

AC P90342;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE ORF YER030C (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP  
 RP SEQUENCE FROM N.A.  
 RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN  
 RN SEQUENCE FROM N.A.  
 RA MIPS;  
 RP  
 RP Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=95112789; PubMed=7813418;  
 RA Feldmann H., Aigle M., Aljinovic G., Andre B., Baclet M.C., Barthe C.,  
 RA Baur A., Becam A.M., Biteau N., Boles E., Brandt T., Brendel M.,  
 RA Brueckner M., Bussereau F., Christiansen C., Contreras R., Crouzet M.,  
 RA Cziepluch C., Demolis N., Delaveau T., Doignon F., Domdey H.,  
 RA Duesternus S., Dubois E., Dujon B., El Bakkoury M., Entian K.D.,  
 RA Feuerhann M., Fiers W., Fobo G.M., Fritz C., Gassenhuber H.,  
 RA Glansdorff N., Goffeau A., Grivell L.A., De haan M., Hein C.,  
 RA Herbert C.J., Hollenberg C.P., Holmstrom K., Jacq C., Jacquet M.,  
 RA Jauniaux J.C., Jonniaux J.L., Kallioe T., Kiesau P., Kirchrath L.,  
 RA Koetter P., Korol S., Liebl S., Loghe M., Lohan A.J.E., Louis E.J.,  
 RA Li Z.Y., Maat M.J., Mallet L., Mannhaupt G., Messenguy F., Miosga T.,  
 RA Molenans F., Mueller S., Nasr F., Obermaier B., Perea J., Pierard A.,  
 RA Piravandi E., Pohl F.M., Pohl T.M., Potier S., Proft M., Farnelle B.,  
 RA Ramezani Rad M., Rieger M., Rose M., Schaaff-Gerstenschlaeger I.,  
 RA Scherens B., Schwarzlose C., Skala J., Slonimski P.P., Smits P.H.M.,  
 RA Souciet J.L., Steensma H.Y., Stucka R., Urestarazu A.,  
 RA Van der Aart Q.J., Van Dyck L., Vassarotti A., Vetter I.,  
 RA Vierendeels F., Vissers S., Wagner G., de Wergifosse P., Wolfe K.H.,  
 RA Zagulski M., Zimmermann F.K., Mewes H.W., Kleine K.;  
 RT "Complete DNA sequence of yeast chromosome II.";  
 RL EMBO J. 13:5795-5809(1994).  
 DR EMBL; Z35957; CAA85041.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1657 MW; C6B3A4A2E8485212 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDV 6  
 Db 12 PDV 14

RESULT 73  
 Q8J1G2  
 ID Q8J1G2 PRELIMINARY; PRT; 14 AA.  
 AC Q8J1G2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE YPL156 (Fragment).  
 DE YPL156  
 GN YPL156  
 OS Ashbya gossypii (Eremothecium gossypii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Ashbya.  
 OX NCBI\_TaxID=33169;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP  
 RP Alberti-Segui C., Dietrich F., Philippsen P.;  
 RT "Identification of kinesin-related proteins in the filamentous fungus  
 Ashbya gossypii.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF378570; AAN87139.1; -.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1646 MW; 8C3A12EB808B1D15 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 VQS 18  
 Db 5 VQS 7

RESULT 74  
 Q9P2A2  
 ID Q9P2A2 PRELIMINARY; PRT; 14 AA.  
 AC Q9P2A2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Truncated aldo-keto reductase (fragment).  
 GN TRUNCATED AKR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP  
 RP TISSUE=Liver;  
 RX MEDLINE=20138537; PubMed=10672042;  
 RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,  
 RA Watanabe K., Ito S.;  
 RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with  
 three aldo-keto reductase genes.";  
 RL Genes Cells 5:111-125(2000).  
 DR EMBL; AB037903; BAA92888.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQP 13  
 Db 7 LQP 9

RESULT 75  
 Q96Q50  
 ID Q96Q50 PRELIMINARY; PRT; 14 AA.  
 AC Q96Q50;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Mitochondrial ribosomal protein L33 (fragment).  
 GN MRPL33.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP  
 RP MEDLINE=21429115; PubMed=11543634;  
 RX Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,  
 RA Watanabe K., Tanaka T.;  
 RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes  
 to the chromosomes and implications for human disorders.";  
 RL Genomics 77:65-70(2001).  
 DR EMBL; AB051623; BAB54951.1; -.  
 KW Ribosomal protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1744 MW; 64ED243E9AED663B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEX 8  
Db 6 VEX 8

Search completed: November 25, 2003, 18:25:14  
Job time : 46.4223 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 58.3085 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18

Sequence: 1 DQPPDVKPKDLQPFQVQS 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

A Geneseq\_19Jun03.\*

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 18    | 100.0       | 18     | 22    | Colostrinin derive |
| 2          | 18    | 100.0       | 18     | 22    | Colostrinin peptid |
| 3          | 18    | 100.0       | 18     | 22    | Colostrinin peptid |
| 4          | 18    | 100.0       | 18     | 22    | Ewe colostrinin pe |
| 5          | 18    | 100.0       | 18     | 23    | Colostrinin consti |
| 6          | 18    | 100.0       | 18     | 23    | Colostrinin consti |
| 7          | 18    | 100.0       | 18     | 23    | Neural cell regula |
| 8          | 18    | 100.0       | 19     | 22    | Ewe colostrinin pe |
| 9          | 5     | 27.8        | 8      | 23    | Human papillomavir |

|    |   |      |    |    |           |                    |
|----|---|------|----|----|-----------|--------------------|
| 10 | 5 | 27.8 | 10 | 22 | AAG96833  | Human complementar |
| 11 | 5 | 27.8 | 15 | 6  | AAp50841  | Sequence of colony |
| 12 | 5 | 27.8 | 15 | 9  | AAp82092  | HRV2-derived pepti |
| 13 | 5 | 27.8 | 15 | 19 | AAW75695  | M. tuberculosis 32 |
| 14 | 5 | 27.8 | 15 | 19 | AAW75696  | M. tuberculosis 32 |
| 15 | 5 | 27.8 | 15 | 23 | ABG67986  | Human ADPI tryptic |
| 16 | 5 | 27.8 | 15 | 23 | AAW47777  | Short chain dehydr |
| 17 | 5 | 27.8 | 19 | 23 | ABG60992  | Dirofilaria immiti |
| 18 | 5 | 27.8 | 19 | 23 | AAW66103  | D. immitis transgl |
| 19 | 5 | 27.8 | 20 | 12 | AAAR11303 | Recombinant 275-29 |
| 20 | 5 | 27.8 | 20 | 12 | AAAR11404 | Human rhinovirus T |
| 21 | 4 | 22.2 | 4  | 22 | AAAS5927  | Human leptin fragm |
| 22 | 4 | 22.2 | 5  | 19 | AAW45571  | Amino-terminal pro |
| 23 | 4 | 22.2 | 6  | 13 | ABO80941  | Peptide #4 used in |
| 24 | 4 | 22.2 | 6  | 15 | AAAS5954  | Peptide signal seq |
| 25 | 4 | 22.2 | 6  | 22 | AAAG63056 | Amino acid sequenc |
| 26 | 4 | 22.2 | 6  | 23 | AAAG6432  | Vector encoded pep |
| 27 | 4 | 22.2 | 6  | 24 | ABUS6263  | Peptide binding to |
| 28 | 4 | 22.2 | 7  | 14 | AAAR33159 | HPV E7 protein - R |
| 29 | 4 | 22.2 | 7  | 22 | AAW44291  | H11 binding site c |
| 30 | 4 | 22.2 | 8  | 12 | AAAR10631 | Human Papilloma Vi |
| 31 | 4 | 22.2 | 8  | 14 | AAAR33158 | HPV E7 protein - R |
| 32 | 4 | 22.2 | 8  | 15 | AAAR6821  | Phytase derived pe |
| 33 | 4 | 22.2 | 8  | 15 | ABG70878  | R. rhodochrous nit |
| 34 | 4 | 22.2 | 9  | 12 | AAAR10635 | Human Papilloma Vi |
| 35 | 4 | 22.2 | 9  | 14 | AAAR33157 | HPV E7 protein - R |
| 36 | 4 | 22.2 | 9  | 14 | AAAR33170 | HPV E7 protein - R |
| 37 | 4 | 22.2 | 9  | 14 | AAAR43741 | MHC Class I allele |
| 38 | 4 | 22.2 | 9  | 14 | AAAR43742 | MHC Class I allele |
| 39 | 4 | 22.2 | 9  | 15 | AAAS9257  | Peptide fragment ( |
| 40 | 4 | 22.2 | 9  | 15 | AAAR61700 | HLA-A2.1 algorithm |
| 41 | 4 | 22.2 | 9  | 15 | AAAR73799 | Antigen fragment 1 |
| 42 | 4 | 22.2 | 9  | 15 | AAAR73800 | Antigen fragment 1 |
| 43 | 4 | 22.2 | 9  | 15 | AAAR73796 | Antigen fragment 1 |
| 44 | 4 | 22.2 | 9  | 16 | AAAR80939 | Peptide for increa |
| 45 | 4 | 22.2 | 9  | 16 | AAAR78899 | HPV16 E7 11-19 cyt |
| 46 | 4 | 22.2 | 9  | 16 | AAAR78894 | HPV16 E7 12-20 cyt |
| 47 | 4 | 22.2 | 9  | 18 | AAW39661  | HPV16/18 E7 peptid |
| 48 | 4 | 22.2 | 9  | 18 | AAW39662  | HPV16/18 E7 peptid |
| 49 | 4 | 22.2 | 9  | 18 | AAW36590  | Hepatitis B virus  |
| 50 | 4 | 22.2 | 9  | 19 | AAW78893  | Human papillomavir |
| 51 | 4 | 22.2 | 9  | 19 | AAW54766  | Peptide from HPV 1 |
| 52 | 4 | 22.2 | 9  | 19 | AAW54767  | Peptide from HPV 1 |
| 53 | 4 | 22.2 | 9  | 20 | AAW48125  | Immunogenic peptid |
| 54 | 4 | 22.2 | 9  | 20 | AAW48135  | Immunogenic peptid |
| 55 | 4 | 22.2 | 9  | 20 | AAW30325  | Potential T cell e |
| 56 | 4 | 22.2 | 9  | 20 | AAW28526  | Beta-1 integrin ce |
| 57 | 4 | 22.2 | 9  | 20 | AAW10346  | T cell epitope/MHC |
| 58 | 4 | 22.2 | 9  | 20 | AAW10511  | HLA Class I motif  |
| 59 | 4 | 22.2 | 9  | 21 | AAAB19059 | Amino acid sequenc |
| 60 | 4 | 22.2 | 9  | 21 | AAAB33705 | MHC class I associ |
| 61 | 4 | 22.2 | 9  | 21 | AAW96374  | HLA-A2 binding pep |
| 62 | 4 | 22.2 | 9  | 21 | AAW86644  | Telomerase peptide |
| 63 | 4 | 22.2 | 9  | 21 | AAW86658  | Telomerase peptide |
| 64 | 4 | 22.2 | 9  | 22 | AAAG93801 | Human papilloma vi |
| 65 | 4 | 22.2 | 9  | 22 | AAAG88547 | HER2/NEU DR superm |
| 66 | 4 | 22.2 | 9  | 22 | AAAG88711 | HER2/NEU DR 3a mot |
| 67 | 4 | 22.2 | 9  | 22 | AAAG88865 | HER2/neu epitope B |
| 68 | 4 | 22.2 | 9  | 22 | AAAB95951 | MHC class-I associ |
| 69 | 4 | 22.2 | 9  | 22 | AAAB95999 | HPV 16 E7 A2 MHC-b |
| 70 | 4 | 22.2 | 9  | 22 | AAAB96001 | HPV 16 E7 A2 MHC-b |
| 71 | 4 | 22.2 | 9  | 22 | AAJ03011  | Hepatitis C virus  |
| 72 | 4 | 22.2 | 9  | 22 | AAAB20215 | HPV strain 16 E7 p |
| 73 | 4 | 22.2 | 9  | 22 | AAAB71116 | Polylinker site fr |
| 74 | 4 | 22.2 | 9  | 22 | AAAB76118 | Tumour associated  |
| 75 | 4 | 22.2 | 9  | 23 | ABG80028  | MHC class I molecu |
| 76 | 4 | 22.2 | 9  | 23 | ABG80194  | MHC class I molecu |
| 77 | 4 | 22.2 | 9  | 23 | ABG69555  | Human CEPI tryptic |
| 78 | 4 | 22.2 | 9  | 23 | AAW49925  | Human D40 associat |
| 79 | 4 | 22.2 | 9  | 23 | AAW49948  | Human D40 associat |
| 80 | 4 | 22.2 | 9  | 23 | AAU82122  | Human papillomavir |
| 81 | 4 | 22.2 | 9  | 23 | AAU82137  | Human papillomavir |
| 82 | 4 | 22.2 | 9  | 23 | AAU82236  | Human papillomavir |

83 4 22.2 9 23 AAU82237 Human papillomavir  
 84 4 22.2 9 23 AAU82288 Human papillomavir  
 85 4 22.2 9 23 AAU82289 Human papillomavir  
 86 4 22.2 9 23 AAU82344 Human papillomavir  
 87 4 22.2 9 23 AAU82344 f8 phage-displayed  
 88 4 22.2 9 24 AAE13683 Human cancer-relat  
 89 4 22.2 9 24 ABR04681 Human cancer-relat  
 90 4 22.2 9 24 ABR05301 Human cancer-relat  
 91 4 22.2 9 24 ABR05467 Human cancer-relat  
 92 4 22.2 9 24 ABR05481 Human cancer-relat  
 93 4 22.2 9 24 ABR20198 Human cancer-relat  
 94 4 22.2 9 24 ABR20227 Human cancer-relat  
 95 4 22.2 9 24 ABR20449 Human cancer-relat  
 96 4 22.2 9 24 ABR20594 Human cancer-relat  
 97 4 22.2 9 24 ABR20830 Human cancer-relat  
 98 4 22.2 9 24 ABR20995 Human cancer-relat  
 99 4 22.2 9 24 ABR21239 Human cancer-relat  
 100 4 22.2 9 24 ABR21594 Human cancer-relat  
 100 4 22.2 9 24 ABR21619 Human cancer-relat

## ALIGNMENTS

RESULT 1  
 AAB72248  
 ID AAB72248 standard; peptide; 18 AA.  
 AC  
 AC AAB72248;  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostromin derived cytokine inducing peptide SEQ ID 3.  
 XX  
 KW Colostromin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 DR  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostromin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostromin,  
 CC a proline rich polypeptide aggregate contained in colostrom. The  
 CC peptides have immune response/modulatory activity, and are capable of  
 CC inducing cytokines. Colostromin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DQPPDVEKPDLPQFQVQS 18  
 Db 1 DQPPDVEKPDLPQFQVQS 18  
 RESULT 2  
 AAB72502  
 ID AAB72502 standard; Peptide; 18 AA.  
 XX  
 AC AAB72502;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostromin peptide #3.  
 XX  
 KW Dermatological; oxidative stress regulator; colostromin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 DR  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostromin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostromin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DQPPDVEKPDLPQFQVQS 18  
 Db 1 DQPPDVEKPDLPQFQVQS 18  
 RESULT 3  
 AAB72534  
 ID AAB72534 standard; Peptide; 18 AA.  
 XX  
 AC AAB72534;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #3.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX Sequence 18 AA;  
 SQ

Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. NO. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DQPPDVERPDLPQFQVQS 18  
 |||||  
 DB 1 DQPPDVERPDLPQFQVQS 18  
 |||||

RESULT 4  
 AAB59325  
 ID AAB59325 standard; Peptide; 18 AA.  
 XX  
 AC AAB59325;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment B-10.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 XX WO200075173-A2.  
 PN  
 PD 14-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 XX Claim 7; Page 27; 63pp; English.  
 PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 18 AA;  
 SQ

Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. NO. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DQPPDVERPDLPQFQVQS 18  
 |||||  
 DB 1 DQPPDVERPDLPQFQVQS 18  
 |||||

RESULT 5  
 AAE20230  
 ID AAE20230 standard; peptide; 18 AA.  
 XX  
 AC AAE20230;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 XX Colostrinin constituent peptide #3.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH 18  
 FT Modified-site /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18  
 Db 1 DQPPDVEKPDLPQFQVQS 18

# RESULT 6

AA051038  
 ID AA051038 standard; Peptide; 18 AA.

AC AA051038;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10. It was one of the  
 CC best overall inducers in almost all cytokine and blood cell  
 CC proliferation experiments conducted.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQFQVQS 18

Db 1 DQPPDVEKPDLPQFQVQS 18

# RESULT 7

AA014579  
 ID AA014579 standard; peptide; 18 AA.

AC AA014579;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 3.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

OS Unidentified.

FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVKEPDLQPFQVQS 18  
 |||||  
 Db 1 DQPPDVKEPDLQPFQVQS 18

RESULT 8

AA859355  
 ID AAB59355 standard; Peptide; 19 AA.

XX AC AAB59355;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment derived sequence #15.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -

XX PS Claim 8; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrum. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 18; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVKEPDLQPFQVQS 18  
 |||||  
 Db 2 DQPPDVKEPDLQPFQVQS 19

RESULT 9

AAU82343

ID AAU82343 standard; Peptide; 8 AA.

XX AC AAU82343;

XX DT 09-APR-2002 (first entry)

XX DE Human papillomavirus (HPV) E7 antigenic peptide #229.

XX KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.

XX OS Homo sapiens.

XX PN WO200200242-A2.

XX PD 03-JAN-2002.

XX PF 26-JUN-2001; 2001WO-US20240.

XX PR 26-JUN-2000; 2000US-214202P.

XX PA (STES-) STESSEN BIOTECHNOLOGIES CORP.

XX PI Neefe J, Goldstone S, Winnett M, Siegel M;

XX DR WPI; 2002-130834/17.

XX PT Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -

XX PS Example; Page 27; 34pp; English.

XX CC The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.

XX SQ Sequence 8 AA;

Query Match 27.8%; Score 5; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPDV 6

Db 2 QPPDV 6

RESULT 10

AAU96833

ID AAG96833 standard; Peptide; 10 AA.

XX AC AAG96833;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 3027.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

PN WO200142277-A2.  
 PD 14-JUN-2001.  
 XX  
 XX 13-DEC-2000; 2000WO-GB04776.  
 XX  
 XX 13-DEC-1999; 99GB-0029464.  
 XX  
 XX (PROT-) PROTEOM LTD.  
 XX  
 XX Roberts GW, Heal JR;  
 XX  
 XX WPI; 2001-408419/43.  
 XX  
 XX A set of peptide ligands consisting of specific complementary peptides  
 PT for proteins encoded by genes of the human genome, useful in an assay  
 PT for screening and identifying of one or more novel peptides which are  
 PT drug candidates or pro-drugs -  
 XX  
 XX Example 4; Page 477; 646pp; English.  
 PS  
 CC The invention relates to a set of complementary peptide ligands  
 CC generated from the human genome. The complementary peptides  
 CC interact with their relevant target proteins encoded in the human  
 CC genome. They can be used as reagents in drug discovery and as lead  
 CC ligands to facilitate drug design and development. The present  
 CC sequence is a complementary peptide provided in the specification.  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 PDLQP 13  
 Db 2 PDLQP 6  
 RESULT 11  
 AAP50841  
 ID AAP50841 standard; protein; 15 AA.  
 XX  
 AC AAP50841;  
 XX  
 DT 18-NOV-1991 (first entry)  
 XX  
 DE Sequence of colony stimulating factor subclass no.1 (CSF 1).  
 XX  
 KW Quantitative assay; clinical diagnosis; therapeutic agent;  
 KW haematopoiesis; immune cell deficiency; cancer therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /label= H,S,E  
 FT  
 XX  
 XX US4504586-A.  
 XX  
 XX 12-MAR-1985.  
 XX  
 XX 03-FEB-1983; 83US-0463516.  
 XX  
 XX 03-FEB-1983; 83US-0463516.  
 XX  
 XX (AMGE-) AMGEN.  
 XX  
 XX Nicolson M;  
 PI  
 XX WPI; 1985-080848/13.  
 DR  
 XX Determn. of colony stimulating factor sub-class 1 - by using

PT monoclonal antibody obtd. from cell lines ATCC HB 8207 and 8208  
 XX  
 PS Example; columns 9-10; 8pp; English.  
 XX  
 CC The inventors claim a novel murine derived hybridoma cell line which  
 CC is capable of producing in a growth medium a monoclonal antibody  
 CC capable of specific binding with human CSF-1 in an antigen-antibody  
 CC complex. A synthetic polypeptide duplicating the sequence of AAs of  
 CC residues 2 through 14 is expected to be successfully employed in  
 CC immunization, cell fusion and cloning procedures as set out in the  
 CC examples.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 PPDVE 7  
 Db 3 PPDVE 7  
 RESULT 12  
 AAP82092  
 ID AAP82092 standard; peptide; 15 AA.  
 XX  
 AC AAP82092;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 26-OCT-1990 (first entry)  
 XX  
 XX HRV2-derived peptide corresponding to amino acids 156-170 of VP2.  
 DE  
 XX synthetic human rhinovirus (HRV) peptides; HRV vaccine.  
 KW  
 XX Human rhinovirus.  
 OS  
 XX EP287395-A.  
 FN  
 XX 19-OCT-1988.  
 PD  
 XX 15-APR-1988; 88EP-0303432.  
 PF  
 XX 16-APR-1987; 87GB-0009274.  
 PR  
 XX (WELL ) WELLCOME FOUND LTD.  
 PA  
 XX Francis MJ, Clarke BE;  
 PI  
 XX WPI; 1988-294751/42.  
 DR  
 XX Vaccine against human rhinovirus -  
 OS comprising synthetic peptides corresp to epitope of VP2 or  
 FT equivalent amino acid residues of human rhinovirus  
 FT  
 XX Claim 4; Page 8; 15pp; English.  
 PS  
 XX Peptide can be chemically synthesised or prepd by recombinant  
 CC techniques ,opt as fusion protein. One or more amino acids may be  
 CC replaced by one or more amino acids which do not affect the  
 CC antigenicity of the peptide. The peptide is coupled to a carrier  
 CC for use in a vaccine.  
 CC See also AAP82093.  
 CC (Updated on 25-MAR-2003 to correct PD field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13  
 |||||  
 Db 9 PDLQP 13

RESULT 13  
 AAW75695  
 ID AAW75695 standard; peptide; 15 AA.  
 XX  
 AC AAW75695;  
 XX  
 DT 23-OCT-1998 (first entry)  
 XX

DE M. tuberculosis 32A kD protein derived peptide 54 (residues 266-280).  
 XX  
 KW Mycobacterium tuberculosis; vaccination; extracellular product;  
 KW immunodominant epitope; interleukin-12; MF59; immune response;  
 KW opsonising humoral response; intracellular pathogen.  
 XX

OS Synthetic.  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO9831388-A1.  
 XX  
 PD 23-JUL-1998.  
 XX  
 PF 15-JAN-1998; 98WO-US00942.  
 XX  
 PR 21-JAN-1997; 97US-0786533.  
 XX

PA (REGC ) UNIV CALIFORNIA.  
 XX

PI Harth G, Horwitz MA, Lee B;  
 XX

DR WPI; 1998-413815/35.  
 XX

PT Vaccines against Mycobacterium containing major extracellular  
 PT proteins - used to, e.g. induce protective and therapeutic immune  
 PT responses, and for detecting an immune response  
 XX

PS Example 29; Page 101; 236pp; English.  
 XX

CC Sequences shown in AAW75642 to AAW75698 represent synthetic peptides  
 CC derived from the native 32A kD major secretory protein of M.  
 CC tuberculosis. These peptides are used for identifying the immunodominant  
 CC T-cell epitope of the 32A kD protein. The invention provides an agent for  
 CC vaccinating mammals against Mycobacterium. The agent comprises at least  
 CC one of the major abundant extracellular 110, 80, 71, 58, 45, 32A, 32B,  
 CC 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M. tuberculosis, or at  
 CC least 1 of their immunodominant epitopes and interleukin-12 (IL-12) or  
 CC MF59 as adjuvants. The agent containing the nucleic acid encoding the  
 CC extracellular products are used to raise a protective or therapeutic  
 CC immune response against Mycobacterium, specifically M. tuberculosis. The  
 CC immunodominant epitopes can also be used (typically in a cutaneous  
 CC hypersensitivity test) to detect an immune response to vaccination.  
 CC Preparation of the agent does not require selection of the most  
 CC immunogenic products, so large scale production and purification are  
 CC easy, resulting in a consistent, standardised formulation, having lower  
 CC toxicity than killed or attenuated vaccines. The agents provide a rapid  
 CC and effective response (including a strong cell-mediated component) and  
 CC are safe even in immunocompromised subjects. They prevent development of  
 CC an opsonising humoral response that might spread intracellular  
 CC pathogens.  
 XX

SQ Sequence 15 AA;  
 XX

Query Match 27.8%; Score 5; DB 19; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDLQ 12  
 |||||  
 Db 10 KPDLQ 14

RESULT 14  
 AAW75696

ID AAW75696 standard; peptide; 15 AA.  
 XX

AC AAW75696;  
 XX

DT 23-OCT-1998 (first entry)  
 XX

DE M. tuberculosis 32A kD protein derived peptide 55 (residues 271-285).  
 XX  
 KW Mycobacterium tuberculosis; vaccination; extracellular product;  
 KW immunodominant epitope; interleukin-12; MF59; immune response;  
 KW opsonising humoral response; intracellular pathogen.  
 XX

OS Synthetic.  
 OS Mycobacterium tuberculosis.  
 XX

PN WO9831388-A1.  
 XX

PD 23-JUL-1998.  
 XX

PF 15-JAN-1998; 98WO-US00942.  
 XX

PR 21-JAN-1997; 97US-0786533.  
 XX

PA (REGC ) UNIV CALIFORNIA.  
 XX

PI Harth G, Horwitz MA, Lee B;  
 XX

DR WPI; 1998-413815/35.  
 XX

PT Vaccines against Mycobacterium containing major extracellular  
 PT proteins - used to, e.g. induce protective and therapeutic immune  
 PT responses, and for detecting an immune response  
 XX

PS Example 29; Page 101; 236pp; English.  
 XX

CC Sequences shown in AAW75642 to AAW75698 represent synthetic peptides  
 CC derived from the native 32A kD major secretory protein of M.  
 CC tuberculosis. These peptides are used for identifying the immunodominant  
 CC T-cell epitope of the 32A kD protein. The invention provides an agent for  
 CC vaccinating mammals against Mycobacterium. The agent comprises at least  
 CC one of the major abundant extracellular 110, 80, 71, 58, 45, 32A, 32B,  
 CC 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M. tuberculosis, or at  
 CC least 1 of their immunodominant epitopes and interleukin-12 (IL-12) or  
 CC MF59 as adjuvants. The agent containing the nucleic acid encoding the  
 CC extracellular products are used to raise a protective or therapeutic  
 CC immune response against Mycobacterium, specifically M. tuberculosis. The  
 CC immunodominant epitopes can also be used (typically in a cutaneous  
 CC hypersensitivity test) to detect an immune response to vaccination.  
 CC Preparation of the agent does not require selection of the most  
 CC immunogenic products, so large scale production and purification are  
 CC easy, resulting in a consistent, standardised formulation, having lower  
 CC toxicity than killed or attenuated vaccines. The agents provide a rapid  
 CC and effective response (including a strong cell-mediated component) and  
 CC are safe even in immunocompromised subjects. They prevent development of  
 CC an opsonising humoral response that might spread intracellular  
 CC pathogens.  
 XX

SQ Sequence 15 AA;  
 XX

Query Match 27.8%; Score 5; DB 19; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDLQ 12  
 |||||  
 Db 5 KPDLQ 9

RESULT 15

ABG67986  
ID ABG67986 standard; Peptide; 15 AA.  
XX  
AC ABG67986;  
XX  
XX  
DT 07-OCT-2002 (first entry)  
DE Human ADPI tryptic digest peptide #695.  
XX  
XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
KW Alzheimer's disease-associated feature; neuroprotective;  
KW Alzheimer's disease-associated protein isoform; nootropic;  
KW ADPI tryptic digest peptide.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200246767-A2.  
XX  
XX 13-JUN-2002.  
XX  
XX 29-NOV-2001; 2001WO-GB05289.  
PF  
XX  
XX 08-DEC-2000; 2000US-254431P.  
PR  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
PA  
XX  
XX Herath HMac, Parekh RB, Rohlf C;  
PI  
XX  
XX WPI; 2002-508575/54.  
DR  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT comprises detecting Alzheimer's disease-associated features or  
PT Alzheimer's disease-associated protein isoforms in brain tissue  
PT from the subject -  
XX  
XX Claim 7; Page 56; 427pp; English.  
XX  
XX The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in  
CC a subject. The method comprises analysing a sample of brain tissue  
CC from a subject by 2D electrophoresis to generate a 2D array of  
CC Alzheimer's disease-associated features (ADFs), whose relative  
CC abundance correlates with the presence, absence, stage or severity of  
CC AD and comparing the abundance of each feature with the abundance of  
CC that chosen feature in brain tissue from persons free from AD. The  
CC invention also describes Alzheimer's disease-associated protein  
CC isoforms (ADPis) detectable in brain tissue. The methods and  
CC compositions of the invention are useful for the screening, diagnosis  
CC or prognosis of AD in a subject, for determining the stage or severity  
CC of AD in a subject, for identifying a subject at risk of developing AD,  
CC or for monitoring the effect of therapy administered to a subject  
CC having AD. Antibodies capable of binding to ADPis are useful for  
CC treating or preventing AD, and for determining the efficacy of a given  
CC treatment regime. An agent that modulates the activity of ADPI is  
CC useful in the manufacture of a medicament for the treatment or  
CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI  
CC tryptic digest peptides.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 27.8%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DQPPD 5  
Db 5 DQPPD 9  
RESULT 16  
AAM47777  
ID AAM47777 standard; Peptide; 15 AA.  
XX

AAM47777;  
XX  
DT 26-FEB-2002 (first entry)  
DE Short chain dehydrogenase 32 peptide fragment.  
XX  
XX Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;  
KW immunological disease; inflammation; gene therapy; cytostatic;  
KW haemostatic; virucide; immunomodulatory; antiinflammatory.  
XX  
OS Unidentified.  
XX  
PN CNI307114-A.  
XX  
XX 08-AUG-2001.  
PD  
XX  
XX 28-JAN-2000; 2000CN-0111584.  
PF  
XX  
XX 28-JAN-2000; 2000CN-0111584.  
PR  
XX  
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.  
PA  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX WPI; 2002-026893/04.  
DR  
XX  
XX New polypeptide for treating malignant tumors and HIV infection,  
PT comprises the polypeptide-short chain dehydrogenase 32 and  
PT polynucleotide for coding said polypeptide -  
XX  
XX Example 6; Page 27 (Disclosure); 33pp; Chinese.  
PS  
XX  
XX The present invention relates to short chain dehydrogenase 32 (AAM47776).  
CC The protein and its coding sequence are useful for treating various  
CC diseases, such as malignant tumours, haemopathy, HIV infection,  
CC immunological diseases and inflammations. The present sequence is an  
CC N-terminal peptide fragment of the protein, which was used in an example  
CC from the present invention.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 27.8%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 PPDVE 7  
Db 5 PPDVE 9  
RESULT 17  
ABG60992  
ID ABG60992 standard; Peptide; 19 AA.  
XX  
XX ABG60992;  
AC  
XX  
XX 27-AUG-2002 (first entry)  
DT  
XX  
XX Dirofilaria immitis transglutaminase peptide #2.  
DE  
XX  
XX Nematode; transglutaminase; nematocide; Dirofilaria immitis;  
KW Brugia malayi; Onchocerca volvulus; antinematode vaccine.  
XX  
XX Dirofilaria immitis.  
OS  
XX  
XX US6383774-B1.  
PN  
XX  
XX 07-MAY-2002.  
PD  
XX  
XX 04-DEC-1997; 97US-0984919.  
PP  
XX  
XX 03-DEC-1996; 96US-0781420.  
PR  
XX  
XX 12-JUN-1997; 97US-0874102.  
PR



```

XX (HESK-) HESKA CORP.
XX
XX Chandrashekar R;
XX
XX WPI; 2002-451385/48.
XX
XX New nucleic acid encoding nematode transglutaminase, useful in vaccines
XX for treating or preventing nematode infestation in humans and animals
XX
XX Example 5; Column 39; 66pp; English.
XX
XX The invention relates to an isolated nucleic acid (I) encoding nematode
XX transglutaminase. (I), optionally incorporated into recombinant viruses
XX or cells, are used to treat or prevent infestation by parasitic nematodes
XX in humans or animals, especially by Dirofilaria immitis, Brugia malayi
XX or Onchocerca volvulus. (I) can also be used for expression of the
XX corresponding recombinant proteins which are also useful in
XX antineoplastic vaccines and for raising antibodies (useful for treatment
XX or diagnosis). ABG60989-ABG61003 represent nematode transglutaminase
XX amino acid sequences of the invention.
XX
XX Sequence 19 AA;
XX
XX Query Match 27.8%; Score 5; DB 23; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 PFQVQ 17
XX |||||
XX Db 11 PFQVQ 15
XX
XX RESULT 19
XX AAR11303
XX ID AAR11303 standard; Protein; 20 AA.
XX
XX AC AAR11303;
XX
XX DT 25-MAR-2003 (updated)
XX DT 30-MAY-1991 (first entry)
XX
XX DE Recombinant 275-294 antigenic peptide from M.tuberculosis 32kD Ag.
XX
XX KW tuberculosis; vaccine; BCG; 32kD antigen.
XX
XX OS Mycobacterium tuberculosis.
XX
XX PN EP419355-A.
XX
XX PD 27-MAR-1991.
XX
XX PF 19-SEP-1990; 90EP-0402590.
XX
XX PR 19-SEP-1989; 89EP-0402571.
XX PR 19-SEP-1990; 90EP-0402590.
XX
XX PA (INNO-) INNOGENETICS NV SA.
XX
XX PI Content J, Dewit L, Debruyne J, Vanvooren JP;
XX WPI; 1991-088933/13.
XX
XX PT Polypeptide comprising recombinant polypeptide - with defined
XX peptide sequence(s) used for diagnosis and for preparing vaccine
XX against tuberculosis
XX
XX PS Claim 45; Page 72; 134pp; English.
XX
XX CC This peptide corresponds to amino acids 275 to 294 of mature 32kD
XX antigen of M.tuberculosis. It is used to produce antibodies,
XX particularly monoclonal antibodies, for the diagnosis of evulsive
XX tuberculosis.
XX CC See also AAR11081-3, AAR11086-Q11090, AAR11101-8, AAR11297-R11302,
XX AAR11304.
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 20 AA;
XX
XX Query Match 27.8%; Score 5; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 PFQVQ 17
XX |||||
XX Db 11 PFQVQ 15
XX
XX RESULT 18
XX AAG66103
XX ID AAG66103 standard; peptide; 19 AA.
XX
XX AC AAG66103;
XX
XX DT 27-FEB-2002 (first entry)
XX
XX DE D. immitis transglutaminase protein internal fragment.
XX
XX KW Transglutaminase protein; disulfide isomerase; antiparasite; vaccine;
XX nematode; heartworm; ss.
XX
XX OS Dirofilaria immitis.
XX
XX PN US6309644-B1.
XX
XX PD 30-OCT-2001.
XX
XX PF 12-JUN-1997; 97US-0874102.
XX
XX PR 03-DEC-1996; 96US-0781420.
XX
XX PA (HESK-) HESKA CORP.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX
XX Chandrashekar R, Mehta K;
XX
XX WPI; 2002-040231/05.
XX
XX Novel Dirofilaria immitis transglutaminase protein which also has
XX protein disulfide isomerase activity, used to identify transglutaminase
XX activity inhibitors that are useful for protecting animals from
XX heartworm
XX
XX Example 5; Column 39; 66pp; English.
XX
XX The invention relates to parasitic nematode transglutaminase proteins and
XX polynucleotides encoding them. The transglutaminase proteins are useful

```

```

CC for identifying a compound capable of inhibiting transglutaminase or
CC protein disulfide isomerase activity. The proteins represent novel
CC targets for antiparasite vaccines and drugs. The products inhibit the
CC crucial steps in nematode molting that involve nematode transglutaminase.
CC The proteins are also useful for preventing an animal (a dog) from
CC heartworm, a disease condition caused by D.immitis. The nematode protein
CC disulfide isomerase or transglutaminase activity inhibitors identified
CC are useful for protecting an animal from heartworm. The proteins are
CC useful as diagnostic agents to detect infection by parasitic nematodes.
CC The present sequence represents a D. immitis transglutaminase protein
CC internal fragment.
XX
XX Sequence 19 AA;
XX
XX Query Match 27.8%; Score 5; DB 23; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 PFQVQ 17
XX |||||
XX Db 11 PFQVQ 15
XX
XX RESULT 19
XX AAR11303
XX ID AAR11303 standard; Protein; 20 AA.
XX
XX AC AAR11303;
XX
XX DT 25-MAR-2003 (updated)
XX DT 30-MAY-1991 (first entry)
XX
XX DE Recombinant 275-294 antigenic peptide from M.tuberculosis 32kD Ag.
XX
XX KW tuberculosis; vaccine; BCG; 32kD antigen.
XX
XX OS Mycobacterium tuberculosis.
XX
XX PN EP419355-A.
XX
XX PD 27-MAR-1991.
XX
XX PF 19-SEP-1990; 90EP-0402590.
XX
XX PR 19-SEP-1989; 89EP-0402571.
XX PR 19-SEP-1990; 90EP-0402590.
XX
XX PA (INNO-) INNOGENETICS NV SA.
XX
XX PI Content J, Dewit L, Debruyne J, Vanvooren JP;
XX WPI; 1991-088933/13.
XX
XX PT Polypeptide comprising recombinant polypeptide - with defined
XX peptide sequence(s) used for diagnosis and for preparing vaccine
XX against tuberculosis
XX
XX PS Claim 45; Page 72; 134pp; English.
XX
XX CC This peptide corresponds to amino acids 275 to 294 of mature 32kD
XX antigen of M.tuberculosis. It is used to produce antibodies,
XX particularly monoclonal antibodies, for the diagnosis of evulsive
XX tuberculosis.
XX CC See also AAR11081-3, AAR11086-Q11090, AAR11101-8, AAR11297-R11302,
XX AAR11304.
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 20 AA;
XX
XX Query Match 27.8%; Score 5; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

| Qy | 8 KPDQ 12                                                                 | 1 KPDQ 5 | Qy | 7 EXPD 10                                                                 | 1 EXPD 4 |
|----|---------------------------------------------------------------------------|----------|----|---------------------------------------------------------------------------|----------|
| DE | Human leptin fragment SEQ ID NO: 45.                                      |          | DE | Human leptin fragment SEQ ID NO: 45.                                      |          |
| XX | leptin; human; LSR; lipolysis stimulated receptor; obesity;               |          | XX | leptin; human; LSR; lipolysis stimulated receptor; obesity;               |          |
| XX | hypertension; anorexia; cachexia; stroke; atherosclerosis.                |          | XX | hypertension; anorexia; cachexia; stroke; atherosclerosis.                |          |
| XX | Homo sapiens.                                                             |          | XX | Homo sapiens.                                                             |          |
| XX | WO200121647-A2.                                                           |          | XX | WO200121647-A2.                                                           |          |
| XX | 29-MAR-2001.                                                              |          | XX | 29-MAR-2001.                                                              |          |
| XX | 22-SEP-2000; 2000WO-IB01470.                                              |          | XX | 22-SEP-2000; 2000WO-IB01470.                                              |          |
| XX | 22-SEP-1999; 99US-0155506.                                                |          | XX | 22-SEP-1999; 99US-0155506.                                                |          |
| XX | (GEST ) GENSET.                                                           |          | XX | (GEST ) GENSET.                                                           |          |
| XX | Yen F, Erickson MR, Fruebis J, Bihain B;                                  |          | XX | Yen F, Erickson MR, Fruebis J, Bihain B;                                  |          |
| XX | WPI; 2001-218642/22.                                                      |          | XX | WPI; 2001-218642/22.                                                      |          |
| XX | New leptin polypeptide fragment and related polynucleotides, useful for   |          | XX | New leptin polypeptide fragment and related polynucleotides, useful for   |          |
| XX | the prevention and treatment of obesity and obesity-related diseases      |          | XX | the prevention and treatment of obesity and obesity-related diseases      |          |
| XX | such as hypertension and diabetes -                                       |          | XX | such as hypertension and diabetes -                                       |          |
| XX | Example 10; Page 237; 247pp; English.                                     |          | XX | Example 10; Page 237; 247pp; English.                                     |          |
| XX | The present invention provides the protein and coding sequences of leptin |          | XX | The present invention provides the protein and coding sequences of leptin |          |
| XX | fragments which modulate the activity of lipolysis stimulated factor      |          | XX | fragments which modulate the activity of lipolysis stimulated factor      |          |
| XX | (LSR). These sequences are useful in the treatment of obesity related     |          | XX | (LSR). These sequences are useful in the treatment of obesity related     |          |
| XX | diseases, including obesity, anorexia, cachexia, cardiac and coronary     |          | XX | diseases, including obesity, anorexia, cachexia, cardiac and coronary     |          |
| XX | insufficiency, stroke, hypertension, atheromatous disease,                |          | XX | insufficiency, stroke, hypertension, atheromatous disease,                |          |
| XX | atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,         |          | XX | atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,         |          |
| XX | hyperuricaemia and syndrome X.                                            |          | XX | hyperuricaemia and syndrome X.                                            |          |
| XX | Sequence 4 AA;                                                            |          | XX | Sequence 4 AA;                                                            |          |
| XX | Query Match 22.2%; Score 4; DB 22; Length 4;                              |          | XX | Query Match 22.2%; Score 4; DB 22; Length 4;                              |          |
| XX | Best Local Similarity 100.0%; Pred. No. 9.3e+05;                          |          | XX | Best Local Similarity 100.0%; Pred. No. 9.3e+05;                          |          |
| XX | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |          | XX | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |          |
| XX | Example 2; Page 7; 24pp; English.                                         |          | XX | Example 2; Page 7; 24pp; English.                                         |          |
| XX | The synthetic insert encoding this epitope was ligated                    |          | XX | The synthetic insert encoding this epitope was ligated                    |          |
| XX | into the NheI restriction site of plasmid pPV-Nhe. The recombinant        |          | XX | into the NheI restriction site of plasmid pPV-Nhe. The recombinant        |          |
| XX | plasmid was transformed into E. coli strain XL-1 Blue. The                |          | XX | plasmid was transformed into E. coli strain XL-1 Blue. The                |          |
| XX | recombinant construct was designed so as to have a diagnostic             |          | XX | recombinant construct was designed so as to have a diagnostic             |          |
| XX | internal MluI restriction site for screening the resulting clones.        |          | XX | internal MluI restriction site for screening the resulting clones.        |          |
| XX | Positive clones were cultured to high density in nutrient broth and       |          | XX | Positive clones were cultured to high density in nutrient broth and       |          |
| XX | induced to express chimaeric protein comprising the HRV2 epitope by       |          | XX | induced to express chimaeric protein comprising the HRV2 epitope by       |          |
| XX | addition of IPTG.                                                         |          | XX | addition of IPTG.                                                         |          |
| XX | (Updated on 25-MAR-2003 to correct PR field.)                             |          | XX | (Updated on 25-MAR-2003 to correct PR field.)                             |          |
| XX | (Updated on 25-MAR-2003 to correct PA field.)                             |          | XX | (Updated on 25-MAR-2003 to correct PA field.)                             |          |
| XX | Sequence 20 AA;                                                           |          | XX | Sequence 20 AA;                                                           |          |
| XX | Query Match 27.8%; Score 5; DB 12; Length 20;                             |          | XX | Query Match 27.8%; Score 5; DB 12; Length 20;                             |          |
| XX | Best Local Similarity 100.0%; Pred. No. 1.4e+02;                          |          | XX | Best Local Similarity 100.0%; Pred. No. 1.4e+02;                          |          |
| XX | Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |          | XX | Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                |          |
| XX | 9 PDLPQ 13                                                                |          | XX | 9 PDLPQ 13                                                                |          |
| XX | 11 PDLPQ 15                                                               |          | XX | 11 PDLPQ 15                                                               |          |
| XX | RESULT 21                                                                 |          | XX | RESULT 21                                                                 |          |
| XX | AAB59927                                                                  |          | XX | AAB59927                                                                  |          |
| XX | ID AAB59927 standard; Peptide; 4 AA.                                      |          | XX | ID AAB59927 standard; Peptide; 4 AA.                                      |          |
| XX | AAB59927;                                                                 |          | XX | AAB59927;                                                                 |          |
| XX | 06-JUN-2001 (first entry)                                                 |          | XX | 06-JUN-2001 (first entry)                                                 |          |
| XX |                                                                           |          | XX |                                                                           |          |

PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX Izu Y, Kato I, Miyagi M, Tanaka T, Tanigawa T;  
 PI Tomono J, Tsunasawa S;  
 XX WPI; 1998-077182/07.  
 DR Pyrococcus furiosus DSM 3638 derived aminopeptidase - is  
 PT thermostable, and used for removing amino-terminal protecting groups  
 XX  
 PS Disclosure; Page 49; 76pp; Japanese.  
 XX This peptide has a N-terminal protecting group and can be used to  
 CC determine the activity of a novel aminopeptidase enzyme derived from  
 CC Pyrococcus furiosus DSM 3638. The enzyme is thermostable and removes  
 CC amino-terminal protecting groups from peptides. It is effective on a  
 CC range of protecting groups including acetyl, pyroglutamyl, formyl and  
 CC myristoyl groups. This aminopeptidase is inhibited by amastatin and  
 CC accelerated by cobalt chloride. This enzyme can be produced by culturing  
 CC microbial, plant or animal cells transformants transformed with an  
 CC expression vector containing the encoding nucleic acid. The enzyme can be  
 CC used for efficient amino-deprotection of peptides, especially in cases  
 CC where the protecting group is of uncertain or unknown structure. This is  
 CC especially applicable to sequence analysis of peptides and proteins.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 22.2%; Score 4; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 DVEK 8  
 Db 2 DVEK 5  
 RESULT 23  
 ABB08941  
 ID ABB08941 standard; peptide; 5 AA.  
 XX  
 AC ABB08941;  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Peptide #4 used in a mass spectrometry method 4.  
 XX  
 KW Argentinated peptide; mass spectrometry; silver;  
 XX sequence determination; peptide sequencing.  
 OS Unidentified.  
 XX  
 PN CA2302877-Al.  
 XX  
 PD 29-SEP-2001.  
 XX  
 PF 29-MAR-2000; 2000CA-2302877.  
 XX  
 PR 29-MAR-2000; 2000CA-2302877.  
 XX  
 PA (UYYO-) UNIV YORK.  
 XX  
 PI Siu KWM, Chu IK, Lau T;  
 XX  
 DR WPI; 2002-106671/15.  
 XX  
 PT Determining peptide or protein sequence by mass spectrometry by  
 PT combining oligopeptides with silver, scanning silver containing peaks  
 PT in optimum collision energies and analysing doublet or triplet peak  
 PT patterns -  
 XX  
 XX Example 5; Table 3; 46pp; English.  
 XX  
 CC The present sequence represents a tryptic peptide unknown to the

CC experimenter analysed using the method of the invention. The  
 CC specification describes a novel method of analysing argentinated peptides  
 CC using mass spectrometry by combining an oligopeptide with silver to  
 CC provide an argentinated oligopeptide, submitting the sample to a mass  
 CC spectrometer, scanning silver containing peaks in optimum collision  
 CC energies, identifying any doublet or triplet peak pattern, and confirming  
 CC with Y ions, and determining partial sequence by mass separation between  
 CC two successive doublet or triplet patterns. The method of the invention  
 CC is used for determining peptide or protein sequences.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 DVEK 8  
 Db 2 DVEK 5  
 RESULT 24  
 AAR59954  
 ID AAR59954 standard; peptide; 6 AA.  
 XX  
 AC AAR59954;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 14-FEB-1995 (first entry)  
 XX  
 DE Peptide signal sequence for treating Semliki Forest virus E1  
 XX infections.  
 XX  
 KW Therapeutic; metabolic interactions; PSS; analogues.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9416328-Al.  
 XX  
 PD 21-JUL-1994.  
 XX  
 PF 30-DEC-1993; 93WO-US12679.  
 XX  
 PR 30-DEC-1992; 92US-0997727.  
 XX  
 PA (RATH/) RATH M.  
 XX  
 PI Rath M;  
 XX  
 DR WPI; 1994-249399/30.  
 XX  
 XX Identifying peptide signal sequences in a protein - and use of  
 PT their synthetic analogues for treating or preventing, e.g.  
 PT cardiovascular and auto-immune disease, infections and cancer.  
 XX  
 PS Claim 24; Page 12; 28pp; English.  
 XX  
 CC The sequence is that of a peptide signal sequence which can be used  
 CC to treat Semliki forest virus E1 viral infections.  
 CC See also AAR59944-83.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 EXPD 10  
 Db 3 EXPD 6

```

RESULT 25
AAG63056
ID AAG63056 standard; peptide; 6 AA.
XX
XX
XX AAG63056;
XX
XX 01-OCT-2001 (first entry)
XX
XX Amino acid sequence of a Porcine parvovirus (PPV)-binding domain.
XX
XX Porcine parvovirus; PPV; Quick Assay for Selecting Affinity Resins;
XX virus binding domain.
XX
XX Unidentified.
XX
XX WO200140265-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US42515.
XX
XX 02-DEC-1999; 99US-0453115.
XX
XX (WITE-) VI TECHNOLOGIES INC.
XX
XX Hammond DJ;
XX
XX WPI; 2001-475677/51.
XX
XX Identifying ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins, involves differentiating specific or
XX non-specific false positive interactions from target-specific
XX interactions -
XX
XX Claim 7; Page 28; 39pp; English.
XX
XX The present sequence represents a Porcine parvovirus (PPV)-binding
XX domain, which binds to PPV in the presence of fibrinogen. It was
XX identified using the method of the invention. The method
XX identifies ligands that interact with a target by Quick Assay for
XX Selecting Affinity Resins. The method comprise differentiating false
XX positive interactions (either specific or non-specific) from
XX target-specific interaction, by distinguishing non-specific binding
XX ligands to agents in the screening solution from specific binding
XX between a ligand and target. The method is useful for identifying
XX ligands that interact with the target, and for multiple screenings of
XX the same surface-immobilized library for a number of different ligands.
XX
XX Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 11 LQPF 14
XX |||||
XX 3 LQPF 6
XX
XX Db
XX
XX RESULT 26
XX AAU86432
XX ID AAU86432 standard; Peptide; 6 AA.
XX
XX AC AAU86432;
XX
XX 21-MAY-2002 (first entry)
XX
XX Vector encoded peptide.
XX
XX Oestrogen receptor; breast cancer; combinatorial peptide library;
XX receptor modulating compound.
XX
XX Synthetic.

```

```

XX WO200204956-A2.
XX
XX 17-JAN-2002.
XX
XX 11-JUL-2001; 2001WO-US21867.
XX
XX 12-JUL-2000; 2000US-0614865.
XX
XX 21-MAY-2001; 2001US-0860688.
XX
XX (KARO-) KARO BIO USA INC.
XX
XX Fowlkes DM, Barnett TR, Buehrer B;
XX
XX WPI; 2002-154969/20.
XX
XX Identifying receptor-binding peptides comprises screening combinatorial
XX peptide library presented in form of cells each of which coexpress one
XX peptide member and receptor with signal producing system for reporting
XX binding -
XX
XX Example 501; Page 112; 175pp; English.
XX
XX The invention relates to identifying a binding peptide which binds a
XX receptor and which is a member of a combinatorial library of peptides,
XX comprising screening a combinatorial peptide library presented in the
XX form of cells which coexpress the receptor or its ligand-binding receptor
XX moiety and one member of the library, together with a signal producing
XX system for reporting binding of the peptide to the receptor. Also
XX included is a method for predicting the receptor-modulating activity of a
XX compound which modulates the biological activity of a receptor
XX comprising (a) identifying peptides which bind the receptor by the
XX method above, (b) using a number of the peptides to predict the receptor-
XX modulating activity of a compound by (i) providing a panel of
XX identified peptides, where the members differ in their ability to bind
XX to the receptor depending on reference conformations the receptor is
XX in, where the effect of a number of reference substances known to
XX modulate the biological activity of the receptor on the binding of each
XX member of the panel is known and is characterised as a reference
XX fingerprint for each reference substance, (ii) screening a test substance
XX of unknown activity relative to the receptor to determine its effect on
XX the binding of each member of the panel to the receptor, thereby
XX obtaining a test fingerprint for the test substance, (iii) comparing the
XX test fingerprint to the reference fingerprints and (iv) predicting the
XX biological activity of the test substance based on the assumption that
XX its biological activity will be similar to that of reference substances
XX with similar fingerprints. The method is useful for identifying a binding
XX peptide which binds a vertebrate, mammalian, preferably human receptor,
XX an intracellular, nuclear, oestrogen or androgen receptor. The identified
XX peptides which bind to the receptor are useful for predicting the
XX receptor-modulating activity of a compound (e.g. ant/agonists).
XX The receptor-binding library members are useful in the prediction of the
XX ability of small organic molecules, suitable for pharmaceutical use
XX (e.g. in the case of oestrogen receptors, for breast cancer treatment),
XX to interact with the receptor. The analyte-binding molecules can also be
XX used for in vivo imaging. The method has several advantages over whole
XX animal-based assay systems in that the same technology can be applied to
XX a variety of different receptors, the system can be used for high
XX throughput screening for agonists and compound characterisation, and gives very
XX distinct patterns for agonists and antagonists of receptor activity using
XX very much less protein. The present sequence is a vector derived
XX peptide which is occasionally included in expressed peptides from a
XX combinatorial peptide library.
XX
XX SQ Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 23; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 DLQP 13
XX |||||
XX 2 DLQP 5
XX
XX Db

```

RESULT 27  
 ABUS8263  
 ID ABUS8263 standard; Peptide; 6 AA.  
 XX AC  
 XX ABUS8263;  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to porcine parvovirus in the presence of fibrinogen #2.  
 XX  
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002155106-A1.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 01-DEC-2000; 2000US-0727963.  
 PF  
 XX 01-DEC-2000; 2000US-0727963.  
 PR  
 XX (HAMM/) HAMMOND D J.  
 PA  
 XX Hammond DJ;  
 PI  
 XX WPI; 2003-198483/19.  
 DR  
 XX  
 XX New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -  
 XX  
 PS Claim 7; Page 31; 35pp; English.  
 XX  
 CC The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 LQPF 14  
 DB 3 LQPF 6  
 RESULT 28  
 AAR33159  
 ID AAR33159 standard; peptide; 7 AA.  
 XX AC  
 XX AAR33159;  
 XX

DT 25-MAR-2003 (updated)  
 DT 25-JUN-1993 (first entry)  
 XX  
 DE HPV E7 protein - RBG protein binding inhibitor peptide.  
 XX  
 KW Human papilloma virus; retinoblastoma gene; genital warts;  
 KW cervical cancer; treatment.  
 XX  
 OS Synthetic.  
 XX  
 XX EP531080-A2.  
 PN  
 XX 10-MAR-1993.  
 PD  
 XX 01-SEP-1992; 92EP-0307905.  
 PF  
 XX 04-SEP-1991; 91US-0754829.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Oliff AI, Riemen MW;  
 PI  
 XX WPI; 1993-078581/10.  
 DR  
 XX  
 XX New polypeptide(s) which inhibit human papilloma virus binding to  
 PT RBG protein - useful for treating genital warts and cervical cancer  
 XX  
 PS Claim 7; Page 15; 15pp; English.  
 XX  
 CC The sequence is that of a peptide which inhibits binding of human  
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
 CC protein. It can be used in the treatment of conditions caused by HPV,  
 CC esp. genital warts and cervical cancer.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 14; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 DB 1 DLQP 4  
 RESULT 29  
 AAM44291  
 ID AAM44291 standard; Peptide; 7 AA.  
 XX  
 AC AAM44291;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #562.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX CA2290722-A1.  
 PN  
 XX 08-JUN-2001.  
 PD  
 XX 08-DEC-1999; 99CA-2290722.  
 PF  
 XX 08-DEC-1999; 99CA-2290722.  
 PR  
 XX 08-DEC-1999; 99CA-2290722.  
 XX

PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maili PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 XX  
 PS Example 4; Page 103; 154pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumors that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPCCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs  
 CC or a population of different SPCCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 LQPF 14  
 Db ||||  
 4 LQPF 7  
 RESULT 30  
 AAR10631  
 ID AAR10631 standard; Protein; 8 AA.  
 XX  
 AC AAR10631;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 18-APR-1991 (first entry)  
 XX  
 XX Human Papilloma Virus-16 "(Gln27]-E7-(20-27)-AMIDE" peptide.  
 DE  
 XX papilloma virus; retinoblastoma gene-binding protein; genital warts;  
 KW cervical cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN EP412762-A.  
 XX  
 PD 13-FEB-1991.  
 XX  
 XX 06-AUG-1990; 90EP-0308652.  
 PF  
 XX 09-APR-1990; 90US-0506981.  
 PR 07-AUG-1989; 89US-0330569.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA (OLIF/ ) OLIFF A I.  
 XX  
 XX Oliff AI, Riemen MW;  
 PI  
 XX WPI; 1991-045887/07.  
 DR

XX Papilloma virus and retinoblastoma gene-binding protein  
 PT inhibitors - involves a specified aminoacid sequence contg. 13  
 PT residues for treatment of genital warts and cervical cancer  
 XX  
 XX Claim 12; Page 11; 11pp; English.  
 XX  
 XX The peptide carries an amide group at the C-terminus. The sequence  
 CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein  
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,  
 CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.  
 CC The peptides are used as screening tools and in the prevention,  
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They  
 CC can also be used to raise antibodies either as vaccines or to  
 CC heighten the immune response to an HPV infection all ready present.  
 CC See also AAR10628-R10630, AAR10632-7.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 DLQP 13  
 Db ||||  
 1 DLQP 4  
 RESULT 31  
 AAR33158  
 ID AAR33158 standard; peptide; 8 AA.  
 XX  
 AC AAR33158;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 25-JUN-1993 (first entry)  
 XX  
 XX HPV E7 protein - RBG protein binding inhibitor peptide.  
 DE  
 XX Human papilloma virus; retinoblastoma gene; genital warts;  
 KW cervical cancer; treatment.  
 XX  
 OS Synthetic.  
 XX  
 PN EP531080-A2.  
 XX  
 PD 10-MAR-1993.  
 XX  
 XX 01-SEP-1992; 92EP-0307905.  
 PF  
 XX 04-SEP-1991; 91US-0754829.  
 PR (MERI ) MERCK & CO INC.  
 PA  
 XX Oliff AI, Riemen MW;  
 PI  
 XX WPI; 1993-078581/10.  
 DR  
 XX New polypeptide(s) which inhibit human papilloma virus binding to  
 PT RBG protein - useful for treating genital warts and cervical cancer  
 XX  
 XX Claim 7; Page 15; 15pp; English.  
 PS  
 XX The sequence is that of a peptide which inhibits binding of human  
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
 CC protein. It can be used in the treatment of conditions caused by HPV,  
 CC esp. genital warts and cervical cancer.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 14; Length 8;  
 DR

|                                                                                                             |                                                                        |  |  |
|-------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|--|--|
| Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                        |  |  |
| QY                                                                                                          | 10 DLQP 13<br>                                                         |  |  |
| Db                                                                                                          | 1 DLQP 4                                                               |  |  |
| RESULT 32                                                                                                   |                                                                        |  |  |
| AA                                                                                                          | AAR46821 standard; Protein; 8 AA.                                      |  |  |
| XX                                                                                                          |                                                                        |  |  |
| AC                                                                                                          | AAR46821;                                                              |  |  |
| XX                                                                                                          |                                                                        |  |  |
| DT                                                                                                          | 25-MAR-2003 (updated)                                                  |  |  |
| DT                                                                                                          | 19-AUG-1994 (first entry)                                              |  |  |
| XX                                                                                                          |                                                                        |  |  |
| DE                                                                                                          | Phytase derived peptide 795.                                           |  |  |
| XX                                                                                                          |                                                                        |  |  |
| KW                                                                                                          | pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid; |  |  |
| KW                                                                                                          | phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;  |  |  |
| KW                                                                                                          | plant; feed composition; filtration.                                   |  |  |
| XX                                                                                                          |                                                                        |  |  |
| OS                                                                                                          | Synthetic.                                                             |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PN                                                                                                          | WO9403612-A1.                                                          |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PD                                                                                                          | 17-FEB-1994.                                                           |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PF                                                                                                          | 30-JUL-1993; 93WO-FI00310.                                             |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PR                                                                                                          | 31-JUL-1992; 92US-0923724.                                             |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PA                                                                                                          | (ALKO-) ALKO LTD.                                                      |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PI                                                                                                          | Cantrell M, Fagerstroem RB, Miettinen-Oinonen ASK;                     |  |  |
| PI                                                                                                          | Nevalainen HK, Paloheimo NT, Piddington C, Rambosek JA;                |  |  |
| PI                                                                                                          | Torkkeli TK, Turunen MK;                                               |  |  |
| XX                                                                                                          |                                                                        |  |  |
| DR                                                                                                          | WPI; 1994-065700/08.                                                   |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PT                                                                                                          | Compsns. contg. phytate degrading enzymes - obtd. by expression        |  |  |
| PT                                                                                                          | of their genes in Trichoderma, used partic. for producing animal       |  |  |
| PT                                                                                                          | feed compsns.                                                          |  |  |
| XX                                                                                                          |                                                                        |  |  |
| PS                                                                                                          | Example 4; Page 44; 142pp; English.                                    |  |  |
| XX                                                                                                          |                                                                        |  |  |
| CC                                                                                                          | The sequences given in AAR46793-824 are peptides derived from the      |  |  |
| CC                                                                                                          | phytase protein. The phytase protein may be used in the composition    |  |  |
| CC                                                                                                          | of the invention. The DNA encoding the phytase protein may be          |  |  |
| CC                                                                                                          | introduced into a Trichoderma host which then expresses it and the     |  |  |
| CC                                                                                                          | protein is collected from the culture medium. By using Trichoderma as  |  |  |
| CC                                                                                                          | a host for Aspergillus phytate degrading enzymes such as this, a       |  |  |
| CC                                                                                                          | totally different enzyme composition compared to that secreted from    |  |  |
| CC                                                                                                          | Aspergillus results. The enzyme composition can be used for removal    |  |  |
| CC                                                                                                          | of phytic acid or inositol hexaphosphoric acid from raw material,      |  |  |
| CC                                                                                                          | particularly plant material. The composition is used in feed           |  |  |
| CC                                                                                                          | compositions for animals. By using Trichoderma as a source of a        |  |  |
| CC                                                                                                          | composition containing phytate degrading enzymes some difficult        |  |  |
| CC                                                                                                          | downstream processing problems, eg. filtration, that occur with        |  |  |
| CC                                                                                                          | similar Aspergillus compositions are avoided and yields are improved.  |  |  |
| CC                                                                                                          | (Updated on 25-MAR-2003 to correct PN field.)                          |  |  |
| XX                                                                                                          |                                                                        |  |  |
| SQ                                                                                                          | Sequence 8 AA;                                                         |  |  |
| Query Match 22.2%; Score 4; DB 15; Length 8;                                                                |                                                                        |  |  |
| Best Local Similarity 100.0%; Pred. No. 9.3e+05;                                                            |                                                                        |  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                  |                                                                        |  |  |
| QY                                                                                                          | 13 PFOV 16<br>                                                         |  |  |
| Db                                                                                                          | 4 PFOV 7                                                               |  |  |

|                                                                                                             |                                                                          |  |  |
|-------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|--|--|
| Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                          |  |  |
| QY                                                                                                          | 10 DLQP 13<br>                                                           |  |  |
| Db                                                                                                          | 1 DLQP 4                                                                 |  |  |
| RESULT 33                                                                                                   |                                                                          |  |  |
| ABG70878                                                                                                    | ABG70878 standard; Peptide; 8 AA.                                        |  |  |
| XX                                                                                                          |                                                                          |  |  |
| AC                                                                                                          | ABG70878;                                                                |  |  |
| XX                                                                                                          |                                                                          |  |  |
| DT                                                                                                          | 29-NOV-2002 (first entry)                                                |  |  |
| XX                                                                                                          |                                                                          |  |  |
| DE                                                                                                          | R. rhodochrous nitrile hydratase alpha subunit peptide #2.               |  |  |
| XX                                                                                                          |                                                                          |  |  |
| KW                                                                                                          | Nitrile hydratase; alpha subunit; enzyme; amide production;              |  |  |
| KW                                                                                                          | cyanide resistance; 2-hydroxy-4-methylthiobutyronitrile;                 |  |  |
| KW                                                                                                          | 2-hydroxy-4-methylthiobutyroamide; alpha-hydroxy amide.                  |  |  |
| XX                                                                                                          |                                                                          |  |  |
| OS                                                                                                          | Rhodococcus rhodochrous strain J1.                                       |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PN                                                                                                          | WO200270717-A2.                                                          |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PD                                                                                                          | 12-SEP-2002.                                                             |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PF                                                                                                          | 01-MAR-2002; 2002WO-JP01912.                                             |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PR                                                                                                          | 02-MAR-2001; 2001JP-0059023.                                             |  |  |
| PR                                                                                                          | 24-JAN-2002; 2002JP-0016222.                                             |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PA                                                                                                          | (DAIL ) DAICEL CHEM IND LTD.                                             |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PI                                                                                                          | Nagasawa T, Matsuyama A;                                                 |  |  |
| XX                                                                                                          |                                                                          |  |  |
| DR                                                                                                          | WPI; 2002-707100/76.                                                     |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PT                                                                                                          | Novel nitrile hydratase which acts on nitrile group of nitrile           |  |  |
| PT                                                                                                          | compound, hydrates nitrile group and converts it to amide group, useful  |  |  |
| PT                                                                                                          | for producing amides using alpha-hydroxy nitrile as starting material    |  |  |
| XX                                                                                                          |                                                                          |  |  |
| PS                                                                                                          | Example 22; Page 55; 96pp; English.                                      |  |  |
| XX                                                                                                          |                                                                          |  |  |
| CC                                                                                                          | The invention relates to a nitrile hydratase which acts on the nitrile   |  |  |
| CC                                                                                                          | group of a nitrile compound, hydrates the nitrile group and converts it  |  |  |
| CC                                                                                                          | to an amide group, and which is resistant to cyanide, or a protein       |  |  |
| CC                                                                                                          | complex consisting of the alpha and beta subunits which act on a nitrile |  |  |
| CC                                                                                                          | group of a nitrile compound, hydrate the nitrile group and covert it to  |  |  |
| CC                                                                                                          | an amide group, and use 2-hydroxy-4-methylthiobutyronitrile as a         |  |  |
| CC                                                                                                          | substrate to produce 2-hydroxy-4-methylthiobutyroamide. Also             |  |  |
| CC                                                                                                          | included are the polynucleotides encoding the alpha and beta subunits,   |  |  |
| CC                                                                                                          | recombinant vector containing either or both polynucleotides, a          |  |  |
| CC                                                                                                          | transformed host containing the vector, producing an amide (comprising   |  |  |
| CC                                                                                                          | contacting a nitrile compound with the hydratase or a microorganism      |  |  |
| CC                                                                                                          | producing it, or their processed products and recovering the amide       |  |  |
| CC                                                                                                          | produced) and stabilising the activity of nitrile hydratase in the       |  |  |
| CC                                                                                                          | presence of nitrile compounds, comprising contacting the nitrile         |  |  |
| CC                                                                                                          | hydratase with divalent metal cations. The nitrile hydratase, complex or |  |  |
| CC                                                                                                          | transformed host is useful for producing an amide which involves         |  |  |
| CC                                                                                                          | contacting a nitrile compound such as alpha-hydroxy- nitrile with the    |  |  |
| CC                                                                                                          | enzymatically active material and recovering the amide (preferably       |  |  |
| CC                                                                                                          | alpha-hydroxy amide) produced. The alpha-hydroxynitrile is represented   |  |  |
| CC                                                                                                          | by formula F1, and the product alpha-hydroxy amide is represented by     |  |  |
| CC                                                                                                          | formula F3 (both detailed in the specification). The present             |  |  |
| CC                                                                                                          | sequence represents a peptide from Rhodococcus rhodochrous strain J1     |  |  |
| CC                                                                                                          | nitrile hydratase alpha subunit used to design a PCR primer for          |  |  |
| CC                                                                                                          | isolation of the DNA encoding Rhodococcus sp. Cr4 nitrile hydratase.     |  |  |
| XX                                                                                                          |                                                                          |  |  |
| SQ                                                                                                          | Sequence 8 AA;                                                           |  |  |
| Query Match 22.2%; Score 4; DB 23; Length 8;                                                                |                                                                          |  |  |
| Best Local Similarity 100.0%; Pred. No. 9.3e+05;                                                            |                                                                          |  |  |
| Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                  |                                                                          |  |  |
| QY                                                                                                          | 4 PDVE 7<br>                                                             |  |  |
| Db                                                                                                          | 3 PDVE 6                                                                 |  |  |







AC AAR59257;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 10-MAY-1995 (first entry)  
 XX  
 DE Peptide fragment (1.0229) of HPV binds HLA-A2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;  
 KW HIV1; core antigen; surface antigen; pharmaceutical composition;  
 KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;  
 KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;  
 KW human leukocyte antigen.  
 XX  
 OS Human papilloma virus.  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 XX  
 PI Grey HM, Kast WM, Sette A, Sidney J;  
 XX  
 DR WPI; 1994-302678/37.  
 XX  
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Example 5; Page 106; 138pp; English.  
 XX  
 CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1  
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity  
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257  
 CC has an IC50 of <0.003 and the sequence occurs at position 14 in the HPV  
 CC E7 protein. The peptides of the invention can induce cytotoxic T  
 CC lymphocytes which can react with target cells. They can be used for the  
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,  
 CC etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 DLQP 13  
 Db 1 DLQP 4  
 RESULT 40  
 AAR61700  
 ID AAR61700 standard; peptide; 9 AA.  
 XX  
 AC AAR61700;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 12-JUN-1995 (first entry)  
 XX  
 DE HLA-A2.1 algorithm predicted binding peptide 33.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;

KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 XX  
 PI Grey HM, Kast WM, Sette A, Sidney J;  
 XX  
 DR WPI; 1994-302678/37.  
 XX  
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 70; 138pp; English.  
 XX  
 CC AAR61668-712 are potential peptide binders of HLA-A2.1 motif. They were  
 CC predicted by using an algorithm which assigns a score for each amino  
 CC acid, at each position along a peptide. A peptide is scored in the  
 CC 'Grouped Ratio' algorithm as a product of the scores of each of its  
 CC residues. This value can then be used to predict a population of  
 CC peptides with the highest occurrence of good binders. This set of  
 CC peptides was comprised of 21 peptides with high algorithm scores, and 20  
 CC peptides with low algorithm scores. This peptide (source WT (sic)) had an  
 CC algorithm score of 0.0017 and an A2.1 binding score of 0.0001. The  
 CC correlation between binding and algorithm score was 0.69 (over all the  
 CC peptides). The peptides of the invention can induce cytotoxic T  
 CC lymphocytes which can react with target cells. They can be used for the  
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,  
 CC etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 KPDL 11  
 Db 6 KPDL 9  
 RESULT 41  
 AAR73799  
 ID AAR73799 standard; peptide; 9 AA.  
 XX  
 AC AAR73799;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 19-JUN-1995 (first entry)  
 XX  
 DE Antigen fragment 115, from HPV(a) has binding affinity for HLA-2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;

KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1.  
 XX  
 OS Human papilloma virus strain 16(a).  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 XX  
 XX Grey HM, Kast WM, Sette A, Sidney J;  
 XX WPI; 1994-302678/37.  
 DR  
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 84; 138pp; English.  
 XX  
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7  
 CC antigen has a binding value of 1.9000. The peptides of the invention can  
 CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db 4 DLQP 7  
 XX  
 AC AAR73800;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 19-JUN-1995 (first entry)  
 XX  
 XX Antigen fragment 116, from HPV has binding affinity for HLA-2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1.  
 XX  
 OS Human papilloma virus strain 16.

XX WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 XX  
 XX Grey HM, Kast WM, Sette A, Sidney J;  
 XX WPI; 1994-302678/37.  
 DR  
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 84; 138pp; English.  
 XX  
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7  
 CC antigen has a binding value of 0.0130. The peptides of the invention can  
 CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db 3 DLQP 6  
 XX  
 AC AAR73796;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 19-JUN-1995 (first entry)  
 XX  
 XX Antigen fragment 112, from HPV has binding affinity for HLA-2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1.  
 XX  
 OS Human papilloma virus strain 16.  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX (CYTE-) CYTEL CORP.  
 PA Grey HM, Kast WM, Sette A, Sidney J;  
 PI WPI; 1994-302678/37.  
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX Disclosure; Page 84; 138pp; English.  
 XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7  
 CC antigen has a binding value of 1.4000. The peptides of the invention can  
 CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 DLQP 13  
 Db 4 DLQP 7  
 RESULT 44  
 AAR80939  
 ID AAR80939 standard; peptide; 9 AA.  
 AC AAR80939;  
 XX  
 DT 03-MAY-1996 (first entry)  
 DE Peptide for increasing HLA-A2.1 cell expression.  
 DE Human melanoma-associated protein; MAGE-2; tumour rejection antigen;  
 KW precursor; major histocompatibility complex; MHC; class 1; HLA-A2.1;  
 KW binding motif; cytolytic T cell; CTL; induction; peptide loading;  
 KW primary immune response.  
 XX Synthetic.  
 OS  
 XX WO9525530-A1.  
 PN  
 XX 28-SEP-1995.  
 PD  
 XX 21-MAR-1995; 95WO-US03535.  
 PF  
 XX 24-MAR-1994; 94US-0217188.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA (UYLE-) RIJKSUNIV LEIDEN.  
 XX  
 XX Boon-Falleur T, Kast WM, Melief CJM, Van Der Bruggen P;  
 PI Visseren MW;  
 PI WPI; 1995-344456/44.  
 XX  
 DR New peptide(s) based on tumour rejection antigen precursor MAGE-2  
 XX

PT which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used  
 PT partic. for treating cancers  
 XX  
 PS Example 3; Page 37; 44pp; English.  
 XX  
 CC Expression of HLA-A2.1 (T2) cells is increased by incubating T2  
 CC cells in medium containing the present peptide. T2 cells will  
 CC present the peptide bound to HLA-A2.1 in high amount and are good  
 CC antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-  
 CC AAR80888) can induce a similar primary immune response.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 DLQP 13  
 Db 3 DLQP 6  
 RESULT 45  
 AAR78889  
 ID AAR78889 standard; peptide; 9 AA.  
 XX  
 AC AAR78889;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HPV16 E7 11-19 cytotoxic T lymphocyte epitope.  
 XX  
 KW HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; antigens; treatment; disease prevention;  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9522317-A1.  
 XX  
 PD 24-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US02121.  
 XX  
 PR 16-FEB-1994; 94US-0197484.  
 XX  
 PA (CYTE-) CYTEL CORP.  
 XX  
 PI Vitiello MA, Chesnut RW, Sette AD, Cellis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 PT Compsn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 XX Example 14; Page 72; 109pp; English.  
 XX  
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a  
 CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a  
 CC lipid conjugated helper T cell inducing peptide. The compsn. is  
 CC useful in the treatment and prevention of HPV associated diseases.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 DLQP 13

```

Db ||||
 4 DLQP 7

RESULT 46
AAR78894
ID AAR78894 standard; peptide; 9 AA.
XX
AC AAR78894;
XX
DT 25-MAR-2003 (updated)
DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;
KW lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
XX
PF 16-FEB-1995; 95WO-US02121.
XX
PR 16-FEB-1994; 94US-0197484.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;
XX
DR WPI; 1995-302545/39.
XX
PT Compens. inducing cytotoxic T lymphocyte response to pref. viral,
PT bacterial, parasitic or tumour antigens - useful in the treatment
PT and prevention of diseases associated with the antigen e.g.
PT hepatitis B
XX
PS Example 14; Page 72; 109pp; English.
XX
CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
CC lipid conjugated helper T cell inducing peptide. The compsn. is
CC useful in the treatment and prevention of HPV associated diseases.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 3 DLQP 6

RESULT 47
AAW39661
ID AAW39661 standard; peptide; 9 AA.
XX
AC AAW39661;
XX
DT 11-JUN-1998 (first entry)
XX
DE HPV16/18 E7 peptide (pos. 11-19).
XX
KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
KW disease; anti-tumour; anti-viral.
XX
OS Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.

RESULT 48
AAW39662
ID AAW39662 standard; peptide; 9 AA.
XX
AC AAW39662;
XX
DT 11-JUN-1998 (first entry)
XX
DE HPV16/18 E7 peptide (pos. 12-20).
XX
KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
KW disease; anti-tumour; anti-viral.
XX
OS Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.

OS Human papillomavirus.
XX
PN WO9741440-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-NL00229.
XX
PR 23-DEC-1996; 96EP-0203670.
PR 26-APR-1996; 96EP-0201145.

Query Match 22.2%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

Peptides AAW39430-W39734 are used in a novel method for the selection of
immunogenic T-cell peptide epitopes present in polypeptide antigens. The
method involves the identification of peptide sequences capable of
binding to an HLA (human leukocyte antigen) class I molecule and
measuring the binding of this epitope peptide to the HLA class I
peptide. The stability of binding of the peptide and MHC (major
histocompatibility complex) class I molecule is measured on intact human
B cells carrying the MHC molecule at their cell surfaces. The method can
be used to select peptide epitopes for generating vaccines against a
disease associated with the polypeptide, e.g. cancers or AIDS. The
peptide epitopes are especially T-cell peptide epitopes with strong
anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived
from the human papillomavirus E7 protein and is capable of binding to the
human MHC Class I allele HLA-A2.1.

```

XX (UYLE-) RIJKSUNIV LEIDEN.  
PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
XX  
XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;  
XX  
DR WPI; 1997-549891/50.  
XX  
XX Method of selecting T cell peptide epitope(s) - by measuring the  
PT stability of HLA class I-peptide complexes on intact B cells  
PT  
XX Example 3; Page 78; 109pp; English.  
XX  
XX Peptides AAW39430-W39734 are used in a novel method for the selection of  
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
CC method involves the identification of peptide sequences capable of  
CC binding to an HLA (human leukocyte antigen) class I molecule and  
CC measuring the binding of this epitope peptide to the HLA class I  
CC peptide. The stability of binding of the peptide and MHC (major  
CC histocompatibility complex) class I molecule is measured on intact human  
CC B cells carrying the MHC molecule at their cell surfaces. The method can  
CC be used to select peptide epitopes for generating vaccines against a  
CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
CC peptide epitopes are especially T-cell peptide epitopes with strong  
CC anti-tumour and anti-viral immune responses. Peptide AAW39462 is derived  
CC from the human papillomavirus E7 protein and is capable of binding to the  
CC human MHC Class I allele HLA-A2.1.  
XX  
SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 DLOP 13  
Db |||||  
3 DLOP 6  
RESULT 49  
AAW36590  
ID AAW36590 standard; peptide; 9 AA.  
XX  
XX AAW36590;  
XX  
XX 25-MAR-2003 (updated)  
DT 09-MAR-1998 (first entry)  
XX  
XX Hepatitis B virus bulk antigen.  
XX  
XX Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV:  
KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;  
KW CTL; induce; production; Hepatitis B virus.  
XX  
XX Hepatitis B virus.  
OS  
XX US5686068-A.  
PN  
XX 11-NOV-1997.  
PD  
XX 25-JUL-1996; 96US-0687226.  
PF  
XX 25-JUL-1996; 96US-0687226.  
PR  
XX 24-MAR-1994; 94US-0217188.  
PR  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX (UYLE-) RIJKSUNIV LEIDEN.  
XX  
XX Boon-Faller T, Melief CJM, Van Der Bruggen P, Van Der Burg S;  
PI Visseren MW;  
XX  
XX WPI; 1997-558084/51.  
DR  
XX

PT Induction of cytolytic T cell production in vivo - by administering  
XX MAGE-2 peptide(s)  
XX  
XX Example 3; Column 9; 24pp; English.  
XX  
XX This peptide sequence represents a hepatitis B virus reference peptide  
CC used in determining the primary induction of the immune response against  
CC MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides  
CC AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)  
CC A2.1 molecule with high affinity and are therefore the only candidates of  
CC the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),  
CC because CTL recognise peptides only when bound to HLA molecules.  
CC Production of CTL in a subject can be induced by administering a MAGE-2  
CC peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who  
CC presents HLA-A2 molecules on cells. The method can be used to treat  
CC subjects in need of additional CTL.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
XX Sequence 9 AA;  
SQ  
Query Match 22.2%; Score 4; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 DLOP 13  
Db |||||  
3 DLOP 6  
RESULT 50  
AAW78893  
ID AAW78893 standard; peptide; 9 AA.  
XX  
XX AAW78893;  
XX  
XX 17-NOV-1998 (first entry)  
DT  
XX  
XX Human papillomavirus 16 E7 protein fragment 11-19.  
DE  
XX  
XX Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;  
KW class II associated peptide; pathogen; gene therapy; genetic disease;  
KW infection; downregulation; immune response.  
XX  
XX Human papillomavirus.  
OS  
XX Synthetic.  
XX  
XX WO9831398-A1.  
PN  
XX 23-JUL-1998.  
PD  
XX 22-JAN-1998; 98WO-US01499.  
PF  
XX 06-JAN-1998; 98US-0003253.  
PR  
XX 22-JAN-1997; 97US-0787547.  
PR  
XX (PANG-) PANGAEA PHARM INC.  
XX  
XX Curley JM, Hedley ML, Langer RS, Lunsford LB;  
XX  
XX WPI; 1998-427556/36.  
XX  
XX New preparations of microparticles - comprising a synthetic polymer  
PT matrix and nucleic acid comprising an expression vector for use in  
PT gene therapy  
XX  
XX Disclosure; Page 10; 101pp; English.  
XX  
XX A microparticle preparation (MP) has been developed, consisting of  
CC microparticles having a diameter of less than 100 nm. The MP  
CC comprises: (a) a polymeric matrix (PM) consisting of one or more  
CC synthetic polymers having a solubility in water of less than 1 mg/l; and  
CC (b) an expression vector selected from RNA molecules (at least 50% of  
CC which are closed circles) or circular plasmid DNA (at least 50% of which

CC are supercoiled). Also described is a MP of at most 20 microns in  
CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression  
CC control sequence operatively linked to a coding sequence, where the  
CC coding sequence encodes an expression product selected from: (i) a  
CC polypeptide at least 7 amino acids in length, having a sequence identical  
CC to the sequence of: (i) a fragment of a naturally-occurring mammalian  
CC protein; or (ii) a fragment of a naturally-occurring protein from an  
CC infectious agent which infects a mammal; (2) a peptide having a length  
CC and sequence which permits it to bind to an MHC class I or II molecule;  
CC and (3) the polypeptide or the peptide linked to a trafficking sequence.  
CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for  
CC use in the present invention. The MPs are highly effective vehicles for  
CC the delivery of polynucleotides into phagocytic cells. They can be used  
CC for gene therapy, e.g. for treating genetic diseases, infections or  
CC tumours or for downregulating an immune response.

XX SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|  
|  
|  
|  
Db 4 DLQP 7

RESULT 51  
AAW54766  
ID AAW54766 standard; peptide; 9 AA.

XX AC AAW54766;

DT 25-SEP-1998 (first entry)

DE Peptide from HPV 16 E7 (11-19).

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
KW vaccine; treatment.

OS Synthetic.

PN WO9813378-A1.

PD 02-APR-1998.

XX 25-SEP-1997; 97WO-NL00536.

XX 26-SEP-1996; 96EP-0202701.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Drijfhout JW, Koning F;

XX WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose  
PT residue(s) to antigen for increasing T cell response, useful in,  
PT e.g. vaccines against viral infection(s)

XX Disclosure; Page 37; 47pp; English.

XX The peptides AAW54559-W54809 are examples of peptides to which at least  
CC 1 (preferably 2) mannose can be attached to increase their uptake as  
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
CC peptides will increase the T cell response, whereas uptake of antagonist  
CC peptides blocks the T cell response. Blocking binding of immunogenic  
CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
CC arthritis, graft rejection etc., also to induce T-cell non-  
CC responsiveness. Vaccines containing mannosylated antigen are used to  
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
CC and parasites.

SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|  
|  
|  
|  
Db 4 DLQP 7

RESULT 52  
AAW54767  
ID AAW54767 standard; peptide; 9 AA.

XX AC AAW54767;

XX 25-SEP-1998 (first entry)

DE Peptide from HPV 16 E7 (12-20).

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
KW vaccine; treatment.

OS Synthetic.

PN WO9813378-A1.

PD 02-APR-1998.

XX 25-SEP-1997; 97WO-NL00536.

XX 26-SEP-1996; 96EP-0202701.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Drijfhout JW, Koning F;

XX WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose  
PT residue(s) to antigen for increasing T cell response, useful in,  
PT e.g. vaccines against viral infection(s)

XX Disclosure; Page 37; 47pp; English.

XX The peptides AAW54559-W54809 are examples of peptides to which at least  
CC 1 (preferably 2) mannose can be attached to increase their uptake as  
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
CC peptides will increase the T cell response, whereas uptake of antagonist  
CC peptides blocks the T cell response. Blocking binding of immunogenic  
CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
CC arthritis, graft rejection etc., also to induce T-cell non-  
CC responsiveness. Vaccines containing mannosylated antigen are used to  
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
CC and parasites.

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|  
|  
|  
|  
Db 3 DLQP 6

RESULT 53  
AAW48125  
ID AAY48125 standard; Peptide; 9 AA.

XX AC AAY48125;

|           |             |                                                                           |               |  |
|-----------|-------------|---------------------------------------------------------------------------|---------------|--|
| XX        |             | 01-DEC-1999                                                               | (first entry) |  |
| DT        | XX          | Immunogenic peptide having a human leukocyte antigen binding motif #2736. |               |  |
| DE        | XX          |                                                                           |               |  |
| DE        | XX          |                                                                           |               |  |
| KW        | XX          | Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;    |               |  |
| KW        | XX          | immune response; T cell activation; major histocompatibility complex;     |               |  |
| KW        | XX          | Cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;   |               |  |
| KW        | XX          | prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;         |               |  |
| KW        | XX          | vaccine; immunisation.                                                    |               |  |
| OS        | XX          | Synthetic.                                                                |               |  |
| OS        | XX          | Homo sapiens.                                                             |               |  |
| XX        | XX          |                                                                           |               |  |
| PV        | XX          | WO9945954-A1.                                                             |               |  |
| PD        | XX          | 16-SEP-1999.                                                              |               |  |
| PF        | XX          | 13-MAR-1998; 98WO-US05039.                                                |               |  |
| PR        | XX          | 13-MAR-1998; 98WO-US05039.                                                |               |  |
| PA        | XX          | (EPIM-) EPIMUNE INC.                                                      |               |  |
| PI        | XX          | Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;                |               |  |
| DR        | XX          | WPI; 1999-551214/46.                                                      |               |  |
| PT        | XX          | New immunogenic peptides with HLA binding motif, useful in treatment      |               |  |
| PT        | XX          | and diagnosis of cancers and viral diseases -                             |               |  |
| PS        | XX          | Claim 1; Page 137; 150pp; English.                                        |               |  |
| CC        | XX          | AA45390 to AA48214 represent specifically claimed immunogenic peptides    |               |  |
| CC        | XX          | having a human major histocompatibility complex (MHC) Class I (also       |               |  |
| CC        | XX          | known as human leukocyte antigen (HLA)) binding motif. The immunogenic    |               |  |
| CC        | XX          | peptides can bind to a specific HLA allele (i.e. HLA-A subtypes           |               |  |
| CC        | XX          | HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  |               |  |
| CC        | XX          | response against the antigen from which the peptide is derived.           |               |  |
| CC        | XX          | Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are    |               |  |
| CC        | XX          | normally induced by an antigen in the form of a peptide fragment bound    |               |  |
| CC        | XX          | to a HLA molecule, rather than the intact foreign antigen itself, and     |               |  |
| CC        | XX          | are particularly important in tumour rejection and in fighting viral      |               |  |
| CC        | XX          | infections. The peptides are therefore useful therapeutically to treat    |               |  |
| CC        | XX          | or prevent viral infections and cancers in mammals (especially humans)    |               |  |
| CC        | XX          | e.g prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.        |               |  |
| CC        | XX          | They can be administered as vaccines to elicit an immune response in      |               |  |
| CC        | XX          | individuals susceptible or otherwise at risk of viral infection or        |               |  |
| CC        | XX          | cancer, or used to treat chronic or acute conditions. They are also       |               |  |
| CC        | XX          | useful diagnostically, and can be used to induce a cytotoxic T cell       |               |  |
| CC        | XX          | response, by contacting a cytotoxic T cell with the peptide e.g. to       |               |  |
| CC        | XX          | produce CTLs ex vivo for infusion back into a patient. The                |               |  |
| CC        | XX          | polynucleotides encoding the immunogenic peptides are also useful         |               |  |
| CC        | XX          | therapeutically and for immunisation as above.                            |               |  |
| XX        | XX          |                                                                           |               |  |
| SQ        | XX          | Sequence 9 AA;                                                            |               |  |
|           |             | Query Match 22.2%; Score 4; DB 20; Length 9;                              |               |  |
|           |             | Best Local Similarity 100.0%; Pred. No. 9.3e+05;                          |               |  |
|           |             | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps                   |               |  |
| Qy        | 8 KPDL 11   |                                                                           |               |  |
|           |             |                                                                           |               |  |
| Dd        | 1 KPDL 4    |                                                                           |               |  |
|           |             |                                                                           |               |  |
| RESULT 54 |             |                                                                           |               |  |
| AA48135   | ID          | AA48135 standard; Peptide; 9 AA.                                          |               |  |
| XX        | XX          |                                                                           |               |  |
| AC        | XX          | AA48135;                                                                  |               |  |
| XX        | XX          |                                                                           |               |  |
| DT        | 01-DEC-1999 | (first entry)                                                             |               |  |



XX TEK protein; TIE2 protein; receptor tyrosine kinase; T cell response;  
 KW immune response; endothelial cell; tumor-associated vasculature;  
 KW coagulation; thrombosis; cancer; anticancer vaccine.  
 XX Homo sapiens.  
 XX OS  
 PN WO9943801-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PF 26-FEB-1999; 99WO-GB00583.  
 XX  
 PR 26-FEB-1998; 98GB-0004121.  
 XX  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Durrant LG, Hewett PW, Ramage JM, Spendlove I;  
 XX  
 DR WPI; 1999-540586/45.  
 XX  
 XX New peptides containing at least one epitope from Tek receptor  
 PT tyrosine kinase, used in vaccines against cancer  
 XX  
 PS Claim 7; Page 31; 56pp; English.  
 XX  
 CC AAY30325-35 represent T cell epitopes of the TEK protein, also known as  
 CC TIE2 protein. TEK is a receptor tyrosine kinase. TEK contains epitopes  
 CC which bind to MHC. The presentation of TEK epitopes can also stimulate  
 CC helper cell and/or cytotoxic T cell responses. The immune response is  
 CC directed against endothelial cells in the tumor-associated  
 CC vasculature and includes production of antibodies that bind to the  
 CC cells, causing coagulation and thrombosis. The immune response is  
 CC targeted to endothelial cells lining blood vessels of the tumor (these  
 CC cells overexpress Tek), so damage to even a few cells will kill many  
 CC tumor cells. These target cells are accessible to the immune response  
 CC and problems of antigenic heterogeneity, MHC loss and resistance to  
 CC apoptosis (associated with epithelial cells) are unlikely to occur in  
 CC normal endothelial cells. TEK epitopes (see AAY30320-24) are used to  
 CC generate antibodies, and for prevention and treatment of cancer.  
 CC The peptides, and recombinant DNA constructs or viral vectors that  
 CC express them, are useful as anticancer vaccines to target endothelial  
 CC cells that line blood vessels of the tumor.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VEKP 9  
 DB 3 VEKP 6  
 RESULT 56  
 AAY28526  
 ID AAY28526 standard; peptide; 9 AA.  
 XX  
 AC AAY28526;  
 XX  
 DT 19-OCT-1999 (first entry)  
 XX  
 DE Beta-1 integrin cell adhesion modulator analogue #38.  
 XX  
 KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;  
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.  
 XX  
 OS Synthetic.  
 OS WO9937669-A1.  
 PN  
 XX 29-JUL-1999.  
 PD

XX 21-JAN-1999; 99WO-US01236.  
 XX  
 PR 12-AUG-1998; 98US-0096212.  
 PR 22-JAN-1998; 98US-0072119.  
 PR 12-AUG-1998; 98US-0096211.  
 XX  
 PA (MINU ) UNIV MINNESOTA.  
 XX  
 XX Brienzo A, Furcht LT, McCarthy JB;  
 PI WPI; 1999-469112/39.  
 XX  
 DR New peptides modulating beta1 integrin subunit dependent cell  
 XX adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin  
 PT dependent adhesion important in tumour cell biology  
 XX  
 PS Claim 21; Fig 14; 47pp; English.  
 XX  
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide  
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides  
 CC AAY28510-Y28549 have been used to show that peptides which modulate this  
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which  
 CC has a side chain including an aromatic group, and a penultimate  
 CC C-terminal amino acid residue (Lip) with an alkyl side chain group, i.e.  
 CC a 'lipAr' motif. Studies with these peptides have also shown that  
 CC inhibiting peptides do not contain D-amino acids and that it is the  
 CC presence of the ArLip motif that conveys effective beta1 integrin  
 CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent  
 CC cell adhesion is important for cell adhesion to extracellular matrix  
 CC proteins, and the subunit is expressed on tumours such as melanomas.  
 CC Therefore these LipAr motif containing peptides may be important in the  
 CC treatment of cancer.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QPPD 5  
 DB 2 QPPD 5  
 RESULT 57  
 AAY10346  
 ID AAY10346 standard; Peptide; 9 AA.  
 XX  
 AC AAY10346;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE T cell epitope/MHC ligand SEQ ID NO:276.  
 XX  
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 OS  
 PN WO9902183-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 10-JUL-1998; 98WO-US14289.  
 XX  
 PR 10-DEC-1997; 97US-0988320.  
 PR 10-JUL-1997; 97CA-2209815.  
 XX  
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX

PI Kuendig TM, Simard JJJ;  
 DR WPI; 1999-120514/10.  
 XX  
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS  
 XX  
 PS Disclosure; Page 34; 1999p; English.  
 XX  
 CC The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db ||||  
 3 DLQP 6  
 RESULT 58  
 AAY10511  
 ID AAY10511 standard; Peptide; 9 AA.  
 XX AC AAY10511;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE HLA Class I motif peptide SEQ ID NO:441.  
 XX  
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 XX  
 PN WO9902183-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 10-JUL-1998; 98WO-US14289.  
 XX  
 PR 10-DEC-1997; 97US-0988320.  
 PR 10-JUL-1997; 97CA-2209815.  
 XX  
 PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX  
 PI Kuendig TM, Simard JJJ;  
 XX  
 DR WPI; 1999-120514/10.  
 XX  
 PT Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 44; 1999p; English.  
 PS  
 XX  
 CC The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db ||||  
 3 DLQP 6  
 RESULT 59  
 AAB19059  
 ID AAB19059 standard; peptide; 9 AA.  
 XX AC AAB19059;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Amino acid sequence of a betal-integrin inhibitor.  
 XX  
 KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;  
 KW central nervous system ischemic injury; myocardial infarction;  
 KW betal-integrin; angioplasty; surgical incision; injury-related trauma;  
 KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200056350-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 22-MAR-2000; 2000WO-US07680.  
 XX  
 PR 22-MAR-1999; 99US-0125634.  
 PR 24-NOV-1999; 99US-0167538.  
 XX  
 PA (MINU ) UNIV MINNESOTA  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (SENT-) SENTRON MEDICAL INC.  
 XX  
 PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;  
 PI Furcht LT;  
 XX  
 DR WPI; 2000-656062/63.  
 XX  
 PT Inhibition of inflammatory leukocyte mediated destruction of tissue in  
 PT a patient, comprises administering a peptide inhibitor of  
 PT betal-integrin, useful for treatment of e.g. cancer and osteoporosis  
 XX  
 PS Claim 3; Page 38; 61pp; English.  
 XX  
 CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit

CC betal-integrin which is responsible for leukocyte mediated tissue  
 CC destruction. The peptides are useful for inhibiting inflammatory  
 CC leukocyte mediated destruction of tissue which occurs as a result of  
 CC central nervous system (CNS) ischemic injury, myocardial infarction,  
 CC angioplasty, surgical incisions, injury-related trauma, and/or  
 CC transplant reperfusion, exposure to heat, cold, light, electricity  
 CC and/or chemicals. They are also useful for the treatment of stroke, a  
 CC burn type injury, cancer, and osteoporosis.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5  
 ||||  
 Db 2 QPPD 5

RESULT 60  
 AAB33705  
 ID AAB33705 standard; Peptide; 9 AA.  
 AC AAB33705;  
 XX  
 DT 26-JAN-2001 (first entry)  
 DE MHC class I associated immunogenic peptide SEQ ID 104.  
 XX  
 KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;  
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..  
 XX  
 OS Unidentified.  
 XX  
 PN WO200053161-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 10-MAR-2000; 2000WO-US06578.  
 XX  
 PR 11-MAR-1999; 99US-0266463.  
 PR 27-MAY-1999; 99US-0321346.  
 XX  
 PA (ZYCO-) ZYCO INC.  
 XX  
 PI Lunsford LB, Putnam D, Hedley ML;  
 XX  
 DR WPI; 2000-638130/61.  
 XX  
 PT Microparticles useful for administering a nucleic acid into the mucosal  
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric  
 PT matrix, a lipid and a nucleic acid molecule -  
 XX  
 PS Disclosure; Page 16; 96pp; English.  
 XX  
 CC The present invention relates to microparticles which are less than 20  
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a  
 CC nucleic acid molecule. The microparticle is specifically not  
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide  
 CC sequence encodes an expression product that binds to major  
 CC histocompatibility complex (MHC) type I or II molecules. Peptides  
 CC AAB3602-B33647 represent MHC class II associated immunogenic peptides,  
 CC and AAB33648-B33710 represent MHC class I associated immunogenic  
 CC peptides. The peptides are examples of the expression products of the  
 CC nucleotide sequences which can be included in the microparticles of the  
 CC invention. Sequences AAB33711-B33716 represent alternative expression  
 CC products and nuclear localisation signals also used in the invention. The  
 CC microparticles are useful for administering a nucleic acid into the  
 CC mucosal tissue preferably vaginal tissue of an animal.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
 ||||  
 Db 4 DLQP 7

RESULT 61  
 AAY96374  
 ID AAY96374 standard; peptide; 9 AA.  
 XX  
 AC AAY96374;  
 XX  
 DT 29-AUG-2000 (first entry)  
 DE HLA-A2 binding peptide hTERT T765.  
 XX  
 KW hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;  
 KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;  
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200025813-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US25438.  
 XX  
 PR 29-OCT-1998; 98US-0106106.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;  
 XX  
 DR WPI; 2000-365402/31.  
 XX  
 PT Universal tumor-associated antigens such as telomerase catalytic  
 PT subunit capable of binding major histocompatibility complex molecule  
 PT useful for diagnosis, prevention and treatment of cancer  
 XX  
 PS Disclosure; Page 75; 136pp; English.  
 XX  
 CC Human telomerase complex reverse transcriptase (hTERT) is expressed in  
 CC more than 85 percent of human cancers. hTERT is useful as a universal  
 CC tumour-associated antigen (TAA) that binds to a major histocompatibility  
 CC complex molecule (MHC). hTERT peptides were analyzed for the ability to  
 CC bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T  
 CC lymphocytes (CTL) were then generated that kill a cell expressing hTERT  
 CC or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.  
 CC Antigen presenting cells (APC) were also generated ex vivo for  
 CC presentation of a TAA peptide or hTERT. The APC can be used to activate  
 CC CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and  
 CC CTL are useful for cancer immunotherapy. Measuring the level of CTL in a  
 CC sample is useful for assessing the level of immunity of a patient to a  
 CC TAA or a peptide, where the sample is obtained before or after a cancer  
 CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also  
 CC useful for diagnosis and prophylactic treatment of cancer.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
 ||||  
 Db 4 DLQP 7

```

RESULT 62
AAY86644
ID AAY86644 standard; Peptide; 9 AA.
XX
AC AAY86644;
XX
DT 05-MAY-2000 (first entry)
XX
DE Telomerase peptide #59.
XX
KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW telomerase T lymphocyte.
XX
OS Homo sapiens.
XX
PN WO200002581-A1.
XX
PD 20-JAN-2000.
XX
PF 30-JUN-1999; 99WO-NO00220.
XX
PR 08-JUL-1998; 98NO-0003141.
XX
PA (NHYP) NORSE HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI Saeboe-Larsen S;
XX
DR WPI; 2000-145727/13.
XX
PT Protein or peptide fragments useful in the treatment and prophylaxis of
PT cancer in mammals -
XX
PS Claim 12; Page 35; 53pp; English.
XX
CC This sequence represents a telomerase peptide of the invention, and can
CC be used in a method for the treatment or prophylaxis of cancer. The
CC sequences are useful in the treatment or prophylaxis of cancer.
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC tract carcinomas. They are useful for generating telomerase T lymphocytes
CC capable of recognising and destroying tumour cells in a mammal.
CC comprising culturing T lymphocytes obtained from the mammal with the
CC peptides. Telomerase protein is expressed only by tumour cells, hence,
CC other body cells are not targeted or destroyed by telomerase specific T
CC cells.
CC Note: This sequence was indexed from WO200002581, which is the first
CC major country equivalent to NO9803141.
XX
SQ Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 63
AAY86658
ID AAY86658 standard; Peptide; 9 AA.
XX
AC AAY86658;
XX
DT 05-MAY-2000 (first entry)
XX
DE Telomerase peptide #73.
XX
KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;

```

```

KW telomerase T lymphocyte.
XX
OS Homo sapiens.
XX
PN WO200002581-A1.
XX
PD 20-JAN-2000.
XX
PF 30-JUN-1999; 99WO-NO00220.
XX
PR 08-JUL-1998; 98NO-0003141.
XX
PA (NHYP) NORSE HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI Saeboe-Larsen S;
XX
DR WPI; 2000-145727/13.
XX
PT Protein or peptide fragments useful in the treatment and prophylaxis of
PT cancer in mammals -
XX
PS Claim 12; Page 35; 53pp; English.
XX
CC This sequence represents a telomerase peptide of the invention, and can
CC be used in a method for the treatment or prophylaxis of cancer. The
CC sequences are useful in the treatment or prophylaxis of cancer.
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC tract carcinomas. They are useful for generating telomerase T lymphocytes
CC capable of recognising and destroying tumour cells in a mammal.
CC comprising culturing T lymphocytes obtained from the mammal with the
CC peptides. Telomerase protein is expressed only by tumour cells, hence,
CC other body cells are not targeted or destroyed by telomerase specific T
CC cells.
CC Note: This sequence was indexed from WO200002581, which is the first
CC major country equivalent to NO9803141.
XX
SQ Sequence 9 AA;
XX
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 4 DLQP 7

RESULT 64
AAG93801
ID AAG93801 standard; Peptide; 9 AA.
XX
AC AAG93801;
XX
DT 17-SEP-2001 (first entry)
XX
DE Human papilloma virus 16 E7 peptide 1.
XX
KW Continuous flow production; microparticle; gene therapy;
KW antisense therapy; vaccination; treatment; autoimmune disease;
KW immune response modulation.
XX
OS Human wart virus.
XX
PN WO200136583-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US31770.
XX
PR 19-NOV-1999; 99US-0443654.
XX

```

(ZYCO-) ZYCOS INC.

Hedley ML, Hsu Y, Tyo M;  
WPI; 2001-425203/45.

Continuous production of microparticles containing nucleic acid for e.g. gene therapy, comprises mixing a solution of polymeric material and nucleic acid with a surfactant solution, removing solvent and drying -

XX Disclosure; Page 12; 47pp; English.

XX The present sequence is that of a peptide of the invention.

CC The invention relates to a method for scalable, continuous flow production of a nucleic acid containing microparticle that maintains the structural integrity of the associated nucleic acid and results in a microparticle having purity suitable for introduction into an animal host. Microparticles prepared according to the method can be used for delivery of a nucleic acid for gene therapy, antisense therapy, vaccination, treatment of autoimmune disease and either specific or non-specific modulation of an immune response. The microparticles may also be used to deliver nucleic acid encoding a protein or peptide useful in any kind of therapy. The method is economical, aseptic and scalable.

CC The method also enables control over the size of microparticles. The microparticles produced are free of impurities such as organic solvents and are readily dispersed in a wide range of dispersing agents.

XX Sequence 9 AA;

XX Query Match 22.2%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||||  
Db 4 DLQP 7

RESULT 65

AAG88547 standard; Peptide; 9 AA.

XX AAG88547;

XX 11-SEP-2001 (first entry)

XX HER2/NEU DR supermotif binding peptide core sequence #130.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell; immune response; vaccine; tumour; cancer; cytostatic; immunostimulant; tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

XX Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US333591.

XX 10-DEC-1999; 99US-0458299.

XX (EPIM-) EPIMMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E; Keogh E;

XX WPI; 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer -

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 XX cellular immune responses for the prevention and treatment of cancer -  
 PS Disclosure; Page 174; 199pp; English.  
 XX  
 CC The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising  
 CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic  
 CC and immunostimulant activities, and can be used in vaccines. (I), (II)  
 CC and (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample form a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 ||||  
 Db 2 KPDL 5

RESULT 67  
 AAG88865  
 ID AAG88865 standard; Peptide; 9 AA.  
 AC  
 AC AAG88865;  
 XX

DT 11-SEP-2001 (first entry)

XX HER2/neu epitope B7 supermotif peptide #25.

XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.  
 OS Synthetic.

XX WO200141787-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33591.

XX 10-DEC-1999; 99US-0458299.

XX (EPIM-) EPIMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

XX Keogh E;

PA

DR WPI; 2001-374995/39.

XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer -  
 PS Claim 1; Page 183; 199pp; English.

XX

CC The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising  
 CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic  
 CC and immunostimulant activities, and can be used in vaccines. (I), (II)  
 CC and (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample form a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 ||||  
 Db 1 KPDL 4

RESULT 68  
 AAB95951  
 ID AAB95951 standard; Peptide; 9 AA.  
 XX  
 AC AAB95951;  
 XX

DT 25-JUN-2001 (first entry)

XX MHC class-I associated HPV epitope SEQ ID 58.

XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;  
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;  
 KW cervical dysplasia; major histocompatibility complex; MHC I.

XX Human papillomavirus.

XX WO200119408-A1.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-US255559.

XX 16-SEP-1999; 99US-0154665.

XX 16-SEP-1999; 99US-0398534.

XX 09-DEC-1999; 99US-0169846.

XX 09-DEC-1999; 99US-0458173.

XX (ZYCO-) ZYCOS INC.

XX Hedley ML, Urban RC, Chicz RM;  
 PI WPI; 2001-265996/27.  
 XX  
 XX Novel nucleic acids encoding polypeptide polypeptides containing  
 PT multiple epitopes from one or more proteins, useful for treating tumors  
 PT and as vaccines against pathogenic agents -  
 XX  
 XX Disclosure; Page 8; 64pp; English.  
 PS  
 XX This invention relates to polynucleotides encoding a hybrid polypeptide  
 CC comprising a signal sequence and three segments that are either  
 CC contiguous or separated by a spacer amino acid or spacer peptide. The  
 CC invention specifically details polynucleotides encoding a polypeptide  
 CC peptide where the peptide segments are tumour antigens or a naturally  
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
 CC antiviral and immunostimulatory activity. The polynucleotide and  
 CC polypeptide peptides are useful for eliciting an immune response in a  
 CC mammal. The polynucleotide and protein are useful as vaccines for  
 CC treating tumours and pathogenic infections. The polynucleotide is also  
 CC useful for preventing or treating human papillomavirus (HPV)-associated  
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical  
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
 CC infection, cervical dysplasia, high grade squamous intraepithelial  
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are  
 CC useful for generating or enhancing prophylactic or therapeutic immune  
 CC response against pathogens, tumours or autoimmune diseases in a  
 CC population of individuals having diverse MHC allotypes, as positive  
 CC controls in T cell stimulation assays in vitro, and as tools to  
 CC understand processing of epitopes within cells. Peptides  
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major  
 CC histocompatibility complex I (MHC I) associated tumour and pathogen  
 CC antigens. The peptides can be used as part of the polypeptide proteins of  
 CC the invention. Also included are examples of the polypeptide proteins  
 CC represented by AAB96050 - AAB96052, and localisation signal peptides  
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of  
 CC the polypeptide peptides.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db ||||  
 4 DLQP 7  
 RESULT 69  
 AAB95999  
 ID AAB95999 standard; Peptide; 9 AA.  
 XX AAB95999;  
 AC  
 XX  
 XX 25-JUN-2001 (first entry)  
 DT  
 XX HPV 16 E7 A2 MHC-binding epitope SEQ ID 101.  
 DE  
 XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;  
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;  
 KW cervical dysplasia; major histocompatibility complex; MHC I.  
 XX Human papillomavirus.  
 OS  
 XX WO200119408-A1.  
 PN  
 XX 22-MAR-2001.  
 PD  
 XX 18-SEP-2000; 2000WO-US25559.  
 FF  
 XX 16-SEP-1999; 99US-0154665.  
 PR

PR 16-SEP-1999; 99US-0398534.  
 PR 03-DEC-1999; 99US-0169846.  
 PR 03-DEC-1999; 99US-0458173.  
 XX  
 XX (ZYCO-) ZYCOs INC.  
 PA  
 XX Hedley ML, Urban RC, Chicz RM;  
 PI WPI; 2001-265996/27.  
 XX  
 XX Novel nucleic acids encoding polypeptide polypeptides containing  
 PT multiple epitopes from one or more proteins, useful for treating tumors  
 PT and as vaccines against pathogenic agents -  
 XX  
 XX Disclosure; Page 22; 64pp; English.  
 PS  
 XX This invention relates to polynucleotides encoding a hybrid polypeptide  
 CC comprising a signal sequence and three segments that are either  
 CC contiguous or separated by a spacer amino acid or spacer peptide. The  
 CC invention specifically details polynucleotides encoding a polypeptide  
 CC peptide where the peptide segments are tumour antigens or a naturally  
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
 CC antiviral and immunostimulatory activity. The polynucleotide and  
 CC polypeptide peptides are useful for eliciting an immune response in a  
 CC mammal. The polynucleotide and protein are useful as vaccines for  
 CC treating tumours and pathogenic infections. The polynucleotide is also  
 CC useful for preventing or treating human papillomavirus (HPV)-associated  
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical  
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
 CC infection, cervical dysplasia, high grade squamous intraepithelial  
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are  
 CC useful for generating or enhancing prophylactic or therapeutic immune  
 CC response against pathogens, tumours or autoimmune diseases in a  
 CC population of individuals having diverse MHC allotypes, as positive  
 CC controls in T cell stimulation assays in vitro, and as tools to  
 CC understand processing of epitopes within cells. Peptides  
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major  
 CC histocompatibility complex I (MHC I) associated tumour and pathogen  
 CC antigens. The peptides can be used as part of the polypeptide proteins of  
 CC the invention. Also included are examples of the polypeptide proteins  
 CC represented by AAB96050 - AAB96052, and localisation signal peptides  
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of  
 CC the polypeptide peptides.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db ||||  
 3 DLQP 6  
 RESULT 70  
 AAB96001  
 ID AAB96001 standard; Peptide; 9 AA.  
 XX AAB96001;  
 AC  
 XX  
 XX 25-JUN-2001 (first entry)  
 DT  
 XX HPV 16 E7 A2 MHC-binding epitope SEQ ID 103.  
 DE  
 XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;  
 KW human papillomavirus-associated disease; condyloma; cervical dysplasia;  
 KW cervical dysplasia; major histocompatibility complex; MHC I.  
 XX Human papillomavirus.  
 OS  
 XX WO200119408-A1.  
 PN  
 XX

PD 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-US25559.  
 PF 16-SEP-1999; 99US-0154665.  
 XX 16-SEP-1999; 99US-0398534.  
 PR 09-DEC-1999; 99US-0169846.  
 PR 09-DEC-1999; 99US-0458173.  
 XX (ZYCO-) ZYCOS INC.  
 PA Hedley ML, Urban RC, Chicx RM;  
 XX WPI; 2001-265996/27.  
 XX Novel nucleic acids encoding polypeptide polypeptides containing  
 PT multiple epitopes from one or more proteins, useful for treating tumors  
 PT and as vaccines against pathogenic agents -  
 XX Disclosure; Page 22; 64pp; English.  
 XX This invention relates to polynucleotides encoding a hybrid polypeptide  
 XX comprising a signal sequence and three segments that are either  
 CC contiguous or separated by a spacer amino acid or spacer peptide. The  
 CC invention specifically details polynucleotides encoding a polypeptide  
 CC peptide where the peptide segments are tumour antigens or a naturally  
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
 CC antiviral and immunostimulatory activity. The polynucleotide and  
 CC polypeptide peptides are useful for eliciting an immune response in a  
 CC mammal. The polynucleotide and protein are useful as vaccines for  
 CC treating tumours and pathogenic infections. The polynucleotide is also  
 CC useful for preventing or treating human papillomavirus (HPV)-associated  
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical  
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
 CC infection, cervical dysplasia, high grade squamous intraepithelial  
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are  
 CC useful for generating or enhancing prophylactic or therapeutic immune  
 CC response against pathogens, tumours or autoimmune diseases in a  
 CC population of individuals having diverse MHC allotypes, as positive  
 CC controls in T cell stimulation assays in vitro, and as tools to  
 CC understand processing of epitopes within cells. Peptides  
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major  
 CC histocompatibility complex I (MHC I) associated tumour and pathogen  
 CC antigens. The peptides can be used as part of the polypeptide proteins of  
 CC the invention. Also included are examples of the polypeptide proteins  
 CC represented by AAB96050 - AAB96052, and localisation signal peptides  
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of  
 CC the polypeptide peptides.  
 XX Sequence 9 AA;  
 SQ Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 DLQP 13  
 Db 1 DLQP 4  
 RESULT 71  
 ID AAJ03011  
 XX AAJ03011 standard; Peptide; 9 AA.  
 AC AAJ03011;  
 XX 02-JUL-2001 (first entry)  
 DT Hepatitis C virus epitope #3002.  
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;  
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;  
 XX antiviral.

OS Hepatitis C virus.  
 XX WO200121189-A1.  
 XX 29-MAR-2001.  
 XX 19-JUL-2000; 2000WO-US19774.  
 PF 19-JUL-1999; 99US-0357737.  
 XX (EPIM-) EPIMMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RI, Grey HM;  
 XX WPI; 2001-308046/32.  
 DR A new composition useful as a vaccines against hepatitis C virus -  
 XX Disclosure; Page 174; 214pp; English.  
 XX The present invention describes a composition comprising a prepared  
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.  
 CC These are derived from HCV HLA-binding motifs. They are useful in  
 CC vaccines for the prevention and treatment of HCV infection in humans. The  
 CC present sequence is an epitope used in the disclosure of the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PDLQ 12  
 Db 4 PDLQ 7  
 RESULT 72  
 ID AAB20215  
 XX AAB20215 standard; Peptide; 9 AA.  
 AC AAB20215;  
 XX 14-MAY-2001 (first entry)  
 DT HPV strain 16 E7 protein immunogenic peptide A2.2.  
 DE Immunogenic peptide; immunogen; HPV; E7 protein; vaccine;  
 KW infection; gene therapy; exophytic condyloma; flat condyloma;  
 KW cervical cancer; respiratory papilloma; conjunctival papilloma;  
 KW cervical dysplasia.  
 XX Human papillomavirus type 16.  
 OS US6183746-B1.  
 XX 06-FEB-2001.  
 PF 09-OCT-1998; 98US-0169425.  
 XX 09-OCT-1997; 97US-0061657.  
 PR (ZYCO-) ZYCOS INC.  
 XX Urban RG, Chicx RM, Collins EJ, Hedley ML;  
 PI WPI; 2001-190939/19.  
 DR Inducing an immune response in a mammal for prophylaxis and treatment  
 PT of human papilloma virus infections such as cervical cancer, comprises  
 PT administering immunogenic peptides from the papilloma virus type 16 E7  
 PT protein -



```
XX PS Example 1; Column 9; 23pp; English.
XX CC
XX CC The present sequence is that of immunogenic peptide A2.2 derived
XX CC from human papillomavirus type 16 (HPV16) E7 protein. It binds
XX CC with high affinity to human class I molecule HLA-A2. Immunogenic
XX CC peptides of the invention are derived from a region of the HPV16 E7
XX CC protein that includes overlapping class I HLA binding, T-cell
XX CC epitopes. Nucleic acids encoding the immunogenic peptides are
XX CC administered to a mammal, especially a human, to prevent or treat
XX CC exophytic condyloma, flat condyloma, cervical cancer, respiratory
XX CC papilloma, conjunctival papilloma, genital-tract HPV infection and
XX CC cervical dysplasia (claimed).
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 4 DLQP 7
 ||||
 ||||

RESULT 73
AAB37116
ID AAB37116 standard; peptide; 9 AA.
AC AAB37116;
XX
XX 09-APR-2001 (first entry)
XX
XX Polylinker site from PUR291 for cloning HTLV-1 gp46 ATLE 495 fragment.
XX
XX HTLV-1; env gene; gp46; ATLE495; beta-galactosidase; fusion protein;
XX serodiagnosis.
XX
XX Escherichia coli.
XX
XX RU2152955-C2.
XX
XX 20-JUL-2000.
XX
XX 15-MAY-1997; 97RU-0107950.
XX
XX 15-MAY-1997; 97RU-0107950.
XX
XX (AMVI=) A MED VIROLOGY RES INST.
XX
XX Bobkov AF, Sankov MN, Selimova LM, Kazemova EV;
XX
XX WPI; 2001-022430/03.
XX
XX N-PSDB; AAP28703.
XX
XX Fragment of gene env HTLV-1, recombinant plasmid DNA pATLE 495, strain
XX of Bacterium Escherichia coli HB101/pATLE 495 as producer of
XX polypeptide E 495.
XX
XX Example 2; Column 7; 5pp; Russian.
XX
XX The invention relates to a method of preparing a novel artificially
XX produced polypeptide consisting of the product of the HTLV-1 env
XX gene encoding gp46 fragment ATLE495 fused to the E. coli
XX beta-galactosidase. This sequence represents the peptide encoded by
XX the polylinker sequence from plasmid pUR291 which is downstream of
XX the inserted HTLV-1 gp46 ATLE 495 fragment (AAP28701). The hybrid
XX protein has the specific polypeptide sequence encoded by region env
XX of the HTLV-1 genome and can be used for the serodiagnosis of HTLV-1.
XX
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
DB 2 DLQP 5
 ||||
 ||||

RESULT 74
AAB76118
ID AAB76118 standard; Peptide; 9 AA.
XX
XX AAB76118;
XX
XX 10-APR-2001 (first entry)
XX
XX Tumour associated antigen Her2/neu immunogenic peptide.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX HLA binding peptide; immune response; glycoprotein; cytostatic;
XX virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX human immunodeficiency virus; protozoacide; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX condyloma acuminatum.
XX
XX Homo sapiens.
XX
XX WO200100225-A1.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US17842.
XX
XX 29-JUN-1999; 99US-0141422.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX
XX WPI; 2001-112389/12.
XX
XX Composition comprising human leukocyte antigen binding peptide which
XX comprises isolated, prepared epitope useful for treating viral
XX infections such as acquired immunodeficiency syndrome, and cancer -
XX
XX Claim 1; Page 48; 50pp; English.
XX
XX The present invention describes a composition (I) which comprises at
XX least one human leukocyte antigen (HLA) binding peptide comprising an
XX isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX immunodeficiency virus) and protozoacide activities, which can be used
XX in vaccine production and is an inducer of cytotoxic T-cell response.
XX (I) is useful for inducing a cytotoxic T cell response against a
XX preselected antigen in a patient expressing a specific major
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX treat and/or prevent viral infection and cancer such as prostate cancer,
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX acuminatum.
XX
XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 35.8085 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-3

Perfect score: 18  
Sequence: 1 DQPPVEXFDLQPFQVQS 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Match | Query Length | ID | Description         |
|------------|-------|---------|--------------|----|---------------------|
| 1          | 18    | 100.0   | 18           | 15 | US-10-281-652-3     |
| 2          | 5     | 27.8    | 8            | 12 | US-10-365-908-98    |
| 3          | 5     | 27.8    | 10           | 11 | US-09-572-404B-3027 |
| 4          | 5     | 27.8    | 15           | 12 | US-10-080-608A-70   |
| 5          | 5     | 27.8    | 15           | 12 | US-10-370-685-159   |
| 6          | 4     | 22.2    | 4            | 9  | US-09-804-866-12    |
| 7          | 4     | 22.2    | 5            | 9  | US-09-804-866-13    |
| 8          | 4     | 22.2    | 6            | 10 | US-09-727-963A-17   |
| 9          | 4     | 22.2    | 9            | 9  | US-09-759-960-17    |
| 10         | 4     | 22.2    | 9            | 9  | US-09-829-549A-4    |
| 11         | 4     | 22.2    | 9            | 10 | US-09-909-460-104   |
| 12         | 4     | 22.2    | 9            | 12 | US-10-350-258-6     |
| 13         | 4     | 22.2    | 9            | 12 | US-10-365-908-3     |
| 14         | 4     | 22.2    | 9            | 12 | US-10-365-908-80    |
| 15         | 4     | 22.2    | 9            | 15 | US-10-033-662-36    |
|            |       |         |              |    | Sequence 3, Appli   |
|            |       |         |              |    | Sequence 98, Appl   |
|            |       |         |              |    | Sequence 3027, Ap   |
|            |       |         |              |    | Sequence 70, Appl   |
|            |       |         |              |    | Sequence 159, App   |
|            |       |         |              |    | Sequence 12, Appl   |
|            |       |         |              |    | Sequence 13, Appl   |
|            |       |         |              |    | Sequence 17, Appl   |
|            |       |         |              |    | Sequence 17, Appl   |
|            |       |         |              |    | Sequence 4, Appli   |
|            |       |         |              |    | Sequence 104, App   |
|            |       |         |              |    | Sequence 6, Appli   |
|            |       |         |              |    | Sequence 3, Appli   |
|            |       |         |              |    | Sequence 80, Appl   |
|            |       |         |              |    | Sequence 36, Appl   |

|   |      |    |    |                     |                   |
|---|------|----|----|---------------------|-------------------|
| 4 | 22.2 | 9  | 15 | US-10-128-711-66    | Sequence 66, Appl |
| 4 | 22.2 | 9  | 15 | US-10-128-711-71    | Sequence 71, Appl |
| 4 | 22.2 | 10 | 9  | US-09-847-185-19    | Sequence 19, Appl |
| 4 | 22.2 | 10 | 10 | US-09-835-853-22    | Sequence 22, Appl |
| 4 | 22.2 | 10 | 12 | US-10-177-390-33    | Sequence 33, Appl |
| 4 | 22.2 | 10 | 12 | US-10-365-908-57    | Sequence 57, Appl |
| 4 | 22.2 | 10 | 12 | US-10-365-908-104   | Sequence 104, App |
| 4 | 22.2 | 10 | 15 | US-10-062-710-228   | Sequence 228, App |
| 4 | 22.2 | 10 | 15 | US-10-155-522-82    | Sequence 82, Appl |
| 4 | 22.2 | 10 | 15 | US-10-133-210-271   | Sequence 271, App |
| 4 | 22.2 | 10 | 15 | US-10-211-088-67    | Sequence 67, Appl |
| 4 | 22.2 | 10 | 15 | US-10-224-386-19    | Sequence 19, Appl |
| 4 | 22.2 | 11 | 10 | US-09-017-743C-122  | Sequence 122, App |
| 4 | 22.2 | 11 | 12 | US-10-367-405-5     | Sequence 5, Appli |
| 4 | 22.2 | 11 | 15 | US-10-062-710-206   | Sequence 206, App |
| 4 | 22.2 | 11 | 15 | US-10-211-088-69    | Sequence 69, Appl |
| 4 | 22.2 | 12 | 7  | US-08-736-019-164   | Sequence 164, App |
| 4 | 22.2 | 12 | 11 | US-09-954-385-190   | Sequence 190, App |
| 4 | 22.2 | 12 | 12 | US-10-367-405-1     | Sequence 1, Appli |
| 4 | 22.2 | 12 | 12 | US-10-367-405-2     | Sequence 2, Appli |
| 4 | 22.2 | 12 | 12 | US-10-367-405-14    | Sequence 14, Appl |
| 4 | 22.2 | 12 | 15 | US-10-075-869-37    | Sequence 37, Appl |
| 4 | 22.2 | 13 | 9  | US-09-935-682-57    | Sequence 57, Appl |
| 4 | 22.2 | 15 | 11 | US-09-880-505-16    | Sequence 16, Appl |
| 4 | 22.2 | 15 | 11 | US-09-563-222-139   | Sequence 139, App |
| 4 | 22.2 | 15 | 12 | US-10-282-960-59    | Sequence 59, Appl |
| 4 | 22.2 | 15 | 14 | US-10-051-643-16    | Sequence 16, Appl |
| 4 | 22.2 | 16 | 10 | US-09-908-322-32    | Sequence 32, Appl |
| 4 | 22.2 | 16 | 11 | US-09-783-931-32    | Sequence 32, Appl |
| 4 | 22.2 | 17 | 9  | US-09-864-761-37550 | Sequence 37550, A |
| 4 | 22.2 | 17 | 12 | US-10-161-791-338   | Sequence 338, App |
| 4 | 22.2 | 17 | 12 | US-10-161-791-341   | Sequence 341, App |
| 4 | 22.2 | 17 | 15 | US-10-225-567A-1370 | Sequence 1370, Ap |
| 4 | 22.2 | 17 | 15 | US-10-225-567A-1974 | Sequence 1974, Ap |
| 4 | 22.2 | 18 | 9  | US-09-864-761-41948 | Sequence 41948, A |
| 4 | 22.2 | 18 | 15 | US-10-140-372-15    | Sequence 15, Appl |
| 4 | 22.2 | 18 | 15 | US-10-281-652-23    | Sequence 23, Appl |
| 4 | 22.2 | 18 | 15 | US-10-225-567A-1996 | Sequence 1996, Ap |
| 4 | 22.2 | 19 | 10 | US-09-814-550-6     | Sequence 6, Appli |
| 4 | 22.2 | 20 | 15 | US-10-094-401-138   | Sequence 138, App |
| 4 | 22.2 | 20 | 15 | US-10-225-567A-755  | Sequence 755, App |
| 4 | 22.2 | 20 | 15 | US-10-225-567A-1649 | Sequence 1649, Ap |
| 3 | 16.7 | 4  | 8  | US-08-610-220A-8    | Sequence 8, Appli |
| 3 | 16.7 | 4  | 9  | US-09-150-623-8     | Sequence 8, Appli |
| 3 | 16.7 | 4  | 10 | US-09-982-172-156   | Sequence 156, App |
| 3 | 16.7 | 4  | 10 | US-09-877-381-4     | Sequence 4, Appli |
| 3 | 16.7 | 4  | 12 | US-10-226-629A-1    | Sequence 1, Appli |
| 3 | 16.7 | 4  | 12 | US-10-239-991-27    | Sequence 27, Appl |
| 3 | 16.7 | 4  | 14 | US-10-006-630-17    | Sequence 17, Appl |
| 3 | 16.7 | 4  | 14 | US-10-146-221-20    | Sequence 20, Appl |
| 3 | 16.7 | 4  | 15 | US-10-097-534-42    | Sequence 42, Appl |
| 3 | 16.7 | 4  | 15 | US-10-198-677-56    | Sequence 56, Appl |
| 3 | 16.7 | 5  | 9  | US-09-779-233-29    | Sequence 29, Appl |
| 3 | 16.7 | 5  | 9  | US-09-989-789-2     | Sequence 2, Appli |
| 3 | 16.7 | 5  | 9  | US-09-851-271A-7    | Sequence 7, Appli |
| 3 | 16.7 | 5  | 9  | US-09-925-796-5     | Sequence 5, Appli |
| 3 | 16.7 | 5  | 9  | US-09-941-450-5     | Sequence 5, Appli |
| 3 | 16.7 | 5  | 10 | US-09-922-261-70    | Sequence 70, Appl |
| 3 | 16.7 | 5  | 10 | US-09-731-558-3     | Sequence 3, Appli |
| 3 | 16.7 | 5  | 10 | US-09-942-087A-5    | Sequence 5, Appli |
| 3 | 16.7 | 5  | 10 | US-09-942-090-5     | Sequence 5, Appli |
| 3 | 16.7 | 5  | 11 | US-09-995-973-7     | Sequence 7, Appli |
| 3 | 16.7 | 5  | 11 | US-09-846-033B-211  | Sequence 211, App |
| 3 | 16.7 | 5  | 11 | US-09-500-700-67    | Sequence 67, Appl |
| 3 | 16.7 | 5  | 11 | US-09-990-186-2     | Sequence 2, Appli |
| 3 | 16.7 | 5  | 11 | US-09-897-844-5     | Sequence 5, Appli |
| 3 | 16.7 | 5  | 11 | US-09-996-484-7     | Sequence 7, Appli |
| 3 | 16.7 | 5  | 11 | US-09-530-139-13    | Sequence 13, Appl |
| 3 | 16.7 | 5  | 11 | US-09-989-994-2     | Sequence 2, Appli |
| 3 | 16.7 | 5  | 12 | US-10-076-047A-239  | Sequence 239, App |
| 3 | 16.7 | 5  | 12 | US-10-076-047A-284  | Sequence 284, App |
| 3 | 16.7 | 5  | 12 | US-10-303-686A-48   | Sequence 48, Appl |
| 3 | 16.7 | 5  | 12 | US-10-203-754A-1    | Sequence 1, Appli |

89 3 16.7 5 12 US-10-316-253-79 Sequence 79, Appl  
90 3 16.7 5 12 US-10-226-629A-3 Sequence 3, Appl  
91 3 16.7 5 12 US-10-226-629A-4 Sequence 4, Appl  
92 3 16.7 5 12 US-10-226-629A-5 Sequence 5, Appl  
93 3 16.7 5 12 US-10-226-629A-6 Sequence 6, Appl  
94 3 16.7 5 12 US-10-226-629A-7 Sequence 7, Appl  
95 3 16.7 5 12 US-10-226-629A-8 Sequence 8, Appl  
96 3 16.7 5 12 US-10-226-629A-9 Sequence 9, Appl  
97 3 16.7 5 12 US-10-226-629A-10 Sequence 10, Appl  
98 3 16.7 5 12 US-10-226-629A-11 Sequence 11, Appl  
99 3 16.7 5 12 US-10-245-415B-5 Sequence 5, Appl  
100 3 16.7 5 12 US-10-412-105-29 Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-3  
; Sequence 3, Application US/10281652  
; Publication No. US20030091608A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-3

Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e-12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPQVQS 18  
Db 1 DQPPDVEKPDLPQVQS 18

RESULT 2  
US-10-365-908-98  
; Sequence 98, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Steven E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-98

Query Match 27.8%; Score 5; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 2 QPPDV 6  
Db 2 QPPDV 6

RESULT 3  
US-09-572-404B-3027  
; Sequence 3027, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 3027  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETG1 OR RETG2 OR GUC1  
; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with Sequence 3028 in this  
US-09-572-404B-3027

Query Match 27.8%; Score 5; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13  
Db 2 PDLQP 6

RESULT 4  
US-10-080-608A-70  
; Sequence 70, Application US/10080608A  
; Publication No. US20030198956A1  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/10/080,608A  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: human rhinovirus 2  
US-10-080-608A-70

Query Match 27.8%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13  
Db 9 PDLQP 13

```

RESULT 5
US-10-370-685-159
; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF-P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

Query Match 27.8%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13
Db 9 PDLQP 13

RESULT 6
US-09-804-866-12
; Sequence 12, Application US/09804866
; Patent No. US20020001814A1
; GENERAL INFORMATION:
; APPLICANT: Chu, Ivan K.
; APPLICANT: Lau, Tai-Chu
; TITLE OF INVENTION: Sequencing of Peptides by Mass Spectrometry
; FILE REFERENCE: 7933.208-US-UI
; CURRENT APPLICATION NUMBER: US/09/804,866
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/193,208
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Bovine ubiquitin
US-09-804-866-12

Query Match 22.2%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 1 DVEK 4

RESULT 7
US-09-804-866-13
; Sequence 13, Application US/09804866
; Patent No. US20020001814A1
; GENERAL INFORMATION:
; APPLICANT: Chu, Ivan K.
; APPLICANT: Lau, Tai-Chu
; TITLE OF INVENTION: Sequencing of Peptides by Mass Spectrometry
; FILE REFERENCE: 7933.208-US-UI

```

```

; CURRENT APPLICATION NUMBER: US/09/804,866
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/193,208
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bovine ubiquitin
US-09-804-866-13

Query Match 22.2%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 2 DVEK 5

RESULT 8
US-09-727-963A-17
; Sequence 17, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence : peptide
; OTHER INFORMATION: ligand
US-09-727-963A-17

Query Match 22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 3 LQPF 6

RESULT 9
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US20010006639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

```

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/759,960  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/169,425  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Praeger, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08191/004002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-543-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-759-960-17

Query Match 22.2%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||  
Db 4 DLQP 7

RESULT 10  
US-09-829-549A-4  
; Sequence 4, Application US/09829549A  
; Patent No. US20020052484A1  
; GENERAL INFORMATION:  
; APPLICANT: The Curators of the University of Missouri  
; TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES  
; FILE REFERENCE: UMO 1521.1  
; CURRENT APPLICATION NUMBER: US/09/829,549A  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/195,785  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: Random peptide insert  
US-09-829-549A-4

Query Match 22.2%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12  
|||  
Db 3 PDLQ 6

RESULT 11  
US-09-909-460-104  
; Sequence 104, Application US/09909460  
; Publication No. US20020182258A1

; GENERAL INFORMATION:  
; APPLICANT: Lunsford, Lynn B.  
; APPLICANT: Putnam, David  
; APPLICANT: Hedley, Mary Lynn  
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
; TITLE OF INVENTION: ACID  
; FILE REFERENCE: 08191/014001  
; CURRENT APPLICATION NUMBER: US/09/909,460  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-09-909-460-104

Query Match 22.2%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||  
Db 4 DLQP 7

RESULT 12  
US-10-350-258-6  
; Sequence 6, Application US/10350258  
; Publication No. US20030139345A1  
; GENERAL INFORMATION:  
; APPLICANT: MATTHIAS RATH  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AN  
; CURRENT APPLICATION NUMBER: US/10/350,258  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/351,317  
; PRIOR FILING DATE: January 23, 2002  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-350-258-6

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPDV 6  
|||  
Db 2 PPDV 5

RESULT 13  
US-10-365-908-3  
; Sequence 3, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19

;; PRIOR APPLICATION NUMBER: US 60/214,202  
;; PRIOR FILING DATE: 2000-06-26  
;; NUMBER OF SEQ ID NOS: 140  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Human papilloma virus  
US-10-365-908-3

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||  
Db 4 DLQP 7

RESULT 14  
US-10-365-908-80  
;; Sequence 80, Application US/10365908  
;; Publication No. US20030170268A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Neefe, John R.  
;; APPLICANT: Boux, Leslie J.  
;; APPLICANT: Winnett, Mark T.  
;; APPLICANT: Goldstone, Stephen E.  
;; APPLICANT: Siegel, Marvin  
;; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
;; FILE REFERENCE: 12071-003001  
;; CURRENT APPLICATION NUMBER: US/10/365,908  
;; CURRENT FILING DATE: 2003-02-13  
;; PRIOR APPLICATION NUMBER: US/09/891,823  
;; PRIOR FILING DATE: 2001-10-19  
;; PRIOR APPLICATION NUMBER: US 60/214,202  
;; PRIOR FILING DATE: 2000-06-26  
;; NUMBER OF SEQ ID NOS: 140  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 80  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Human papilloma virus  
US-10-365-908-80

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5  
|||  
Db 2 QPPD 5

RESULT 15  
US-10-033-662-36  
;; Sequence 36, Application US/10033662  
;; Publication No. US2003092197A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Herman, et al.  
;; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card  
;; FILE REFERENCE: 9195-081  
;; CURRENT APPLICATION NUMBER: US/10/033,662  
;; CURRENT FILING DATE: 2001-12-27  
;; NUMBER OF SEQ ID NOS: 72  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 36  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-033-662-36

Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
|||  
Db 1 KPDL 4

RESULT 16  
US-10-128-711-66  
;; Sequence 66, Application US/10128711  
;; Publication No. US2003009634A1  
;; GENERAL INFORMATION:  
;; APPLICANT: VITIELLO, Maria A.  
;; CHESTNUT, Robert W.  
;; SETTE, Alessandro D.  
;; CELIS, Esteban  
;; GRAY, Howard  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
;; NUMBER OF SEQUENCES: 153  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Kourie and Crew  
;; STREET: Steuart Street Tower, One Market Plaza  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94105-1493  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/128,711  
;; FILING DATE: 22-Apr-2002  
;; CLASSIFICATION: <unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/197,484  
;; FILING DATE: 16-FEB-1994  
;; APPLICATION NUMBER: US 07/935,811  
;; FILING DATE: 26-AUG-1992  
;; APPLICATION NUMBER: US 07/874,491  
;; FILING DATE: 27-APR-1992  
;; APPLICATION NUMBER: US 07/827,682  
;; FILING DATE: 29-JAN-1992  
;; APPLICATION NUMBER: US 07/749,568  
;; FILING DATE: 26-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 14137-26-4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (206) 623-6793  
;; INFORMATION FOR SEQ ID NO: 66:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-10-128-711-66

Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||  
Db 4 DLQP 7

RESULT 17  
US-10-128-711-71  
; Sequence 71, Application US/10128711  
; Publication No. US20030099634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; CHESTNUT, Robert W.  
; SETTE, Alessandro D.  
; CELIS, Esteban  
; GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; CIL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/128,711  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:  
US-10-128-711-71  
Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 DLQP 13  
Db 3 DLQP 6  
RESULT 18  
US-09-847-185-19  
; Sequence 19, Application US/09847185  
; Patent No. US20020076392A1  
; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/847,185  
; FILING DATE: 01-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/201,931  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 2442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)535-9001  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-847-185-19  
Query Match 22.2%; Score 4; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 DLQP 13  
Db 4 DLQP 7  
RESULT 19  
US-09-835-853-22  
; Sequence 22, Application US/09835853  
; Patent No. US20020165136A1  
; GENERAL INFORMATION:  
; APPLICANT: BASERGA, Renato L.  
; APPLICANT: RESNICOFF, Mariana  
; APPLICANT: HUANG, Ziwei  
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE and DORR LLP  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/835,853



```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/704,344
; APPLICATION NUMBER:
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, Henry N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8459
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-835-853-22

Query Match 22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 20
US-10-177-390-33
; Sequence 33, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Getold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-177-390-33

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 21
US-10-365-908-57
; Sequence 57, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001

```

```

; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-57

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5
Db 5 QPPD 8

RESULT 22
US-10-365-908-104
; Sequence 104, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-104

Query Match 22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPD 5
Db 1 QPPD 4

RESULT 23
US-10-062-710-228
; Sequence 228, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498

```

; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 228  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Epstein-Barr Virus  
US-10-062-710-228

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13  
Db 4 DLQP 7

RESULT 24  
US-10-155-922-82  
; Sequence 82, Application US/1015922  
; Publication No. US20030086893A1  
; GENERAL INFORMATION:  
; APPLICANT: Hirai, Yohei  
; APPLICANT: Oka, Yumiko  
; APPLICANT: Takebe, Kyoko  
; APPLICANT: Tsuda, Hokari  
; APPLICANT: Tochigi, Keiko  
; APPLICANT: Shinagawa, Toko  
; APPLICANT: Murakami, Kayoko  
; APPLICANT: Koshida, Shogo  
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH  
; FILE REFERENCE: 46739200220  
; CURRENT APPLICATION NUMBER: US/10/155,922  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: PCT/JP01/04691  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: JP 2000-166903  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: JP 2001-347340  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: JP 2001-347338  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: JP 2001-371175  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: JP 2001-371366  
; PRIOR FILING DATE: 2001-12-05  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-155-922-82

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKP 9  
Db 2 VEKP 5

RESULT 25  
US-10-133-210-271  
; Sequence 271, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: Delisi, Charles  
; APPLICANT: Berzofsky, Jay

; APPLICANT: Gulukota, Kamalakar  
; APPLICANT: Vaccaro, Dennis  
; APPLICANT: Wang, Zhiping  
; APPLICANT: Zhang, Chao  
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
; TITLE OF INVENTION: COMPOSITIONS THEREOF  
; FILE REFERENCE: BU-035AX  
; CURRENT APPLICATION NUMBER: US/10/133,210  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 271  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-133-210-271

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13  
Db 4 DLQP 7

RESULT 26  
US-10-211-088-67  
; Sequence 67, Application US/10211088  
; Publication No. US20030104479A1  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Binding domain  
US-10-211-088-67

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11  
Db 3 KPDL 6

RESULT 27  
US-10-224-286-19  
; Sequence 19, Application US/10224286  
; Publication No. US20030108517A1  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; COMPRISEING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: CAMPBELL & FLORES, LLP  
;/ STREET: 4370 La Jolla Village Drive, Suite 700  
;/ CITY: San Diego  
;/ STATE: California  
;/ COUNTRY: United States  
;/ ZIP: 92121  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/10/224,286  
;/ FILING DATE: 19-Aug-2002  
;/ CLASSIFICATION: <Unknown>  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/902,516  
;/ FILING DATE: 29-JUL-1997  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Campbell, Cathryn A.  
;/ REGISTRATION NUMBER: 31,815  
;/ REFERENCE/DOCKET NUMBER: P-IM 2442  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (619)535-9001  
;/ TELEFAX: (619)535-8949  
;/ INFORMATION FOR SEQ ID NO: 19:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
;/ US-10-224-286-19

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 10 DLOP 13  
Db 4 DLOP 7

RESULT 28  
US-09-017-743C-122  
; Sequence 122, Application US/09017743C  
; Patent No. US20020177694A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; Southwood, Scott  
; TITLE OF INVENTION: HIA Binding Peptides and Their  
; Uses  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/017,743C  
; FILING DATE: 03-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/590,298

;/ FILING DATE: 23-JAN-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Parent, Annette S.  
;/ REGISTRATION NUMBER: 42,058  
;/ REFERENCE/DOCKET NUMBER: 018623-008050US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415-576-0200  
;/ TELEFAX: 415-576-0300  
;/ TELEX: <Unknown>  
;/ INFORMATION FOR SEQ ID NO: 122:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 11 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 122:  
;/ US-09-017-743C-122

Query Match 22.2%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 8 KPDL 11  
Db 6 KPDL 9

RESULT 29  
US-10-367-405-5  
; Sequence 5, Application US/10367405  
; Publication No. US20030215438A1  
; GENERAL INFORMATION:  
; APPLICANT: Felix Hausch  
; APPLICANT: Gary Gray  
; APPLICANT: Lu Shan  
; APPLICANT: Chaitan Khosla  
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE  
; FILE REFERENCE: STAN-258US1  
; CURRENT APPLICATION NUMBER: US/10/367,405  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: 60/357,238  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: 60/380,761  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 60/392,782  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/422,933  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: 60/428,033  
; PRIOR FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: 60/435,881  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; US-10-367-405-5

Query Match 22.2%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 11 LQPF 14  
Db 2 LQPF 5

RESULT 30  
US-10-062-710-206  
; Sequence 206, Application US/10062710

; Publication No. US20030049253A1

; GENERAL INFORMATION:

; APPLICANT: Li, Frank Q.

; APPLICANT: Chu, Yong-Liang

; APPLICANT: Qiu, Jian-Tai

; TITLE OF INVENTION: Polymeric Conjugates for Delivery of

; TITLE OF INVENTION: MHC-Recognized Epitopes

; TITLE OF INVENTION: Via Peptide Vaccines

; FILE REFERENCE: 3781-001-27

; CURRENT APPLICATION NUMBER: US/10/062,710

; CURRENT FILING DATE: 2002-02-05

; PRIOR APPLICATION NUMBER: US 60/310,498

; PRIOR FILING DATE: 2001-08-08

; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 206

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: T Cell epitopes

US-10-062-710-206

Query Match 22.2%; Score 4; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 10 DLQP 13

Db 5 DLQP 8

RESULT 31

US-10-211-088-69

; Sequence 69, Application US/10211088

; Publication No. US20030104479A1

; GENERAL INFORMATION:

; APPLICANT: Bright, Gary R.

; APPLICANT: Premkumar, D. David

; APPLICANT: Chen, Yih-Tai

; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi

; FILE REFERENCE: 01-1022-US

; CURRENT APPLICATION NUMBER: US/10/211,088

; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: 60/309,395

; PRIOR FILING DATE: 2001-08-01

; PRIOR APPLICATION NUMBER: 60/341,589

; PRIOR FILING DATE: 2001-12-13

; NUMBER OF SEQ ID NOS: 366

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 69

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Binding domain

US-10-211-088-69

Query Match 22.2%; Score 4; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.1e+02; Indels 0;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 8 KPDL 11

Db 4 KPDL 7

RESULT 32

US-08-736-019-164

; Sequence 164, Application US/08736019

; Publication No. US20030207799A1

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew

; APPLICANT: Stroobant, Paul

; APPLICANT: Minghetti, Luisa

; APPLICANT: Waterfield, Michael

; APPLICANT: Marchionni, Mark

; APPLICANT: Chen, Mario

; APPLICANT: Hiles, Ian

; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

; TITLE OF INVENTION: PREPARATION AND USE

; NUMBER OF SEQUENCES: 189

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Clark & Elbing LLP

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible Pentium

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/736,019

; FILING DATE: 22-OCT-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/471,833

; FILING DATE: 06-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/036,555

; FILING DATE: 24-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/965,173

; FILING DATE: 23-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/907,138

; FILING DATE: 30-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/940,389

; FILING DATE: 03-SEP-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/863,703

; FILING DATE: 03-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 91 07566.3

; FILING DATE: 10-APR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Bieker-Brady, Kristina

; REGISTRATION NUMBER: 39,109

; REFERENCE/DOCKET NUMBER: 04585/00200Q

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 428-0200

; TELEFAX: (617) 428-7045

; TELEX:

; INFORMATION FOR SEQ ID NO: 164:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: Xaa in position 1 is unknown.

US-08-736-019-164

Query Match 22.2%; Score 4; DB 7; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 DVEK 8

Db 9 DVEK 12

```

RESULT 33
US-09-954-385-190
; Sequence 190, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetcky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-190

Query Match 22.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
 ||||
Db 2 DLQP 5

RESULT 34
US-10-367-405-1
; Sequence 1, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: PYRROLIDONE CAR
; LOCATION: (1)...(1)
; OTHER INFORMATION: N terminal pyroglutamate
US-10-367-405-2

Query Match 22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
 ||||
Db 2 LQPF 5

RESULT 36
US-10-367-405-14
; Sequence 14, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033

```

```
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: triticum aestivum
US-10-367-405-14

Query Match 22.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LQPF 14
Db 2 LQPF 5

RESULT 37
US-10-075-869-37
; Sequence 37, Application US/10075869
; Publication No. US20030104622A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Gambotto, Andrea
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
; TITLE OF INVENTION: FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR TRANSPORT
; FILE REFERENCE: AP32573-AAA 072396.0237
; CURRENT APPLICATION NUMBER: US/10/075,869
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-10-075-869-37

Query Match 22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 6 DLQP 9

RESULT 38
US-09-935-682-57
; Sequence 57, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified Nucleotid
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25

; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-57

Query Match 22.2%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9
Db 7 VEKP 10

RESULT 39
US-09-880-505-16
; Sequence 16, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-16

Query Match 22.2%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 40
US-09-563-222-139
; Sequence 139, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-139
```

Query Match 22.2%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EKPD 10  
|||||  
Db 4 EKPD 7

## RESULT 41

US-10-282-960-59  
; Sequence 59, Application US/10282960  
; Publication No. US20030143228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Si-Yi  
; APPLICANT: Zhao, You  
; APPLICANT: Schroers, Roland  
; TITLE OF INVENTION: Human telomerase Reverse Transcriptase as a Class-II Restricted T  
; FILE REFERENCE: P02193US1  
; CURRENT APPLICATION NUMBER: US/10/282,960  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: US 60/345,012  
; PRIOR FILING DATE: 2001-10-29  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 59  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human  
US-10-282-960-59

Query Match 22.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
|||||  
Db 3 DLQP 6

## RESULT 42

US-10-051-643-16  
; Sequence 16, Application US/10051643  
; Publication No. US20020197265A1  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Tan, Paul L. J.  
; TITLE OF INVENTION: Methods and Compounds for the Treatment  
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory  
; TITLE OF INVENTION: System using Mycobacterium Vaccae  
; FILE REFERENCE: 11000.1008c2  
; CURRENT APPLICATION NUMBER: US/10/051,643  
; CURRENT FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US09/156,181  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: US 08/996,624  
; PRIOR FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
US-10-051-643-16

Query Match 22.2%; Score 4; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12  
|||||  
Db 4 PDLQ 7

## RESULT 43

US-09-908-322-32  
; Sequence 32, Application US/09908322  
; Patent No. US20020107194A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowitz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/908,322  
; FILING DATE: 17-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-908-322-32

Query Match 22.2%; Score 4; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QVQS 18  
|||||  
Db 6 QVQS 9

## RESULT 44

US-09-783-931-32  
; Sequence 32, Application US/09783931  
; Publication No. US20030073620A1  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowitz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; AND FRAGMENTS

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/783,931  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/981,392  
FILING DATE: 22-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Antlex, Adriane M.  
REGISTRATION NUMBER: 32,605  
REFERENCE/DOCKET NUMBER: 7326-122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-783-931-32

Query Match 22.2%; Score 4; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 QVQS 18  
|||  
Db 6 QVQS 9

RESULT 45  
US-09-864-761-37550  
; Sequence 37550, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aemica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-03-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 37550  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC010681.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
US-09-864-761-37550

Query Match 22.2%; Score 4; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 PDLQ 12  
|||  
Db 8 PDLQ 11

RESULT 46  
US-10-161-791-338  
; Sequence 338, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York



; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 338:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-338  
  
Query Match 22.2%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PDVE 7  
Db 1 PDVE 4  
  
RESULT 47  
US-10-161-791-341  
; Sequence 341, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 341:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-341  
  
Query Match 22.2%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PDVE 7  
Db 13 PDVE 16  
  
RESULT 48  
US-10-225-567A-1370  
; Sequence 1370, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1370  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-225-567A-1370  
  
Query Match 22.2%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 PDLQ 12  
Db 8 PDLQ 11  
  
RESULT 49  
US-10-225-567A-1974  
; Sequence 1974, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1974
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1974

Query Match
Best Local Similarity 22.2%; Score 4; DB 15; Length 17;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVE 7
Db 1 PDVE 4

RESULT 50
US-09-864-761-41948
; Sequence 41948, Application US/09864761
; Publication No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41948
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

```
; OTHER INFORMATION: MAP TO AC002477.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EST_HUMAN HIT: AA906517.1, EVALUATE 7.00e-04
US-09-864-761-41948
```

```
Query Match
Best Local Similarity 22.2%; Score 4; DB 9; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 9 PDLQ 12
Db 14 PDLQ 17
```

## RESULT 51

```
US-10-140-372-15
; Sequence 15, Application US/10140372
; Publication No. US20030021789A1
; GENERAL INFORMATION:
; APPLICANT: XU, Yi
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: SURFACE PROTEINS FROM GRAM-POSITIVE BACTERIA
; FILE REFERENCE: P07196US01/BAS
; CURRENT APPLICATION NUMBER: US/10/140,372
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,132
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-140-372-15
```

```
Query Match
Best Local Similarity 22.2%; Score 4; DB 15; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 6 VEKP 9
Db 6 VEKP 9
```

## RESULT 52

```
US-10-281-652-23
; Sequence 23, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-23

Query Match 22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 6 DVEK 9

RESULT 53
US-10-225-567A-1996
; Sequence 1996, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1996
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1996

Query Match 22.2%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 11 PDLQ 14

RESULT 54
US-09-814-550-6
; Sequence 6, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-6
```

```

Query Match 22.2%; Score 4; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 3 PDLQ 6

RESULT 55
US-10-094-401-138
; Sequence 138, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Cohen, Edward H.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
; CURRENT APPLICATION NUMBER: US/10/094,401
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/331,352
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/292,975
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: albumin binding peptide
US-10-094-401-138

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 7 PDLQ 10

RESULT 56
US-10-225-567A-755
; Sequence 755, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 755
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-755

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PDVE 7
```

```
Db |||||
 7 PDVE 10

RESULT 57
US-10-225-567A-1649
; Sequence 1649, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1649
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1649

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
 |||||
Db 14 DVEK 17

RESULT 58
US-08-610-220A-8
; Sequence 8, Application US/08610220A
; Publication No. US20030099638A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,220A
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Query Match 16.7%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVE 7
 |||||
Db 1 DVE 3

RESULT 60
US-09-982-172-156
; Sequence 156, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
```

```

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-156

Query Match 16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEK 8
 |||
Db 2 VEK 4

RESULT 61
US-09-877-381-4
; Sequence 4, Application US/09877381
; Patent No. US20020146796A1
; GENERAL INFORMATION:
; APPLICANT: Richard Drake
; APPLICANT: Trenton Hinds
; APPLICANT: Cesar Compadre
; APPLICANT: Barry Hurlburt
; APPLICANT: Tammy Rechtin
; TITLE OF INVENTION: Mutated Herpes Simplex Virus Type I Thymidine
; TITLE OF INVENTION: Kinases and Uses Thereof
; FILE REFERENCE: D6128
; CURRENT APPLICATION NUMBER: US/09/877,381
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 09/338,308
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: a peptide substrate used for a colorimetric assay
US-09-877-381-4

Query Match 16.7%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVE 7
 |||
Db 1 DVE 3

RESULT 62
US-10-226-629A-1
; Sequence 1, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182

```

```

; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Equine infectious anemia virus
US-10-226-629A-1

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
 |||
Db 2 PDL 4

RESULT 63
US-10-299-991-27
; Sequence 27, Application US/10299991
; Publication No. US20030194725A1
; GENERAL INFORMATION:
; APPLICANT: Greener et al.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AND VALIDATING POTENTIAL DRUG TARGETS
; FILE REFERENCE: PROL-P01-004
; CURRENT APPLICATION NUMBER: US/10/299,991
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/331701
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Retroviral
US-10-299-991-27

Query Match 16.7%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDL 11
 |||
Db 2 PDL 4

RESULT 64
US-10-006-630-17
; Sequence 17, Application US/10006630
; Publication No. US20020150926A1
; GENERAL INFORMATION:
; APPLICANT: Jindal, Satish
; APPLICANT: Regnier, Fred
; APPLICANT: Evans, David
; APPLICANT: Williams, Kevin
; APPLICANT: Afeyan, No. US20020150926A1bar
; APPLICANT: Paliwal, Sandeep
; APPLICANT: Pingali, Aruna
; TITLE OF INVENTION: High Speed, automated, continuous flow,
; TITLE OF INVENTION: multi-dimensional molecular selection and analysis
; FILE REFERENCE: SYP-101DV
; CURRENT APPLICATION NUMBER: US/10/006,630
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 09/267,993
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/000,518
; PRIOR FILING DATE: 1995-06-26
; PRIOR APPLICATION NUMBER: 08/670,670
; PRIOR FILING DATE: 1996-06-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17

```

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif with
; OTHER INFORMATION: similarity to TVTEK
US-10-006-630-17

Query Match 16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEK 8
 |||
Db 2 VEK 4

RESULT 65
US-10-146-221-20
; Sequence 20, Application US/10146221
; Publication No. US20020173006A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers
; FILE REFERENCE: 019496-002510US
; CURRENT APPLICATION NUMBER: US/10/146,221
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/260,629
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: linker sequence
US-10-146-221-20

Query Match 16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
 |||
Db 2 EXP 4

RESULT 66
US-10-097-534-42
; Sequence 42, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; TITLE OF INVENTION: MATURATION
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: Gag protein motif
US-10-097-534-42

Query Match 16.7%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDL 11
 |||
Db 2 PDL 4

RESULT 67
US-10-198-677-56
; Sequence 56, Application US/10198677
; Publication No. US20030119023A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: MOORE, Michael
; APPLICANT: KLUG, Aaron
; TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
; TITLE OF INVENTION: FLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 8325-2011 / G11-US1
; CURRENT APPLICATION NUMBER: US/10/198,677
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: canonical linker
; OTHER INFORMATION: sequence variant
US-10-198-677-56

Query Match 16.7%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 EXP 9
 |||
Db 2 EXP 4

RESULT 68
US-09-779-233-29
; Sequence 29, Application US/09779233
; Patent No. US20020045158A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-779-233-29

Query Match 16.7%; Score 3; DB 9; Length 5;
```

Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 7 EXP 9  
Db 3 EXP 5

## RESULT 69

US-09-989-789-2  
; Sequence 2, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Oiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide linker  
US-09-989-789-2

Query Match 16.7%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 7 EXP 9  
Db 3 EXP 5

## RESULT 70

US-09-851-271A-7  
; Sequence 7, Application US/09851271A  
; Patent No. US20020064824A1  
; GENERAL INFORMATION:  
; APPLICANT: Gendag Limited  
; TITLE OF INVENTION: Screening System  
; FILE REFERENCE: 674538-2003  
; CURRENT APPLICATION NUMBER: US/09/851,271A  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: PCT/GB99/03730  
; PRIOR FILING DATE: 1999-11-09  
; PRIOR APPLICATION NUMBER: GB9824544.2  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(5)  
; OTHER INFORMATION: linker  
US-09-851-271A-7

Query Match 16.7%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 7 EXP 9  
Db 3 EXP 5

## RESULT 71

US-09-925-796-5  
; Sequence 5, Application US/09925796  
; Patent No. US20020081614A1  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Zhang, Lei  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins  
; FILE REFERENCE: 019496-002000US  
; CURRENT APPLICATION NUMBER: US/09/925,796  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/395,448  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/229,037  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: linker  
US-09-925-796-5

Query Match 16.7%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 7 EXP 9  
Db 3 EXP 5

## RESULT 72

US-09-941-450-5  
; Sequence 5, Application US/09941450  
; Patent No. US20020094529A1  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey C.  
; APPLICANT: Urnov, Fyodor  
; TITLE OF INVENTION: GENE IDENTIFICATION  
; FILE REFERENCE: S7.US3 / 8325-0007.20  
; CURRENT APPLICATION NUMBER: US/09/941,450  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 09/395,448  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: linker  
US-09-941-450-5

Query Match 16.7%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 7 EXP 9  
Db 3 EXP 5

## RESULT 73

US-09-922-261-70  
; Sequence 70, Application US/09922261  
; Patent No. US2002011471A1  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.

```
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-70
```

```
Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 PDV 6
 |||
Db 3 PDV 5
```

## RESULT 74

```
US-09-731-558-3
; Sequence 3, Application US/09731558
; Patent No. US20020146691A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; TITLE OF INVENTION: Proteins for the Identification of Gene Function
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:flexible
; OTHER INFORMATION: polypeptide linker
US-09-731-558-3
```

```
Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 EXP 9
 |||
Db 3 EXP 5
```

## RESULT 75

```
US-09-942-087A-5
; Sequence 5, Application US/09942087A
; Patent No. US20020160940A1
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
```

```
; APPLICANT: Wolffe, Alan
; APPLICANT: Urtov, Fyodor
; APPLICANT: Lai, Albert
; APPLICANT: Snowden, Andrew
; APPLICANT: Tan, Siyuan
; APPLICANT: Gregory, Philip
; TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; FILE REFERENCE: 8325-0002.21 / S2-US5
; CURRENT APPLICATION NUMBER: US/09/942,087A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/229,037
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:linker
US-09-942-087A-5
```

```
Query Match 16.7%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 7 EXP 9
 |||
Db 3 EXP 5
```

```
Search completed: November 25, 2003, 20:25:28
Job time : 37.8085 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 19.6277 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-3  
Perfect score: 18  
Sequence: 1 DQPPVEXKPLQFFQVQS 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description        |
|------------|-------|-------------|--------|-------------------|--------------------|
| 1          | 18    | 100.0       | 18     | US-09-641-803-3   | Sequence 3, Appli  |
| 2          | 5     | 27.8        | 15     | US-09-914-259-70  | Sequence 70, Appli |
| 3          | 5     | 27.8        | 19     | US-08-781-420-4   | Sequence 4, Appli  |
| 4          | 5     | 27.8        | 19     | US-08-874-102-4   | Sequence 4, Appli  |
| 5          | 5     | 27.8        | 19     | US-08-984-919A-4  | Sequence 4, Appli  |
| 6          | 5     | 27.8        | 19     | US-09-006-595A-4  | Sequence 4, Appli  |
| 7          | 5     | 27.8        | 20     | US-08-447-430A-30 | Sequence 30, Appli |
| 8          | 5     | 27.8        | 20     | US-09-342-673-30  | Sequence 30, Appli |
| 9          | 4     | 22.2        | 4      | US-08-810-720-12  | Sequence 12, Appli |
| 10         | 4     | 22.2        | 5      | US-09-202-832-6   | Sequence 6, Appli  |
| 11         | 4     | 22.2        | 6      | PCT-US93-12679-11 | Sequence 11, Appli |
| 12         | 4     | 22.2        | 8      | US-07-923-724-48  | Sequence 48, Appli |
| 13         | 4     | 22.2        | 8      | US-08-609-426A-48 | Sequence 48, Appli |
| 14         | 4     | 22.2        | 8      | US-08-374-652C-38 | Sequence 38, Appli |
| 15         | 4     | 22.2        | 9      | US-08-078-176-9   | Sequence 9, Appli  |
| 16         | 4     | 22.2        | 9      | US-08-078-176-10  | Sequence 10, Appli |
| 17         | 4     | 22.2        | 9      | US-08-078-175-4   | Sequence 4, Appli  |
| 18         | 4     | 22.2        | 9      | US-08-217-188A-62 | Sequence 62, Appli |
| 19         | 4     | 22.2        | 9      | US-08-687-326-62  | Sequence 62, Appli |
| 20         | 4     | 22.2        | 9      | US-08-787-547-104 | Sequence 104, App  |
| 21         | 4     | 22.2        | 9      | US-08-948-378A-17 | Sequence 17, Appli |
| 22         | 4     | 22.2        | 9      | US-08-667-725B-62 | Sequence 67, Appli |
| 23         | 4     | 22.2        | 9      | US-09-007-748-62  | Sequence 62, Appli |
| 24         | 4     | 22.2        | 9      | US-09-169-425C-17 | Sequence 17, Appli |
| 25         | 4     | 22.2        | 9      | US-08-197-484-66  | Sequence 66, Appli |
| 26         | 4     | 22.2        | 9      | US-08-197-484-71  | Sequence 71, Appli |
| 27         | 4     | 22.2        | 9      | US-09-759-960-17  | Sequence 17, Appli |

|     |   |      |    |   |                     |                    |
|-----|---|------|----|---|---------------------|--------------------|
| 28  | 4 | 22.2 | 9  | 5 | PCT-US95-02121-66   | Sequence 66, Appli |
| 29  | 4 | 22.2 | 9  | 5 | PCT-US95-02121-71   | Sequence 71, Appli |
| 30  | 4 | 22.2 | 10 | 2 | US-08-538-387A-25   | Sequence 25, Appli |
| 31  | 4 | 22.2 | 10 | 2 | US-08-538-387A-26   | Sequence 26, Appli |
| 32  | 4 | 22.2 | 10 | 2 | US-08-902-516-19    | Sequence 19, Appli |
| 33  | 4 | 22.2 | 10 | 2 | US-08-723-423-25    | Sequence 25, Appli |
| 34  | 4 | 22.2 | 10 | 2 | US-08-723-423-26    | Sequence 26, Appli |
| 35  | 4 | 22.2 | 10 | 3 | US-08-709-435-25    | Sequence 25, Appli |
| 36  | 4 | 22.2 | 10 | 3 | US-08-709-435-26    | Sequence 26, Appli |
| 37  | 4 | 22.2 | 10 | 3 | US-08-567-746A-25   | Sequence 26, Appli |
| 38  | 4 | 22.2 | 10 | 3 | US-08-567-746A-26   | Sequence 26, Appli |
| 39  | 4 | 22.2 | 10 | 3 | US-08-633-410-25    | Sequence 25, Appli |
| 40  | 4 | 22.2 | 10 | 3 | US-08-633-410-26    | Sequence 26, Appli |
| 41  | 4 | 22.2 | 10 | 3 | US-08-704-344-22    | Sequence 22, Appli |
| 42  | 4 | 22.2 | 10 | 3 | US-08-711-426-25    | Sequence 25, Appli |
| 43  | 4 | 22.2 | 10 | 3 | US-08-711-426-26    | Sequence 26, Appli |
| 44  | 4 | 22.2 | 10 | 4 | US-08-669-252-25    | Sequence 25, Appli |
| 45  | 4 | 22.2 | 10 | 4 | US-08-669-252-26    | Sequence 26, Appli |
| 46  | 4 | 22.2 | 10 | 4 | US-09-098-122-25    | Sequence 25, Appli |
| 47  | 4 | 22.2 | 10 | 4 | US-09-098-122-26    | Sequence 26, Appli |
| 48  | 4 | 22.2 | 10 | 4 | US-09-847-185-19    | Sequence 19, Appli |
| 49  | 4 | 22.2 | 10 | 6 | 516058-8            | Patent No. 516058  |
| 50  | 4 | 22.2 | 12 | 1 | US-08-036-555B-164  | Sequence 164, App  |
| 51  | 4 | 22.2 | 12 | 1 | US-08-469-569-164   | Sequence 164, App  |
| 52  | 4 | 22.2 | 12 | 1 | US-08-249-322A-164  | Sequence 164, App  |
| 53  | 4 | 22.2 | 12 | 1 | US-08-469-526A-164  | Sequence 164, App  |
| 54  | 4 | 22.2 | 12 | 2 | US-08-734-591A-164  | Sequence 164, App  |
| 55  | 4 | 22.2 | 12 | 2 | US-08-469-660-164   | Sequence 164, App  |
| 56  | 4 | 22.2 | 12 | 3 | US-08-470-335-164   | Sequence 164, App  |
| 57  | 4 | 22.2 | 12 | 3 | US-08-735-021-164   | Sequence 164, App  |
| 58  | 4 | 22.2 | 12 | 3 | US-08-734-664A-164  | Sequence 164, App  |
| 59  | 4 | 22.2 | 12 | 3 | US-08-470-339-164   | Sequence 164, App  |
| 60  | 4 | 22.2 | 12 | 4 | US-08-467-602-164   | Sequence 164, App  |
| 61  | 4 | 22.2 | 12 | 4 | US-09-555-352-16    | Sequence 16, Appli |
| 62  | 4 | 22.2 | 12 | 5 | PCT-US94-05083C-160 | Sequence 160, App  |
| 63  | 4 | 22.2 | 15 | 2 | US-08-687-956A-164  | Sequence 3, Appli  |
| 64  | 4 | 22.2 | 15 | 2 | US-08-997-080-16    | Sequence 16, Appli |
| 65  | 4 | 22.2 | 15 | 2 | US-08-997-362-16    | Sequence 16, Appli |
| 66  | 4 | 22.2 | 15 | 3 | US-08-873-970-16    | Sequence 16, Appli |
| 67  | 4 | 22.2 | 15 | 3 | US-09-095-855-16    | Sequence 16, Appli |
| 68  | 4 | 22.2 | 15 | 3 | US-08-705-347A-16   | Sequence 16, Appli |
| 69  | 4 | 22.2 | 15 | 4 | US-09-324-542-16    | Sequence 16, Appli |
| 70  | 4 | 22.2 | 15 | 4 | US-09-205-426-16    | Sequence 16, Appli |
| 71  | 4 | 22.2 | 15 | 4 | US-09-200-643-16    | Sequence 16, Appli |
| 72  | 4 | 22.2 | 15 | 4 | US-07-145-002B-62   | Sequence 62, Appli |
| 73  | 4 | 22.2 | 16 | 1 | US-07-942-245-77    | Sequence 77, Appli |
| 74  | 4 | 22.2 | 16 | 1 | US-07-942-245-92    | Sequence 92, Appli |
| 75  | 4 | 22.2 | 16 | 1 | US-07-942-245-93    | Sequence 93, Appli |
| 76  | 4 | 22.2 | 16 | 1 | US-08-615-942A-9    | Sequence 9, Appli  |
| 77  | 4 | 22.2 | 16 | 3 | US-08-750-145A-8    | Sequence 8, Appli  |
| 78  | 4 | 22.2 | 16 | 3 | US-08-975-698A-5    | Sequence 5, Appli  |
| 79  | 4 | 22.2 | 16 | 3 | US-09-361-434-2     | Sequence 2, Appli  |
| 80  | 4 | 22.2 | 16 | 3 | US-09-417-090-5     | Sequence 5, Appli  |
| 81  | 4 | 22.2 | 16 | 3 | US-08-981-392-32    | Sequence 32, Appli |
| 82  | 4 | 22.2 | 16 | 4 | US-09-727-578-5     | Sequence 5, Appli  |
| 83  | 4 | 22.2 | 16 | 4 | US-09-635-025-2     | Sequence 2, Appli  |
| 84  | 4 | 22.2 | 16 | 4 | US-09-433-466-3     | Sequence 3, Appli  |
| 85  | 4 | 22.2 | 17 | 1 | US-08-370-567-24    | Sequence 24, Appli |
| 86  | 4 | 22.2 | 17 | 1 | US-08-438-759-24    | Sequence 24, Appli |
| 87  | 4 | 22.2 | 17 | 1 | US-08-729-152-46    | Sequence 46, Appli |
| 88  | 4 | 22.2 | 17 | 3 | US-09-195-666A-21   | Sequence 21, Appli |
| 89  | 4 | 22.2 | 17 | 3 | US-08-836-922-18    | Sequence 18, Appli |
| 90  | 4 | 22.2 | 17 | 3 | US-08-602-999A-338  | Sequence 338, App  |
| 91  | 4 | 22.2 | 17 | 3 | US-08-602-999A-341  | Sequence 341, App  |
| 92  | 4 | 22.2 | 17 | 4 | US-09-635-705-21    | Sequence 21, Appli |
| 93  | 4 | 22.2 | 17 | 4 | US-09-500-124-338   | Sequence 338, App  |
| 94  | 4 | 22.2 | 17 | 4 | US-09-500-124-341   | Sequence 341, App  |
| 95  | 4 | 22.2 | 17 | 4 | US-09-634-858A-21   | Sequence 21, Appli |
| 96  | 4 | 22.2 | 17 | 4 | US-08-869-927C-21   | Sequence 21, Appli |
| 97  | 4 | 22.2 | 17 | 4 | US-08-869-927C-21   | Sequence 21, Appli |
| 98  | 4 | 22.2 | 17 | 4 | PCT-US94-05684-24   | Sequence 24, Appli |
| 99  | 4 | 22.2 | 18 | 2 | US-08-929-922B-11   | Sequence 11, Appli |
| 100 | 4 | 22.2 | 18 | 2 |                     |                    |

ALIGNMENTS

```

RESULT 1
US-09-641-803-3
; Sequence 3, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-3

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPQFQVQS 18
 |||||
DB 1 DQPPDVEKPDLPQFQVQS 18

RESULT 2
US-09-914-259-70
; Sequence 70, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-09-914-259-70

Query Match 27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQP 13
 |||||
DB 9 PDLQP 13

RESULT 3
US-08-781-420-4
; Sequence 4, Application US/08781420
; Patent No. 6248872
```

```

; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Mehta, Kapil
; TITLE OF INVENTION: Parasitic Nematode Transglutaminase
; TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,420
; FILING DATE: December 3, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-420-4

Query Match 27.8%; Score 5; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17
 |||||
DB 11 PFQVQ 15

RESULT 4
US-08-874-102-4
; Sequence 4, Application US/08874102
; Patent No. 6309644
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Kapil Mehta
; TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/874,102  
FILING DATE: 12-JUN-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: HW-2-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-874-102-4

Query Match 27.8%; Score 5; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17  
Db 11 PFQVQ 15

RESULT 5  
US-08-984-919A-4  
Sequence 4, Application US/08984919A  
Patent No. 6383774  
GENERAL INFORMATION:  
APPLICANT: Chandrashekar, Ramaswamy  
APPLICANT: Mehta, Kapil  
TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE  
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Hesk Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,919A  
FILING DATE: 04-DEC-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: HW-2-C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-984-919A-4

Query Match 27.8%; Score 5; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17  
Db 11 PFQVQ 15

RESULT 6  
US-09-006-595A-4  
Sequence 4, Application US/09006595A  
Patent No. 6414115  
GENERAL INFORMATION:  
APPLICANT: Chandrashekar, Ramaswamy  
APPLICANT: Mehta, Kapil  
TITLE OF INVENTION: Parasitic Nematode Transglutaminase  
Proteins, Nucleic Acid Molecules and  
Uses Thereof  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Hesk Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,595A  
FILING DATE: 13-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/781,420  
FILING DATE: December 3, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: HW-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-006-595A-4

Query Match 27.8%; Score 5; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQVQ 17  
Db 11 PFQVQ 15

RESULT 7  
US-08-447-430A-30  
Sequence 30, Application US/08447430A  
Patent No. 5916558  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Recombinant polypeptides and peptides,  
TITLE OF INVENTION: nucleic acids coding for the same and use of these  
TITLE OF INVENTION: polypeptides and peptides in the diagnostic of  
TITLE OF INVENTION: tuberculosis.  
NUMBER OF SEQUENCES: 43

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,430A
; FILING DATE:
; CLASSIFICATION: 424
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-447-430A-30

Query Match 27.8%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDLQ 12
Db 1 KPDLQ 5

RESULT 8
US-09-342-673-30
; Sequence 30, Application US/09342673
; Patent No. 6531138
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant polypeptides and peptides,
; TITLE OF INVENTION: nucleic acids coding for the same and use of these
; TITLE OF INVENTION: polypeptides and peptides in the diagnostic of
; TITLE OF INVENTION: tuberculosis.
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342.673
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/447,430
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-09-342-673-30

Query Match 27.8%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDLQ 12
Db 1 KPDLQ 5

RESULT 9
US-08-810-720-12
; Sequence 12, Application US/08810720
; Patent No. 6037527
; GENERAL INFORMATION:

```

```

; APPLICANT: Barton, Kenneth A.
; APPLICANT: Umbeck, Paul F.
; TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay
; STREET: One South Finckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,720
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 670513.90163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608/251-5000
; TELEFAX: 608/251-9166
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-810-720-12

Query Match 22.2%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DOPP 4
Db 1 DOPP 4

RESULT 10
US-09-202-832-6
; Sequence 6, Application US/09202832
; Patent No. 6194190
; GENERAL INFORMATION:
; APPLICANT: IZU, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,832
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa = N-acetyl-glycine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide
; US-09-202-832-6

```

```

Query Match 22.2%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 2 DVEK 5

RESULT 11
PCT-US93-12679-11
; Sequence 11, Application PC/TUS9312679
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
; TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHELDON & MAK
; STREET: 401 Florence Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12679
; FILING DATE: 30-DEC-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cranfill, Raymond B
; REGISTRATION NUMBER: 32,845
; REFERENCE/DOCKET NUMBER: RATH-10016PC
; TELEPHONE: 415-322-5333
; TELEFAX: 415-322-5499
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-12679-11

```

```

Query Match 22.2%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 EKPD 10
Db 3 EKPD 6

```

```

RESULT 12
US-07-923-724-48
; Sequence 48, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.

```

```

; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,724
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0240004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-07-923-724-48

```

```

Query Match 22.2%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 13 PFQV 16
Db 4 PFQV 7

```

```

RESULT 13
US-08-609-426A-48
; Sequence 48, Application US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-609-426A-48

```

```

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 13 PPOV 16
 |||||
Db 4 PPOV 7

```

```

RESULT 14
US-08-374-652C-38
; Sequence 38, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-374-652C-38

```

```

Query Match 22.2%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 13 PPOV 16
 |||||
Db 4 PPOV 7

```

```

RESULT 15
US-08-078-176-9
; Sequence 9, Application US/08078176
; Patent No. 549784
; GENERAL INFORMATION:
; APPLICANT: BIRD, Colin R.
; APPLICANT: RAY, John A.
; APPLICANT: SCHUCH, Wolfgang W.
; TITLE OF INVENTION: PLANT DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,176
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9027616.3
; FILING DATE: 20-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/11372
; FILING DATE: 19-DEC-1991

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200889/SEE36096A/USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-078-176-9

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 6 KPDL 9

RESULT 17
US-08-078-175-4
; Sequence 4, Application US/08078175
; Patent No. 5484906
; GENERAL INFORMATION:
; APPLICANT: BIRD, Colin R.
; APPLICANT: RAY, John A.
; APPLICANT: SCHUCH, Wolfgang W.
; TITLE OF INVENTION: DNA, DNA CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,175
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9027616.3
; FILING DATE: 20-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/02272
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200621/SEE36096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-078-175-4

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 6 KPDL 9

RESULT 18
US-08-217-188A-62
; Sequence 62, Application US/08217188A

; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200889/SEE36096A/USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```

; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Faller, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 19
US-08-687-226-62
; Sequence 62, Application US/08687225
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Faller, Thierry
; APPLICANT: Boon-Faller, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

```

```

; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 3 DLQP 6

RESULT 20
US-08-787-547-104
; Sequence 104, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

```



```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-104

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 21
US-08-948-378A-17
; Sequence 17, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-948-378A-17

Query Match 22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7

RESULT 22
US-08-667-725B-62
; Sequence 62, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

```

US-09-169-425C-17  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/007,748  
; FILING DATE: 15 January 1998  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 6147187man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 318-3000  
; TELEFAX: (212) 752-5958  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acid residues  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-007-748-62  
Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Oy 10 DLQP 13  
Db 3 DLQP 6  
RESULT 24  
US-09-169-425C-17  
; Sequence 17, Application US/09169425C  
; Patent No. 6183746  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chic, Roman M.  
; APPLICANT: Collins, Edward J.  
; APPLICANT: Hedley, Mary Lynn  
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/169,425C  
; FILING DATE: 09-OCT-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/061,657  
; FILING DATE: 09-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08191/004002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-543-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-09-169-425C-17  
Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Oy 10 DLQP 13  
Db 4 DLQP 7  
RESULT 25  
US-08-197-484-66  
; Sequence 66, Application US/08197484  
; Patent No. 6419331  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-197-484-66  
Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Oy 10 DLQP 13

```
Db 4 DLQP 7
|||||
RESULT 26
US-08-197-484-71
; Sequence 71, Application US/08197484
; Patent No. 641931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-71

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
|||||
Db 3 DLQP 6

RESULT 27
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiczo, Roman M.
; APPLICANT: COLLINS, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-960-17

Query Match 22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
|||||
Db 4 DLQP 7

RESULT 28
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US95-02121-66

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
Db 4 DLQP 7

RESULT 29  
PCT-US95-02121-71  
Sequence 71, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US95-02121-71

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
Db 3 DLQP 6

RESULT 30  
US-08-538-387A-25  
Sequence 25, Application US/08538387A  
Patent No. 5874214  
GENERAL INFORMATION:  
APPLICANT: No. 5874214a, Michael Phillip  
APPLICANT: Senyei, Andrew E.  
APPLICANT: David, Gary S.  
TITLE OF INVENTION: REMOTELY PROGRAMMABLE  
TITLE OF INVENTION: MATRICES WITH MEMORIES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/538,387A  
FILING DATE: 03-OCT-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/473,660  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,196  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,504  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,486  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,147  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/428,662  
FILING DATE: 04/25/95  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6444-300G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
TELEX:

```
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
US-08-538-387A-25

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 31
US-08-538-387A-26
/ Sequence 26, Application US/08538387A
/ Patent No. 5874214
/ GENERAL INFORMATION:
/ APPLICANT: No. 5874214a, Michael Phillip
/ APPLICANT: Senyei, Andrew E.
/ APPLICANT: David, Gary S.
/ TITLE OF INVENTION: REMOTELY PROGRAMMABLE
/ TITLE OF INVENTION: MATRICES WITH MEMORIES
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Brown, Martin, Haller & McClain
/ STREET: 1660 Union Street
/ CITY: San Diego
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92101-2926
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/538,387A
/ FILING DATE: 03-OCT-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/473,660
/ FILING DATE: 06/07/95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/480,196
/ FILING DATE: 06/07/95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/484,504
/ FILING DATE: 06/07/95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/484,486
/ FILING DATE: 06/07/95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/480,147
/ FILING DATE: 06/07/95
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/428,662
/ FILING DATE: 04/25/95
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 6444-300G
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-238-0999

/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
US-08-538-387A-26

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 32
US-08-902-516-19
/ Sequence 19, Application US/08902516
/ Patent No. 5891432
/ GENERAL INFORMATION:
/ APPLICANT: Soo Hoo, William
/ TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
/ TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
/ TITLE OF INVENTION: RESPONSE USING SAME
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CAMPBELL & FLORES, LLP
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/902,516
/ FILING DATE: 29-JUL-1997
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-IM 2442
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619)535-9001
/ TELEFAX: (619)535-8949
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-902-516-19

Query Match 22.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 4 DLQP 7
```

RESULT 33  
US-08-723-423-25  
; Sequence 25, Application US/08723423  
; Patent No. 5961923  
; GENERAL INFORMATION:  
; APPLICANT: No. 5961923a, Michael Phillip  
; APPLICANT: Parandoosh, Zahra  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: Xiao, Xiao-Yi  
; APPLICANT: David, Gary S.  
; APPLICANT: Yozo, Satoda  
; APPLICANT: Zhao, Chanfeng  
; APPLICANT: Potash, Hanan  
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,423  
; FILING DATE: 09/30/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 09/06/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 09/05/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/669,252  
; FILING DATE: 06/24/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/633,410  
; FILING DATE: 06/10/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06145  
; FILING DATE: 04/25/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/639,813  
; FILING DATE: 04/02/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/567,746  
; FILING DATE: 12/05/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/538,387  
; FILING DATE: 10/03/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/473,660  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,196  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/480,147  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,662  
; FILING DATE: 04/25/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6444-302E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-723-423-25  
Query Match 22.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KPDL 11  
Db 7 KPDL 10  
RESULT 34  
US-08-723-423-26  
; Sequence 26, Application US/08723423  
; Patent No. 5961923  
; GENERAL INFORMATION:  
; APPLICANT: No. 5961923a, Michael Phillip  
; APPLICANT: Parandoosh, Zahra  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: Xiao, Xiao-Yi  
; APPLICANT: David, Gary S.  
; APPLICANT: Yozo, Satoda  
; APPLICANT: Zhao, Chanfeng  
; APPLICANT: Potash, Hanan  
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,423  
; FILING DATE: 09/30/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 09/06/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 08/669,252  
FILING DATE: 06/24/96  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 08/633,410  
FILING DATE: 06/10/96  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: PCT/US96/06145  
FILING DATE: 04/25/96  
PRIOR APPLICATION DATA: 08/639,813  
FILING DATE: 04/02/96  
PRIOR APPLICATION DATA: 08/567,746  
FILING DATE: 12/05/95  
PRIOR APPLICATION DATA: 08/538,387  
FILING DATE: 10/03/95  
PRIOR APPLICATION DATA: 08/473,660  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA: 08/480,196  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA: 08/484,504  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA: 08/484,486  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA: 08/480,147  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA: 08/428,662  
FILING DATE: 04/25/95  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6444-302E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-723-423-26

Query Match 22.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11  
Db 7 KPDL 10

RESULT 35  
US-08-709-435-25  
Sequence 25, Application US/08709435  
Patent No. 6017496

GENERAL INFORMATION:  
APPLICANT: No. 6017496a, Michael Phillip  
APPLICANT: Zahra Parandoosh  
APPLICANT: Senyei, Andrew E.  
APPLICANT: Xiao, Xiao-Yi  
APPLICANT: David, Gary S.  
APPLICANT: Yozo, Satoda  
APPLICANT: Zhao, Chanfeng  
APPLICANT: Potash, Hanan  
TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,435  
FILING DATE: 09/06/96  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,252  
FILING DATE: 06/24/96  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/633,410  
FILING DATE: 06/10/96  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/06145  
FILING DATE: 04/25/96  
APPLICATION NUMBER: 08/639,813  
FILING DATE: 04/02/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/567,746  
FILING DATE: 12/05/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/538,387  
FILING DATE: 10/03/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/473,660  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,196  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,504  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,486  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,147  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/428,662  
FILING DATE: 04/25/95  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6444-302D

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-709-435-25

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No.1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11  
Db 7 KPDL 10

## RESULT 36

US-08-709-435-26  
; Sequence 26, Application US/08709435  
; Patent No. 6017496  
; GENERAL INFORMATION:  
; APPLICANT: NO. 6017496a, Michael Phillip  
; APPLICANT: Zahra Parandoosh  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: Xiao, Xiao-Yi  
; APPLICANT: David, Gary S.  
; APPLICANT: Yozo, Satoda  
; APPLICANT: Zhao, Chanfeng  
; APPLICANT: Potash, Hanan  
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/709,435  
; FILING DATE: 09/06/96  
; CLASSIFICATION: 422  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 09/05/96  
; CLASSIFICATION: 422  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/669,252  
; FILING DATE: 06/24/96  
; CLASSIFICATION: 422  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/633,410  
; FILING DATE: 06/10/96  
; CLASSIFICATION: 422  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06145  
; FILING DATE: 04/25/96  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/639,813  
; FILING DATE: 04/02/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/567,746  
; FILING DATE: 12/05/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/538,387  
; FILING DATE: 10/03/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/473,660  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,196  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,147  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,662  
; FILING DATE: 04/25/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6444-302D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-709-435-26

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No.1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11  
Db 7 KPDL 10

## RESULT 37

US-08-567-746A-25  
; Sequence 25, Application US/08567746A  
; Patent No. 6025129  
; GENERAL INFORMATION:  
; APPLICANT: NO. 6025129a, Michael Phillip  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: Parandoosh, Zahra  
; APPLICANT: David, Gary S.  
; TITLE OF INVENTION: ASSAYS USING REMOTELY  
; PROGRAMMABLE MATRICES WITH MEMORIES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA



COUNTRY: USA  
 ZIP: 92101-2926  
 CITY: San Diego  
 STATE: CA  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/567,746A  
 FILING DATE: 05-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/473,660  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/480,196  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,504  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,486  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/428,662  
 FILING DATE: 04/25/95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6444-300G  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-567-746A-25

Query Match 22.2%; Score 4; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 7 KPDL 10

RESULT 38  
 US-08-567-746A-26  
 ; Sequence 26, Application US/08567746A  
 ; Patent No. 6025129  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. 6025129a, Michael Phillip  
 ; APPLICANT: Senyei, Andrew E.  
 ; APPLICANT: Parandoosh, Zahra  
 ; APPLICANT: David, Gary S.  
 ; TITLE OF INVENTION: ASSAYS USING REMOTELY  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street  
 CITY: San Diego  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92101-2926  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/567,746A  
 FILING DATE: 05-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/473,660  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/480,196  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,504  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,486  
 FILING DATE: 06/07/95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/428,662  
 FILING DATE: 04/25/95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seidman, Stephanie L  
 REGISTRATION NUMBER: 33,779  
 REFERENCE/DOCKET NUMBER: 6444-300G  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-238-0999  
 TELEFAX: 619-238-0062  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-567-746A-26

Query Match 22.2%; Score 4; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
 Db 7 KPDL 10

RESULT 39  
 US-08-633-410-25  
 ; Sequence 25, Application US/08633410  
 ; Patent No. 6100026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. 6100026a, Michael Phillip  
 ; APPLICANT: Parandoosh, Zahra  
 ; APPLICANT: David, Gary S.  
 ; APPLICANT: Senyei, Andrew E.  
 ; APPLICANT: Potash, Hanan  
 ; APPLICANT: Xiao, Xiao-Yi

;; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
;; NUMBER OF SEQUENCES: 33  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Brown, Martin, Haller & McClain  
;; STREET: 1660 Union Street  
;; CITY: San Diego  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 92101-2926  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSEQ Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/633,410  
;; FILING DATE: 06/10/96  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US96/06145  
;; FILING DATE: 04/25/96  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/639,813  
;; FILING DATE: 04/02/96  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/567,746  
;; FILING DATE: 12/05/95  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/538,387  
;; FILING DATE: 10/03/95  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/473,660  
;; FILING DATE: 06/07/95  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/480,196  
;; FILING DATE: 06/07/95  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/484,486  
;; FILING DATE: 06/07/95  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/428,662  
;; FILING DATE: 04/25/95  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seidman, Stephanie L  
;; REGISTRATION NUMBER: 33,779  
;; REFERENCE/DOCKET NUMBER: 6444-302PC  
;; TELEPHONE: 619-238-0999  
;; TELEFAX: 619-238-0062  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
US-08-633-410-25

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 KPDL 11  
Db |||||  
7 KPDL 10  
RESULT 40  
US-08-633-410-26  
; Sequence 26, Application US/08633410  
; Patent No. 6100026  
; GENERAL INFORMATION:  
; APPLICANT: No. 6100026a, Michael Phillip  
; APPLICANT: Parandosh, Zahra  
; APPLICANT: David, Gary S.  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: Potash, Hanan  
; APPLICANT: Xiao, Xiao-Yi  
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,410  
; FILING DATE: 06/10/96  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06145  
; FILING DATE: 04/25/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/639,813  
; FILING DATE: 04/02/96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/567,746  
; FILING DATE: 12/05/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/538,387  
; FILING DATE: 10/03/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/473,660  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,196  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,147  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,662  
; FILING DATE: 04/25/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6444-302PC  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-633-410-25

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-633-410-26

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11  
DB 7 KPDL 10

RESULT 41  
US-08-704-344-22  
Sequence 22, Application US/08704344  
Patent No. 6218363  
GENERAL INFORMATION:  
APPLICANT: BASERGA, Renato L.  
APPLICANT: RESNICOFF, Mariana  
APPLICANT: HUANG, Ziwei  
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE and DORR LLP  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, Henry N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.196  
TELEPHONE: (202) 942-8459  
TELEFAX: (202) 942-8484  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-704-344-22

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13  
DB 4 DLQP 7

RESULT 42  
US-08-711-426-25  
Sequence 25, Application US/08711426  
Patent No. 628459  
GENERAL INFORMATION:  
APPLICANT: NO. 6284459a, Michael Phillip  
APPLICANT: Zahra Parandoosh  
APPLICANT: Senyei, Andrew E.  
APPLICANT: Xiao, Xiao-Yi  
APPLICANT: David, Gary S.  
APPLICANT: Yozo, Satoda  
APPLICANT: Zhao, Chanfeng  
TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/711,426  
FILING DATE:  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/669,252  
FILING DATE: 06/24/96  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 06/10/96  
CLASSIFICATION: 422  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/06145  
FILING DATE: 04/25/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/639,813  
FILING DATE: 04/02/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/567,746  
FILING DATE: 12/05/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/538,387  
FILING DATE: 10/03/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/473,660  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,196  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,504  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,486  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,147  
FILING DATE: 06/07/95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/428,662  
FILING DATE: 04/25/95  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779

```

; REFERENCE/DOCKET NUMBER: 6444-302C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-711-426-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 43
US-08-711-426-26
; Sequence 26, Application US/08711426
; Patent No. 6284459
; GENERAL INFORMATION:
; APPLICANT: No. 6284459a, Michael Phillip
; APPLICANT: Zahra Parandoosh
; APPLICANT: Senyei, Andrew E.
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: David, Gary S.
; APPLICANT: Yozo, Satoda
; APPLICANT: Zhao, Chanfeng
; APPLICANT: Potash, Hanan
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711.426
; FILING DATE:
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,252
; FILING DATE: 06/24/96
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06/10/96
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:

; REFERENCE/DOCKET NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-711-426-25

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 44
US-08-669-252-25
; Sequence 25, Application US/08669252
; Patent No. 6319668
; GENERAL INFORMATION:
; APPLICANT: No. 6319668a, Michael Phillip
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:

```

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
; CURRENT APPLICATION DATA: US/08/669,252
; FILING DATE: 06/10/96
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,147
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-669-252-25

Query Match 22.2%, Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPDL 11
Db 7 KPDL 10

RESULT 45
US-08-669-252-26
; Sequence 26, Application US/08669252
; Patent No. 6319668
; GENERAL INFORMATION:
; APPLICANT: No. 6319668a, Michael Phillip
; APPLICANT: Potash, Hanan
; APPLICANT: Xiao, Xiao-Yi
; APPLICANT: Parandoosh, Zahra
; APPLICANT: David, Gary S.
; TITLE OF INVENTION: MATRICES WITH MEMORIES AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,252
; FILING DATE: 06/10/96
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06145
; FILING DATE: 04/25/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639,813
; FILING DATE: 04/02/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,746
; FILING DATE: 12/05/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/538,387
; FILING DATE: 10/03/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,196
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,486
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,504
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/473,660
; FILING DATE: 06/07/95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,662
; FILING DATE: 04/25/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6444-302PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-669-252-26
```

Query Match 22.2%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11  
Db 7 KPDL 10

## RESULT 46

US-09-098-122-25  
; Sequence 25, Application US/09098122  
; Patent No. 6372428  
; GENERAL INFORMATION:  
; APPLICANT: No. 6372428a, Michael Phillip  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: David, Gary S.  
; TITLE OF INVENTION: REMOTELY PROGRAMMABLE MATRICES WITH  
; TITLE OF INVENTION: MEMORIES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/098,122  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/473,660  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,196  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,147  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,662  
; FILING DATE: 04/25/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6444-300H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-09-098-122-25

Query Match 22.2%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPDL 11  
Db 7 KPDL 10

## RESULT 47

US-09-098-122-26  
; Sequence 26, Application US/09098122  
; Patent No. 6372428  
; GENERAL INFORMATION:  
; APPLICANT: No. 6372428a, Michael Phillip  
; APPLICANT: Senyei, Andrew E.  
; APPLICANT: David, Gary S.  
; TITLE OF INVENTION: REMOTELY PROGRAMMABLE MATRICES WITH  
; TITLE OF INVENTION: MEMORIES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/098,122  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/538,387  
; FILING DATE: 03-OCT-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/473,660  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,196  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,504  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,486  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/480,147  
; FILING DATE: 06/07/95  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/428,662  
; FILING DATE: 04/25/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6444-300H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:

```

; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-098-122-26

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPDL 11
Db 7 KPDL 10

RESULT 48
US-09-847-185-19
; Sequence 19, Application US/09847185
; Patent No. 6482407
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMBINING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
Db 11

```

```

Db 4 DLQP 7

RESULT 49
5166058-8
; Patent No. 5166058
; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSSEN, VICKI A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
; PROTEINS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/378,537
; FILING DATE: 11-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 943,332
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO: 8:
; LENGTH: 10
5166058-8

Query Match 22.2%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FQVQ 17
Db 2 FQVQ 5

RESULT 50
US-08-036-555B-164
; Sequence 164, Application US/08036555B
; Patent No. 5530109
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703

```

```

; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA: U.K. 91 07566.3
; APPLICATION NUMBER: 34,266
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELEPHONE: (212) 888-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-036-555B-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 51
US-08-469-569-164
; Sequence 164, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3

```

```

; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELEPHONE: (212) 888-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-569-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 52
US-08-249-322A-164
; Sequence 164, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Teai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 888-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-249-322A-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 53
US-08-469-526A-164
; Sequence 164, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Hiles, Ian
; APPLICANT: Chen, Maio Su
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 54
US-08-734-591A-164
; Sequence 164, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; APPLICATION NUMBER: UK 91 07566.3

```

```
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 55
US-08-469-660-164
; Sequence 164, Application US/08469660
; Patent No. 5676973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 164:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-164

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 56
US-08-470-335-164
; Sequence 164, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-335-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DVEK 8
Db 9 DVEK 12

RESULT 57
US-08-735-021-164
; Sequence 164, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
```

```

; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: FRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)....(1)
; OTHER INFORMATION: Xaa in 1 is unknown.
US-08-735-021-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 58
US-08-734-664A-164
; Sequence 164, Application US/08734664A
; Patent No. 6204241
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-664A-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 59
US-08-470-339-164
; Sequence 164, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1993-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT

```

```
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-470-339-164

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 60
US-08-467-602-164
; Sequence 164, Application US/08467602C
; Patent No. 644642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; DISORDERS
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-467-602-164

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 61
US-09-555-352-16
; Sequence 16, Application US/09555352
; Patent No. 654479
; GENERAL INFORMATION:
; APPLICANT: Cichutek, Klaus
; APPLICANT: Mergel-Millitzer, Heike
; TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
; MODIFIABLE SURFACE CAPSID PROTEINS
; FILE REFERENCE: 11692-005001
; CURRENT APPLICATION NUMBER: US/09/555,352
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/DE98/03542
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: DE 197 52 855.4
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16

Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12

RESULT 62
PCT-US94-05083C-160
; Sequence 160, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-MAY-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is
; OTHER INFORMATION: unknown.
PCT-US94-05083C-160

Query Match 22.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8
Db 9 DVEK 12
```

## RESULT 63

PCT-US95-06846A-164  
; Sequence 164, Application PC/TUS9506846A  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew David, Stroobant, Paul;  
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;  
; APPLICANT: Chen, Maio Su; Hiles, Ian  
; TITLE OF INVENTION: Glial Mitogenic Factors, Their  
; TITLE OF INVENTION: Preparation and Use  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/06846A  
; FILING DATE: 25-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,322  
; FILING DATE: 26-MAY-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APRIL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.K. 91 07566.3  
; FILING DATE: 10-APRIL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, Norman D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5250.5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 689-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 164:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: Xaa in position 1 is unknown.  
PCT-US95-06846A-164

Query Match 22.2%; Score 4; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8  
|||  
Db 9 DVEK 12

## RESULT 64

US-08-687-956A-3  
; Sequence 3, Application US/08687956A  
; Patent No. 5861157  
; GENERAL INFORMATION:  
; APPLICANT: BURNIE, JAMES P  
; APPLICANT: MATTHEWS, RUTH C  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP  
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,956A  
; FILING DATE: 29-JUL-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9401689.6  
; FILING DATE: 28-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 50885/222892  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/861-3000  
; TELEFAX: 202/822-0944  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus oralis  
; US-08-687-956A-3

Query Match 22.2%; Score 4; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKP 9  
|||  
Db 3 VEKP 6

## RESULT 65

US-08-997-080-16  
; Sequence 16, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA



; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-873-970-16

Query Match 22.2%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQ 12  
Db 4 PDLQ 7

## RESULT 68

US-09-095-855-16  
; Sequence 16, Application US/09095855  
; Patent No. 6160093  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Compounds and Methods for  
; TITL OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095.855  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/705,347  
; FILING DATE: 29-AUG-1996  
; APPLICATION NUMBER: 08/873,970  
; FILING DATE: 12-JUN-1997  
; APPLICATION NUMBER: 08/997,362  
; FILING DATE: 23-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1002c3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-095-855-16

Query Match 22.2%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQ 12  
Db 4 PDLQ 7

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-873-970-16

Query Match 22.2%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQ 12  
Db 4 PDLQ 7

RESULT 69  
US-08-705-347A-16  
; Sequence 16, Application US/08705347A  
; Patent No. 6284255  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Hiyama, Jun  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Scott, Linda  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND  
; TITL OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Speckman Picard PLLC  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/705,347A  
; FILING DATE: 28-AUG-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206.269.0565  
; TELEFAX: 206.269.0563  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-705-347A-16

Query Match 22.2%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQ 12  
Db 4 PDLQ 7

## RESULT 70

US-09-324-542-16  
; Sequence 16, Application US/09324542  
; Patent No. 6328978  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Tan, Paul L.J.  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Methods and Compounds for the Treatment  
; TITL OF INVENTION: of Immunologically-Mediated Skin Disorders  
; FILE REFERENCE: 11000.1007c1  
; CURRENT APPLICATION NUMBER: US/09/324,542  
; CURRENT FILING DATE: 1999-06-02  
; EARLIER APPLICATION NUMBER: US 08/997,080  
; EARLIER FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: FastSEQ for Windows Version 3.0

```
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 71
US-09-205-426-16
; Sequence 16, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 72
US-09-200-643-16
; Sequence 16, Application US/09200643
; Patent No. 6410720
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002CON
; CURRENT APPLICATION NUMBER: US/09/200,643
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-200-643-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PDLQ 12
Db 4 PDLQ 7

RESULT 73
US-07-145-002B-62
; Sequence 62, Application US/07145002B
; Patent No. 6482613
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Pestka, Sidney
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF MATURE HUMAN
; TITLE OF INVENTION: LEUKOCYTE INTERFERONS
; FILE REFERENCE: 1803-0088-999
; CURRENT APPLICATION NUMBER: US/07/145,002B
; CURRENT FILING DATE: 1989-01-19
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-145-002B-62

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLQP 13
Db 5 DLQP 8

RESULT 74
US-07-942-245-77
; Sequence 77, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 77:
```



; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-942-245-77

Query Match 22.2%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8  
Db 12 DVEK 15

RESULT 75  
US-07-942-245-92  
; Sequence 92, Application US/07942245  
; Patent No. 5639641  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Jan T.  
; APPLICANT: SEARLE, Stephen M.J.  
; APPLICANT: REES, Anthony R.  
; APPLICANT: ROGUSKA, Michael A.  
; APPLICANT: GUILD, Braydon C.  
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 522  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: HP 9000/700 Workstation  
; OPERATING SYSTEM: UNIX  
; SOFTWARE: In house  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/942,245  
; FILING DATE: 09-SEP-1992  
; CLASSIFICATION: 530  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-942-245-92

Query Match 22.2%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DVEK 8  
Db 12 DVEK 15

Search completed: November 25, 2003, 20:15:59  
Job time : 21.6277 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 11.0426 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-4  
Perfect score: 12  
Sequence: 1 LFRPLPVNVLP 12

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 4     | 33.3        | 17     | 2 J02030  | hypothetical 1.9K  |
| 2          | 4     | 33.3        | 18     | 2 I40062  | shikimate 5-dehydr |
| 3          | 4     | 33.3        | 18     | 2 S53125  | cysteine-rich secr |
| 4          | 4     | 33.3        | 20     | 2 S09022  | carboxylesterase ( |
| 5          | 4     | 33.3        | 20     | 2 S09025  | carboxylesterase ( |
| 6          | 4     | 33.3        | 20     | 2 S09023  | carboxylesterase ( |
| 7          | 3     | 25.0        | 10     | 2 A44646  | neurotoxin-associa |
| 8          | 3     | 25.0        | 10     | 2 I44644  | neurotoxin-associa |
| 9          | 3     | 25.0        | 10     | 2 B56899  | serum heterodimer, |
| 10         | 3     | 25.0        | 10     | 2 S36849  | Ig heavy chain V r |
| 11         | 3     | 25.0        | 11     | 2 S69349  | neuropeptide Ffami |
| 12         | 3     | 25.0        | 11     | 2 S09024  | carboxylesterase ( |
| 13         | 3     | 25.0        | 12     | 1 LFECEP  | pyrE leader peptid |
| 14         | 3     | 25.0        | 12     | 2 S26555  | T-cell receptor be |
| 15         | 3     | 25.0        | 12     | 2 S26556  | T-cell receptor be |
| 16         | 3     | 25.0        | 12     | 2 S26554  | T-cell receptor be |
| 17         | 3     | 25.0        | 12     | 2 PA0037  | plastocyanin 2 - A |
| 18         | 3     | 25.0        | 12     | 2 A60528  | insulin-like growt |
| 19         | 3     | 25.0        | 12     | 2 A33520  | inhibitory diffusi |
| 20         | 3     | 25.0        | 12     | 2 PH0785  | T-cell receptor al |
| 21         | 3     | 25.0        | 12     | 4 PC2123  | aminotransferase c |
| 22         | 3     | 25.0        | 13     | 2 JZVHP1  | crabrolin - Europe |
| 23         | 3     | 25.0        | 13     | 2 S09395  | hypothetical prote |
| 24         | 3     | 25.0        | 13     | 2 S09018  | hemolytic protein  |
| 25         | 3     | 25.0        | 13     | 2 S09019  | hemolytic protein  |
| 26         | 3     | 25.0        | 13     | 2 PL0157  | Ig kappa chain V-I |
| 27         | 3     | 25.0        | 13     | 2 S47371  | T-cell antigen rec |
| 28         | 3     | 25.0        | 13     | 2 S47390  | T-cell antigen rec |
| 29         | 3     | 25.0        | 14     | 1 LFECEFS | pheST operon leade |

|     |   |      |    |          |                     |
|-----|---|------|----|----------|---------------------|
| 30  | 3 | 25.0 | 14 | 2 JN0390 | histamine-releasin  |
| 31  | 3 | 25.0 | 14 | 2 S50900 | chlorophyll a/b-b1  |
| 32  | 3 | 25.0 | 14 | 2 S27140 | hypothetical prote  |
| 33  | 3 | 25.0 | 14 | 2 S58862 | botulinum neurotox  |
| 34  | 3 | 25.0 | 14 | 2 S58866 | botulinum neurotox  |
| 35  | 3 | 25.0 | 14 | 2 C33098 | 223K exoantigen -   |
| 36  | 3 | 25.0 | 14 | 2 A23986 | beta-granin - rat   |
| 37  | 3 | 25.0 | 14 | 2 AF0296 | phenylalanyl-tRNA   |
| 38  | 3 | 25.0 | 14 | 2 F90931 | pheST operon leade  |
| 39  | 3 | 25.0 | 14 | 2 B85780 | pheST operon leade  |
| 40  | 3 | 25.0 | 14 | 2 AG0705 | phenylalanyl-tRNA   |
| 41  | 3 | 25.0 | 15 | 1 LFECEP | phe operon leader   |
| 42  | 3 | 25.0 | 15 | 2 E91061 | hypothetical prote  |
| 43  | 3 | 25.0 | 15 | 2 T09463 | ribosomal protein   |
| 44  | 3 | 25.0 | 15 | 2 PA0029 | protein QA100012 -  |
| 45  | 3 | 25.0 | 15 | 2 PS0276 | phosphoribulokinase |
| 46  | 3 | 25.0 | 15 | 2 B61457 | alpha-glucosidase   |
| 47  | 3 | 25.0 | 15 | 2 S57577 | T-cell receptor V-  |
| 48  | 3 | 25.0 | 15 | 2 E56978 | collagen alpha 2(X  |
| 49  | 3 | 25.0 | 15 | 2 PH0784 | T-cell receptor al  |
| 50  | 3 | 25.0 | 15 | 2 A31902 | bone acidic glycop  |
| 51  | 3 | 25.0 | 15 | 2 AF0832 | phe leader peptide  |
| 52  | 3 | 25.0 | 16 | 2 I40065 | shikimate 5-dehydr  |
| 53  | 3 | 25.0 | 16 | 2 G49039 | T-cell receptor be  |
| 54  | 3 | 25.0 | 16 | 2 H49039 | T-cell receptor be  |
| 55  | 3 | 25.0 | 16 | 2 G24887 | T-cell receptor be  |
| 56  | 3 | 25.0 | 16 | 2 A28587 | T-cell receptor be  |
| 57  | 3 | 25.0 | 16 | 2 PH1476 | T-cell receptor be  |
| 58  | 3 | 25.0 | 16 | 2 PH1475 | T-cell receptor be  |
| 59  | 3 | 25.0 | 16 | 2 PH1474 | T-cell receptor be  |
| 60  | 3 | 25.0 | 16 | 2 PH1472 | T-cell receptor be  |
| 61  | 3 | 25.0 | 16 | 2 PH1477 | T-cell receptor be  |
| 62  | 3 | 25.0 | 16 | 2 PH1473 | T-cell receptor be  |
| 63  | 3 | 25.0 | 16 | 2 PH0766 | T-cell receptor be  |
| 64  | 3 | 25.0 | 16 | 2 PH0767 | T-cell receptor be  |
| 65  | 3 | 25.0 | 16 | 2 PH1480 | T-cell receptor be  |
| 66  | 3 | 25.0 | 17 | 2 I65274 | glutathione S-tran  |
| 67  | 3 | 25.0 | 17 | 2 C37520 | glutathione transf  |
| 68  | 3 | 25.0 | 17 | 2 I49425 | mitogen regulated   |
| 69  | 3 | 25.0 | 17 | 2 S05913 | chorion class A pr  |
| 70  | 3 | 25.0 | 17 | 2 I49593 | cystic fibrosis tr  |
| 71  | 3 | 25.0 | 17 | 2 I84733 | gene CFTR protein   |
| 72  | 3 | 25.0 | 17 | 2 S66213 | glucose 1-dehydrog  |
| 73  | 3 | 25.0 | 17 | 2 S59481 | hydroxyproline-ric  |
| 74  | 3 | 25.0 | 17 | 2 PS0454 | 38k protein 3129 -  |
| 75  | 3 | 25.0 | 17 | 2 E22595 | bombolitin V - Ame  |
| 76  | 3 | 25.0 | 17 | 2 E28587 | T-cell receptor be  |
| 77  | 3 | 25.0 | 17 | 2 B31769 | T-cell receptor de  |
| 78  | 3 | 25.0 | 17 | 2 PC2196 | zymogen granule me  |
| 79  | 3 | 25.0 | 17 | 2 E23734 | insulin-like growt  |
| 80  | 3 | 25.0 | 17 | 2 D53284 | T-cell receptor be  |
| 81  | 3 | 25.0 | 18 | 2 S04229 | N4-(beta-N-acetyl   |
| 82  | 3 | 25.0 | 18 | 2 A32220 | T-cell receptor de  |
| 83  | 3 | 25.0 | 18 | 2 B4995  | alkanal monooxygen  |
| 84  | 3 | 25.0 | 18 | 2 S49026 | ribosomal protein   |
| 85  | 3 | 25.0 | 18 | 2 S23971 | alpha-macroglobuli  |
| 86  | 3 | 25.0 | 18 | 2 S09026 | carboxylesterase (  |
| 87  | 3 | 25.0 | 18 | 2 S57518 | T cell receptor be  |
| 88  | 3 | 25.0 | 18 | 2 S57520 | T cell receptor be  |
| 89  | 3 | 25.0 | 18 | 4 I54078 | hypothetical PML/R  |
| 90  | 3 | 25.0 | 19 | 2 C56049 | superoxide dismuta  |
| 91  | 3 | 25.0 | 19 | 2 S13046 | calreticulin - rab  |
| 92  | 3 | 25.0 | 19 | 2 I40063 | shikimate 5-dehydr  |
| 93  | 3 | 25.0 | 19 | 2 B33708 | thionin, soluble -  |
| 94  | 3 | 25.0 | 19 | 2 S69153 | Neb-colloostatin -  |
| 95  | 3 | 25.0 | 19 | 2 D49404 | T-cell receptor be  |
| 96  | 3 | 25.0 | 19 | 2 A44356 | 37k adherens junct  |
| 97  | 3 | 25.0 | 19 | 2 A41077 | protein-disulfide   |
| 98  | 3 | 25.0 | 19 | 2 S68394 | H+-transporting tw  |
| 99  | 3 | 25.0 | 20 | 2 S17461 | flavodoxin B - Azo  |
| 100 | 3 | 25.0 | 20 | 2 S04961 | malate dehydrogena  |

## ALIGNMENTS

```

RESULT 1
JQ2030
hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
N;Alternate names: ORF2 mini gene protein
C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: JQ2030
R;Russell, R.L.O.; Rohmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsug
A;Reference number: PQ6633; MUID:93286576; PMID:8389803
A;Accession: JQ2030
A;Molecule type: DNA
A;Residues: 1-17 <RUS>
A;Cross-references: DDBJ:DL3375; NID:g222217; PIDN:BAA02640.1; PID:dl003144; PID:g222222

Query Match 33.3%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11
Db 5 VNVL 8

RESULT 2
I40062
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C;Species: Buchnera aphidicola
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40062
R;Roubbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endos
A;Reference number: I40061; MUID:95212914; PMID:7535281
A;Accession: I40062
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18 <RES>
A;Cross-references: EMBL:U10496; NID:g854711; PIDN:AAA79125.1; PID:g854712
C;Genetics:
A;Gene: aroE
C;Keywords: oxidoreductase

Query Match 33.3%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 7 NVLP 10

RESULT 3
S53125
cysteine-rich secretory protein-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S53125; S56161
R;Schwiderzky, U.; Haendler, B.; Schleuning, W.D.
submitted to the EMBL Data Library, March 1995
A;Description: Isolation and characterization of the androgen-dependent mouse cysteine-r
A;Reference number: S53125
A;Accession: S53125
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <SCH>
A;Cross-references: EMBL:X85321
R;Schwiderzky, U.; Haendler, B.; Schleuning, W.D.
Biochem. J. 309, 831-836, 1995

```

```

A;Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich
A;Reference number: S56161; MUID:95366959; PMID:7639699
A;Accession: S56161
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <SC2>
A;Cross-references: EMBL:X85321

```

```

Query Match 33.3%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFPL 5
Db 4 PFPL 7

```

```

RESULT 4
S09022
carboxylesterase (EC 3.1.1.1) RH1, microsomal - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09022
R;Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A;Title: Characterization of molecular species of liver microsomal carboxylesterases (
A;Reference number: S09021; MUID:90179180; PMID:2310190
A;Accession: S09022
A;Molecule type: protein
A;Residues: 1-20 <HOS>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase

```

```

Query Match 33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVVN 9
Db 6 PVVN 9

```

```

RESULT 5
S09025
carboxylesterase (EC 3.1.1.1), microsomal - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09025
R;Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A;Title: Characterization of molecular species of liver microsomal carboxylesterases (
A;Reference number: S09021; MUID:90179180; PMID:2310190
A;Accession: S09025
A;Molecule type: protein
A;Residues: 1-20 <HOS>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase

```

```

Query Match 33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVVN 9
Db 6 PVVN 9

```

```

RESULT 6
S09023
carboxylesterase (EC 3.1.1.1) RL2, microsomal - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09023

```

R;Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A;Reference number: S09021; MUID:90179180; PMID:2310190  
A;Accession: S09023  
A;Molecule type: protein  
A;Residues: 1-20 <HOS>  
C;Superfamily: cholinesterase; cholinesterase homology  
C;Keywords: carboxylic ester hydrolase

Query Match 33.3%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PVVN 9  
DB 6 PVVN 9

RESULT 7  
A44646  
neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)  
C;Species: Clostridium botulinum  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: A44646  
R;Somers, E.; DasGupta, B.R.  
J. Protein Chem. 10, 415-425, 1991  
A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he  
A;Reference number: A44644; MUID:92143938; PMID:1781887  
A;Contents: type A  
A;Accession: A44646  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SOM>  
A;Note: sequence extracted from NCBI backbone (NCBIP:83774)  
A;Note: 6-Trp was also found  
C;Keywords: hemagglutinin

Query Match 25.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 VLP 12  
DB 7 VLP 9

RESULT 8  
I44644  
neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)  
C;Species: Clostridium botulinum  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: I44644  
R;Somers, E.; DasGupta, B.R.  
J. Protein Chem. 10, 415-425, 1991  
A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he  
A;Reference number: A44644; MUID:92143938; PMID:1781887  
A;Contents: type B  
A;Accession: I44644  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SOM>  
A;Note: sequence extracted from NCBI backbone (NCBIP:83783)  
C;Keywords: hemagglutinin

Query Match 25.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 VLP 12  
DB 7 VLP 9

RESULT 9  
B56899  
serum heterodimer, 24K chain - sandbar shark (fragment)  
C;Species: Carcharhinus plumbeus (sandbar shark)  
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Jun-2000  
C;Accession: B56899  
R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.  
Comp. Biochem. Physiol. B 103, 563-568, 1992  
A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum  
A;Reference number: A56899; MUID:93092592; PMID:1458832  
A;Accession: B56899  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <VAZ>  
C;Keywords: glycoprotein; plasma

Query Match 25.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 VVN 9  
DB 7 VVN 9

RESULT 10  
S36849  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Nov-1999  
C;Accession: S36849  
R;Jacob, J.; Kelsoe, G.  
submitted to the EMBL Data Library, July 1992  
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph  
A;Reference number: S25024  
A;Accession: S36849  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-10 <JAC>  
A;Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:gl33386  
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 VVN 9  
DB 7 VVN 9

RESULT 11  
S69349  
neuropeptide FFamide - great pond snail  
C;Species: Lymnaea stagnalis (great pond snail)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 17-Mar-1999  
C;Accession: S69349  
R;Li, K.W.; El Filali, Z.; van Golen, F.A.; Geraerts, W.P.M.  
Eur. J. Biochem. 229, 70-72, 1995  
A;Title: Identification of a novel amide peptide, GLTFNNNSLFF-NH(2), involved in the  
A;Reference number: S69349; MUID:95262689; PMID:774051  
A;Accession: S69349  
A;Molecule type: protein  
A;Residues: 1-11 <LIK>  
A;Experimental source: penis complex  
C;Function:  
A;Description: enhances the contraction frequency and contraction amplitude of the va  
A;Note: control of male reproductive behavior  
C;Keywords: amidated carboxyl end; neuropeptide  
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
|||  
Db 9 LFF 11

## RESULT 12

S09024  
carboxylesterase (EC 3.1.1.1), microsomal - golden hamster (fragment)  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 28-Apr-1993  
C:Accession: S09024  
R:Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09024  
A:Molecule type: protein  
A:Residues: 1-11 <HOS>  
C:Keywords: carboxylic ester hydrolase

Query Match 25.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVN 9  
|||  
Db 7 VVN 9

## RESULT 13

LFECPE  
pyrE leader peptide - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 31-Mar-1993  
C:Accession: A30400; A05110; Q00495  
R:Poulsen, P.; Bonekamp, F.; Jensen, K.F.  
EMBO J. 3, 1783-1790, 1984  
A:Title: Structure of the Escherichia coli pyrE operon and control of pyrE expression by  
A:Reference number: A30400; MUID:85003588; PMID:6207018  
A:Accession: A30400  
A:Molecule type: DNA  
A:Residues: 1-12 <POU>  
R:Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.  
Eur. J. Biochem. 135, 223-229, 1983  
A:Title: Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front of  
A:Reference number: A05110; MUID:83287414; PMID:634999  
A:Accession: A05110  
A:Molecule type: DNA  
C:Genetics:  
A:Gene: pyrE-LP  
A:Map position: 82 min  
C:Superfamily: pyrE leader peptide

Query Match 25.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
|||  
Db 4 LFF 6

## RESULT 14

S26555  
T-cell receptor beta chain (clone Cw3/1B4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C:Accession: S26555  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid

J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: S26555  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Cross-references: EMBL:X68005  
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/1B4  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
|||  
Db 9 LFF 11

## RESULT 15

S26556  
T-cell receptor beta chain (clone Cw3/2C3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C:Accession: S26556  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: S26556  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Cross-references: EMBL:X68006  
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/2C3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
|||  
Db 9 LFF 11

## RESULT 16

S26554  
T-cell receptor beta chain (clone Cw3/Cas7) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C:Accession: S26554  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.;  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recep  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: S26554  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Cross-references: EMBL:X68004  
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas7  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
|||  
Db 9 LFF 11

## RESULT 17

PA0037  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
 C:Accession: PA0037  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0037  
 A:Molecule type: protein  
 A:Residues: 1-12 <KAM>  
 A:Experimental source: stem

Query Match 25.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLP 12  
 ||||  
 Db 5 VLP 7

## RESULT 18

A60528  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
 C:Accession: A60528  
 R:Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D.  
 Comp. Biochem. Physiol. B 92, 561-567, 1989  
 A:Title: Purification of the serum acid-stable insulin-like growth factor binding protein  
 A:Reference number: A60528; MUID:89209787; PMID:2468442  
 A:Accession: A60528  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <WAL>

Query Match 25.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8  
 ||||  
 Db 9 PVV 11

## RESULT 19

A33520  
 C:Species: Mus musculus (house mouse)  
 C:Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 30-Sep-1993  
 C:Accession: A33520  
 R:Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.  
 J. Biol. Chem. 264, 6021-6024, 1989  
 A:Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh)  
 A:Reference number: A33520; MUID:89197888; PMID:2703477  
 A:Accession: A33520  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <BLA>

Query Match 25.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8  
 ||||  
 Db 9 PVV 11

## RESULT 20

PH0785  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PH0785  
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.  
 A:Reference number: PH0746; MUID:92078846; PMID:1836010  
 A:Accession: PH0785  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <CAS>  
 A:Cross-references: EMBL:X60887  
 A:Experimental source: T lymphocyte  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
 ||||  
 Db 7 NVL 9

## RESULT 21

PC2123  
 C:Species: synthetic  
 C:Date: 28-May-1999 #sequence\_revision 28-May-1999 #text\_change 28-May-1999  
 C:Accession: PC2123  
 R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.  
 J. Biochem. 115, 568-577, 1994  
 A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp  
 A:Reference number: JX0315; MUID:94334304; PMID:8056774  
 A:Accession: PC2123  
 A:Molecule type: DNA  
 A:Residues: 1-12 <MIY>  
 C:Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (C) and the parental enzymes catalyze the reversible amino group transfer reaction  
 C:Keywords: aminotransferase

Query Match 25.0%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNV 10  
 ||||  
 Db 2 VNV 4

## RESULT 22

JZVHP1  
 C:Species: Vespa crabro (European hornet)  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C:Accession: A01781  
 R:Argiolas, A.; Pisano, J.J.  
 J. Biol. Chem. 259, 10106-10111, 1984  
 A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin  
 A:Reference number: A92441; MUID:84289390; PMID:6206053  
 A:Accession: A01781  
 A:Molecule type: protein  
 A:Residues: 1-13 <ARG>  
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.  
 C:Keywords: amidated carboxyl end; venom  
 F:13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 23

S09395  
hypothetical protein - fruit fly (*Drosophila melanogaster*) (fragment)  
C:Species: *Drosophila melanogaster*  
C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 24-Jul-1997  
R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtkamp, J. 8, 2359-2364, 1989  
A:Title: The interference of truncated with normal potassium channel subunits leads to a EMBO J. 8, 2359-2364, 1989  
A:Reference number: S09395; MUID:90005442; PMID:2551680  
A:Accession: S09395  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <GIS>

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
|||  
Db 5 LPV 7

## RESULT 24

S09018  
hemolytic protein A1 - edible frog (fragment)  
C:Species: *Rana esculenta* (edible frog)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.; Bossa, F.; Biochim. Biophys. Acta 1033, 318-323, 1990  
A:Title: Purification and characterization of bioactive peptides from skin extracts of *Rana esculenta*  
A:Reference number: S09018; MUID:90198965; PMID:2317508  
A:Accession: S09018  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 25

S09019  
hemolytic protein B9 - edible frog (fragment)  
C:Species: *Rana esculenta* (edible frog)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
R:Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.; Bossa, F.; Biochim. Biophys. Acta 1033, 318-323, 1990  
A:Title: Purification and characterization of bioactive peptides from skin extracts of *Rana esculenta*  
A:Reference number: S09019; MUID:90198965; PMID:2317508  
A:Accession: S09019  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6

Db |||  
1 FLP 3

## RESULT 26

PL0157  
IG kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)  
C:Species: *Homo sapiens* (man)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Feb-1997  
C:Accession: PL0157; C61458  
R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E. J. Exp. Med. 170, 1551-1558, 1989  
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein (A61458; MUID:90039128; PMID:2478651)  
A:Reference number: A61458; MUID:90039128; PMID:2478651  
A:Accession: PL0157  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
A:Accession: C61458  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BR2>

A:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein (A61458; MUID:90039128; PMID:2478651)  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
|||  
Db 11 LPV 13

## RESULT 27

S47371  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: *Homo sapiens* (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
R:Lehner, P.J.  
A:Title: Purification and characterization of bioactive peptides from skin extracts of *Rana esculenta*  
A:Reference number: S47371  
A:Accession: S47371  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>  
A:Cross-references: EMBL:Z35696; NID:G527483; PIDN:CAA84765.1; PID:G527484  
C:Keywords: T-cell receptor

submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by A:Reference number: S47355  
A:Accession: S47371  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>  
A:Cross-references: EMBL:Z35696; NID:G527483; PIDN:CAA84765.1; PID:G527484  
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3  
|||  
Db 11 LFF 13

## RESULT 28

S47390  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: *Homo sapiens* (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
R:Lehner, P.J.  
A:Title: Purification and characterization of bioactive peptides from skin extracts of *Rana esculenta*  
A:Reference number: S47390  
A:Accession: S47390  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>

submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by A:Reference number: S47355  
A:Accession: S47390  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35703; NID:g527499; PIDN:CAA84772.1; PID:g527500  
C;Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3  
|||  
Db 11 LFF 13

## RESULT 29

LFFCFS

pheST operon leader peptide - Escherichia coli (strain K-12)  
N;Alternate names: phenylalanyl-tRNA synthetase operon leader peptide  
C;Species: Escherichia coli  
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 01-Mar-2002  
C;Accession: S11551; I53984; C64930; S06908  
R;Fayot, G.; Mayaux, J.F.; Sacerdot, C.; Fromant, M.; Grunberg-Manago, M.;  
J. Mol. Biol. 171, 239-261, 1983  
A;Title: Escherichia coli phenylalanyl-tRNA synthetase operon region. Evidence for an at  
A;Reference number: A30391; MUID:84090239; PMID:6317865  
A;Accession: S11551  
A;Molecule type: DNA  
A;Residues: 1-14 <FR>  
A;Cross-references: EMBL:V00291; NID:g43065; PIDN:CAA23563.1; PID:g43069  
R;Mayaux, J.  
Gene 30, 137-146, 1984  
A;Title: IS4 transposition in the attenuator region of the Escherichia coli pheS, T oper  
A;Reference number: I53984; MUID:85077605; PMID:6096210  
A;Accession: I53984  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-14 <RES>  
A;Cross-references: GB:M13251; NID:gl47182; PIDN:AAA24333.1; PID:gl47185  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: C64930  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-14 <BLAT>  
A;Cross-references: GB:AE000266; GB:U00096; NID:gl787997; PIDN:AACT4785.1; PID:gl788008;  
A;Experimental source: strain K-12, substrain MGL655  
C;Genetics:  
A;Gene: pheM  
A;Map position: 37 min  
A;Function:  
C;Description: probably involved in attenuation regulation of phenylalanyl-tRNA syntheta  
C;Superfamily: pheST leader peptide

Query Match 25.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4  
|||  
Db 8 PFF 10

## RESULT 30

JN0390

histamine-releasing peptide II - oriental hornet  
N;Alternate names: venom protein HR-2  
C;Species: Vespa orientalis (oriental hornet)  
C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 23-Aug-1997  
C;Accession: JN0390; S10919  
R;Miroschnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus  
Bloor, Khim. 7, 1467-1477, 1981  
A;Title: Structure and properties of histamine releasing peptides from the venom of Vesp

A;Reference number: JN0389

A;Accession: JN0390

A;Molecule type: protein

A;Residues: 1-14 <MIR>

R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.  
Biochemistry (N.Y.) 53, 183-190, 1988

A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.

A;Reference number: S06445

A;Accession: S10919

A;Molecule type: protein

A;Residues: 1-14 <TUI>

C;Superfamily: crabrolin

C;Keywords: amidated carboxyl end; venom

F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 31

S50900

chlorophyll a/b-binding protein lhcb5 - spinach (fragment)

N;Alternate names: light-harvesting complex LHCIIc protein

C;Species: Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence\_revision 23-Apr-1999 #text\_change 23-Apr-1999

C;Accession: S50900

R;Walters, R.G.; Ruban, A.V.; Horton, P.

Eur. J. Biochem. 226, 1063-1069, 1994

A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyc

A;Reference number: S50900; MUID:95112835; PMID:7813461

A;Accession: S50900

A;Molecule type: protein

A;Residues: 1-14 <WAL>

C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photos

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 2 FLP 4

## RESULT 32

S27140

hypothetical protein 1 estrogen receptor 5'-region - human

C;Species: Homo sapiens (man)

C;Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 18-Aug-2000

C;Accession: S27140

R;Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor g

A;Reference number: S27140; MUID:93075998; PMID:1476547

A;Accession: S27140

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202

C;Superfamily: unassigned leader peptides

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||



Db 6 FLP 8

RESULT 33

S58862

botulinum neurotoxin type A and B hemagglutinin component II - Clostridium botulinum (strain N; Alternate names: HA-II protein

C;Species: Clostridium botulinum

C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 15-Oct-1999

C;Accession: S58862; S58858

R;East, A.K.; Stacey, J.M.; Collins, M.D.

Syst. Appl. Microbiol. 17, 306-312, 1994

A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin

A;Reference number: S58855

A;Accession: S58862

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EAS>

A;Cross-references: EMBL:X79104; NID:g870937; PIDN:CAA55719.1; PID:g870941

A;Experimental source: strain NCTC 7272

A;Accession: S58858

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EA2>

A;Cross-references: EMBL:X79103; NID:g870932; PIDN:CAA55715.1; PID:g870936

A;Experimental source: strain Eklund 17B

C;Keywords: hemagglutinin; neurotoxin

Query Match 25.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6

Db 7 FLP 9

RESULT 34

S58866

botulinum neurotoxin type B hemagglutinin component II - Clostridium botulinum (NCTC 7272)

N;Alternate names: protein HA-II

C;Species: Clostridium botulinum

A;Variety: NCTC 7273

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Oct-1999

C;Accession: S58866

R;East, A.K.; Stacey, J.M.; Collins, M.D.

Syst. Appl. Microbiol. 17, 306-312, 1994

A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin

A;Reference number: S58855

A;Accession: S58866

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EAS>

A;Cross-references: EMBL:X79102; NID:g870942; PIDN:CAA55711.1; PID:g870946

A;Experimental source: NCTC 7273

C;Keywords: hemagglutinin; neurotoxin

Query Match 25.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6

Db 7 FLP 9

RESULT 35

C33098

223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: C33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: C33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NIC>

Query Match 25.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLP 12

Db 1 VLP 3

RESULT 36

A23396

beta-granin - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Jun-1993

C;Accession: A23396

R;Hutton, J.C.; Hansen, F.; Peshavaria, M.

FEBS Lett. 185, 336-340, 1985

A;Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely related to beta-granin

A;Reference number: A23396; MUID:85385598; PMID:3896848

A;Accession: A23396

A;Molecule type: protein

A;Residues: 1-14 <HUT>

Query Match 25.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPV 7

Db 1 LPV 3

RESULT 37

AF0296

phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C;Accession: AF0296

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barral

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0296

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-14 <KUP>

A;Cross-references: GB:AL590842; PIDN:CAC91234.1; PID:gi5980423; GSPDB:GN00175

C;Genetics:

A;Gene: pheM

Query Match 25.0%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4

Db 8 FFF 10

RESULT 38

F90931

phst operon leader peptide - Escherichia coli (strain O157:H7, substrain RIMD 050995

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 27-Nov-2001

C;Accession: F90931  
 R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: F90931  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-14 <HAY>  
 A;Cross-references: GB:BA000007; PIDN:BA035845.1; PID:g13361889; GSPDB:GN00154  
 A;Experimental source: strain O157:H7, substrain RMD 050952  
 C;Genetics:  
 A;Gene: ECs2422

Query Match 25.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFF 4  
 |||  
 Db 8 FFF 10

RESULT 39  
 B85780  
 pheST operon leader peptide - *Escherichia coli* (strain O157:H7, substrain EDL933)  
 C;Species: *Escherichia coli*  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 27-Nov-2001  
 C;Accession: B85780  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: B85780  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-14 <STO>  
 A;Cross-references: GB:AE005174; MID:g12515726; PIDN:AAG56702.1; GSPDB:GN00145; UWGP:227  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: pheM

Query Match 25.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFF 4  
 |||  
 Db 8 FFF 10

RESULT 40  
 AG0705  
 phenylalanyl-tRNA synthetase operon leader peptide [imported] - *Salmonella enterica* subsp.  
 C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
 A;Note: this species has also been called *Salmonella typhi*  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AG0705  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AG0705  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-14 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD02016.1; PID:g16502854; GSPDB:GN00176  
 C;Genetics:

A;Gene: STV1774

Query Match 25.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
 |||  
 Db 8 FFF 10

RESULT 41

LFECP

phe operon leader peptide - *Escherichia coli* (strain K-12)

N;Alternate names: attenuator peptide

C;Species: *Escherichia coli*

C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 01-Mar-2002

C;Accession: A03593; B36494; A65038

R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of *Esch*

A;Reference number: A03593; MUID:79033820; PMID:360214

A;Accession: A03593

A;Molecule type: DNA

A;Residues: 1-15 &lt;ZUR&gt;

A;Cross-references: GB:V00314; GB:J01658; MID:g42378; PIDN:CAA23600.1; PID:g42379

R;Gavini, N.; Davidson, B.E.

J. Biol. Chem. 265, 21532-21535, 1990

A;Title: pheA mutants of *Escherichia coli* have a defective pheA attenuator.

A;Reference number: A36494; MUID:91072346; PMID:2254312

A;Accession: B36494

A;Molecule type: DNA

A;Residues: 1-15 &lt;GNV&gt;

A;Cross-references: GB:M58024; GB:J05694; MID:g147178; PIDN:AAA62783.1; PID:g147180

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: A65038

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-15 &lt;BLAT&gt;

A;Cross-references: GB:AE000346; GB:U00096; MID:g2367141; PIDN:AA075647.1; PID:g17889

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: pheL; pheAe

A;Map position: 56 min

C;Superfamily: pheA leader peptide

Query Match 25.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
 |||  
 Db 6 FFF 8

RESULT 42

E91061

hypothetical protein ECs3461 [imported] - *Escherichia coli* (strain O157:H7, substrainC;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001

C;Accession: E91061

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and g

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: E91061

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAE36884.1; PID:G33362932; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 050952  
C;Genetics:  
A;Gene: ECs3461

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
|||  
DB 6 FFF 8

#### RESULT 43

T09463  
ribosomal protein S14 - brown alga (*Pyraliella littoralis*) mitochondrion (fragment)  
C;Species: mitochondrion *Pyraliella littoralis*  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 13-Aug-1999  
C;Accession: T09463

R;Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.

J. Mol. Biol. 277, 1047-1057, 1998

A;Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial gene

A;Reference number: Z16681; MUID:98239704; PMID:9571021

A;Accession: T09463

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-15 <ROU>

A;Cross-references: EMBL:AF034976; NID:G32431103; PID:G32431104

A;Experimental source: strain Roscoff

C;Genetics:

A;Gene: rps14

A;Genome: mitochondrion

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12  
|||  
DB 6 VLP 8

#### RESULT 44

PA0029

Protein QA100012 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C;Accession: PA0029

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A;Reference number: PA0001

A;Accession: PA0029

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: callus

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9  
|||  
DB 10 VVN 12

#### RESULT 45

PS0276

phosphoribulokinase (EC 2.7.1.19) - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
C;Accession: PS0276

R;Tsugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0276

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: leaf, chlorophyll, stem

C;Keywords: phosphotransferase

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8  
|||  
DB 5 PVV 7

#### RESULT 46

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)  
C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification

A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGC5

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; me

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12  
|||  
DB 1 VLP 3

#### RESULT 47

S57577

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999

C;Accession: S57577

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversifie

A;Reference number: S57494

A;Accession: S57577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <BUR>

A;Cross-references: EMBL:Z49945; NID:G887492; PIDN:CAA90216.1; PID:G887493

C;Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3  
|||  
DB 12 LFF 14

#### RESULT 48

E56978  
collagen alpha 2(XI) chain - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Oct-1995  
C:Accession: E56978  
R:Wu, J.J.; Eyre, D.R.  
J. Biol. Chem. 270, 18865-18870, 1995  
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins  
A:Reference number: A56978; MUID:95370194; PMID:7642541  
A:Accession: E56978  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <WUR>  
A:Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in FS

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8  
|||  
DB 11 PVV 13

RESULT 49  
PH0784  
T-cell receptor alpha chain (F1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PH0784  
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0784  
A:Molecule type: mRNA  
A:Residues: 1-15 <CAS>  
A:Cross-references: EMBL:X60885  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11  
|||  
DB 10 NVL 12

RESULT 50  
A31902  
bone acidic glycoprotein-75 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 31-Dec-1993  
C:Accession: A31902  
R:Gorski, J.P.; Shimizu, K.  
J. Biol. Chem. 263, 15938-15945, 1988  
A:Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone tha  
A:Reference number: A31902; MUID:89034045; PMID:2846530  
A:Accession: A31902  
A:Molecule type: protein  
A:Residues: 1-15 <GOR>  
A:Note: 14-Glu and 15-Glu were also found  
C:Keywords: glycoprotein

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
|||

DB 1 LPV 3

RESULT 51  
AF0832  
pne leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (str  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AF0832  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra  
S.; Moulie, S.; O'Gea, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AF0832  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:g16503820; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2853a

Query Match 25.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4  
|||  
DB 6 PFF 8

RESULT 52  
I40065  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C:Species: Buchnera aphidicola  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C:Accession: I40065  
R:Roubbakhsh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (end  
A:Reference number: I40061; MUID:95212914; PMID:7535281  
A:Accession: I40065  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <RES>  
A:Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718  
C:Genetics:  
A:Gene: aroE  
C:Keywords: oxidoreductase

Query Match 25.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3  
|||  
DB 3 LFF 5

RESULT 53  
G49039  
T-cell receptor beta chain V-D-J-C region (V beta 4, J beta 2.2) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C:Accession: G49039  
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
Eur. J. Immunol. 22, 541-549, 1992  
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis usi  
A:Reference number: A49039; MUID:92164737; PMID:1311263  
A:Accession: G49039

A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-16 <ROS>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:90719)  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 13 LFF 15

## RESULT 54

H49039 T-cell receptor beta chain V-D-J-C region (V beta 5, J beta 1.4) - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
 C:Accession: H49039  
 R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
 Eur. J. Immunol. 22, 541-549, 1992  
 A>Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using  
 A:Reference number: A49039; MUID:92164737; PMID:1311263  
 A:Accession: H49039  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-16 <ROS>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:90720)  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 13 LFF 15

## RESULT 55

G24687 T-cell receptor beta-1 chain J-B1.4 segment - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
 C:Accession: G24687  
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A>Title: Organization and sequences of the diversity, joining, and constant region genes  
 A:Reference number: A94081; MUID:86094276; PMID:3866244  
 A:Accession: G24687  
 A:Molecule type: DNA  
 A:Residues: 1-16 <TOY>  
 A:Cross-references: GB:M14158; NID:G338844; PIDN:AAA60671.1; PID:G553683  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 5 LFF 7

## RESULT 56

A28587 T-cell receptor beta-2 chain J-B2.2 segment - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
 C:Accession: A28587  
 R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A>Title: Organization and sequences of the diversity, joining, and constant region ge.  
 A:Reference number: A94081; MUID:86094276; PMID:3866244  
 A:Accession: A28587  
 A:Molecule type: DNA  
 A:Residues: 1-16 <TOY>  
 A:Cross-references: GB:M14159; NID:G338852; PIDN:AAA60676.1; PID:G553687  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 5 LFF 7

## RESULT 57

PH1476 T-cell receptor beta chain (clone 223/14) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C:Accession: PH1476  
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;  
 J. Exp. Med. 177, 811-820, 1993  
 A>Title: T cell receptor selection by and recognition of two class I major histocompa  
 A:Reference number: PH1430; MUID:93171821; PMID:8436911  
 A:Accession: PH1476  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <CAS>  
 A:Experimental source: cytolytic T-lymphocyte  
 C:Superfamily: immunoglobulin homology  
 C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 13 LFF 15

## RESULT 58

PH1475 T-cell receptor beta chain (clone 223/S) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C:Accession: PH1475  
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;  
 J. Exp. Med. 177, 811-820, 1993  
 A>Title: T cell receptor selection by and recognition of two class I major histocompa  
 A:Reference number: PH1430; MUID:93171821; PMID:8436911  
 A:Accession: PH1475  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <CAS>  
 A:Experimental source: cytolytic T-lymphocyte  
 C:Superfamily: immunoglobulin homology  
 C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
 Db 13 LFF 15

## RESULT 59

PH1474 T-cell receptor beta chain (clone A2/25) - mouse (fragment)

```
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1474
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1474
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 13 LFF 15

RESULT 60
PH1472
T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1472
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1472
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 13 LFF 15

RESULT 61
PH1477
T-cell receptor beta chain (clone A3/H2R5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1477
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1477
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 13 LFF 15

RESULT 62
PH1473
T-cell receptor beta chain (clone A3/IIIC5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1473
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.;
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompa
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1473
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 13 LFF 15

RESULT 63
PH0766
T-cell receptor beta chain (J3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0766
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0766
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60860; NID:g52745; PIDN:CAA43250.1; PID:g52746
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 25.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 13 LFF 15

RESULT 64
PH0767
T-cell receptor beta chain (J5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0767
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0767
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: EMBL:X60861; NID:g52752; PIDN:CAA43251.1; PID:g52753
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor
```

Query Match 25.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
Db 13 LFF 15

## RESULT 65

PH1480  
T-cell receptor beta chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 27-Oct-1995  
C:Accession: PH1480; PH1478  
R; Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kojima, Y.; Exp. Med. 177; 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1480  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS1>  
A:Experimental source: cytolytic T-lymphocyte, clone A3/C80b  
A:Accession: PH1478  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS2>  
A:Experimental source: cytolytic T-lymphocyte, clone A24/PBFS  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 25.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3  
Db 13 LFF 15

## RESULT 66

165274  
glutathione S-transferase Ya subunit (put.) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 18-Jun-1999  
C:Accession: I65274  
R; Rothkopf, G.S.; Telakowski-Hopkins, C.A.; Stotish, R.L.; Pickett, C.B.  
Biochemistry 25; 993-1002, 1986  
A:Title: Multiplicity of glutathione S-transferase genes in the rat and association with glutathione S-transferase Ya subunit (put.) - rat (fragment)  
A:Reference number: I52395; MUID:86187772; PMID:2421763  
A:Accession: I65274  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-17 <RSS>  
A:Cross-references: GB:M12894; NID:g204504; PIDN:AAA1289.1; PID:g204505  
C:Superfamily: glutathione transferase

Query Match 25.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPV 7  
Db 1 LPV 3

## RESULT 67

C37520  
glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 30-Sep-1993  
C:Accession: C37520; N24735  
R; Mannervik, B.; Allin, P.; Guichenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jornvall, J. Proc. Natl. Acad. Sci. U.S.A. 82; 7202-7206, 1985

A:Title: Identification of three classes of cytosolic glutathione transferase common  
A:Reference number: A24735; MUID:86042634; PMID:3864155  
A:Accession: C37520  
A:Molecule type: protein  
A:Residues: 1-17 <MAN>  
C:Superfamily: glutathione transferase  
C:Keywords: transferase

Query Match 25.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVV 8  
Db 9 PVV 11

## RESULT 68

I49425  
mitogen regulated protein - western wild mouse (fragment)  
C:Species: Mus spretus (western wild mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
C:Accession: I49425  
R; Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J. Mamm. Genome 5; 349-355, 1994  
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A:Reference number: I48934; MUID:94319082; PMID:8043949  
A:Accession: I49425  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-17 <RSS>  
A:Cross-references: EMBL:U05748; NID:g497088; PIDN:AAB60483.1; PID:g497089  
C:Superfamily: prolactin

Query Match 25.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
Db 5 NVL 7

## RESULT 69

S05913  
chorion class A protein L2 precursor - silkworm (fragment)  
C:Species: Bombyx mori (silkworm)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999  
C:Accession: S05913  
R; Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.  
J. Mol. Biol. 209; 1-19, 1989  
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization of Bombyx mori chorion class A protein L2 precursor - silkworm (fragment)  
A:Reference number: S05913; MUID:90040707; PMID:2810362  
A:Accession: S05913  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-17 <SPO>  
A:Cross-references: EMBL:X15558; NID:g5771; PIDN:CAA33567.1; PID:g5772  
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989  
C:Genetics:  
A:Map position: 2  
C:Superfamily: chorion class A protein pc292

Query Match 25.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFL 5  
Db 6 FFL 8

## RESULT 70

I49593  
 cystic fibrosis transmembrane conductance regulator - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C:Accession: I49593  
 R:Denamur, E.; Chehab, F.F.  
 Hum. Mol. Genet. 3, 1089-1094, 1994  
 A:Title: Analysis of the mouse and rat CFTR promoter regions.  
 A:Reference number: I49593; MUID:95072572; PMID:7526924  
 A:Accession: I49593  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-17 <RES>  
 A:Cross-references: GB:I04873; NID:G414726; PIDN:AAA73562.1; PID:G553892  
 C:Genetics:  
 A:Gene: CFTR  
 C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFF 3  
 |||  
 Db 15 LFF 17

RESULT 71  
 I84733  
 gene CFTR protein - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
 C:Accession: I84733  
 R:Denamur, E.; Chehab, F.F.  
 Hum. Mol. Genet. 3, 1089-1094, 1994  
 A:Title: Analysis of the mouse and rat CFTR promoter regions.  
 A:Reference number: I49593; MUID:95072572; PMID:7526924  
 A:Accession: I84733  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-17 <RES>  
 A:Cross-references: GB:I26098; NID:G425185; PIDN:AAA73561.1; PID:G915270  
 C:Genetics:  
 A:Gene: CFTR  
 C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFF 3  
 |||  
 Db 15 LFF 17

RESULT 72  
 S66213  
 Glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei (fragment)  
 C:Species: Haloferax mediterranei  
 C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 30-Oct-1998  
 C:Accession: S66213  
 R:Bonete, M.J.; Pire, C.; Llorca, F.I.; Camacho, M.L.  
 FEBS Lett. 383, 227-229, 1996  
 A:Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzymatic properties and molecular cloning.  
 A:Reference number: S66213; MUID:96198607; PMID:8925901  
 A:Accession: S66213  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-17 <BON>  
 C:Keywords: oxidoreductase

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFF 3  
 |||  
 Db 15 LFF 17

RESULT 73  
 S59481  
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C>Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
 C:Accession: S59481  
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A:Title: Specificity in the immobilisation of cell wall proteins in response to different pH values.  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59481  
 A:Molecule type: protein  
 A:Residues: 1-17 <WOJ>  
 C:Keywords: glycoprotein; hydroxyproline  
 F:6,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PVV 8  
 |||  
 Db 11 PVV 13

RESULT 74  
 PS0454  
 38K protein 3129 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
 C:Accession: PS0454  
 R:Tsuji, A.  
 submitted to JPIPI, April 1993  
 A:Reference number: PS0206  
 A:Accession: PS0454  
 A:Molecule type: protein  
 A:Residues: 1-17 <TSU>  
 A:Experimental source: leaf, chloroplast, stem  
 A>Note: molecular weight 38K, pI 5.9

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 VVN 9  
 |||  
 Db 9 VVN 11

RESULT 75  
 E22595  
 Bombolitin V - American common bumblebee  
 C:Species: Bombus pennsylvanicus (American common bumblebee)  
 C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 08-Dec-1995  
 C:Accession: E22595  
 R:Argiolas, A.; Pisano, J.J.  
 J. Biol. Chem. 260, 1437-1444, 1985  
 A:Title: Bombolitin, a new class of mast cell degranulating peptides from the venom of the bumblebee.  
 A:Reference number: A92504; MUID:85105003; PMID:2578459  
 A:Accession: E22595  
 A:Molecule type: protein  
 A:Residues: 1-17 <ARG>  
 C:Keywords: amidated carboxyl end; hemolysis; venom  
 F:17/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 VVN 9  
 |||  
 Db 9 VVN 11



Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
    |||  
Db 2 NVL 4

Search completed: November 25, 2003, 18:28:16  
Job time : 12.0426 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 5.80851 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 5     | 41.7        | 17     | 1     | UP36_UPEMJ  |
| 2          | 4     | 33.3        | 14     | 1     | UC15_MAIZE  |
| 3          | 3     | 25.0        | 5      | 1     | PAP2_PARMA  |
| 4          | 3     | 25.0        | 12     | 1     | GRAR_RANRU  |
| 5          | 3     | 25.0        | 12     | 1     | TM2A_METWA  |
| 6          | 3     | 25.0        | 12     | 1     | UN39_CLOPA  |
| 7          | 3     | 25.0        | 12     | 1     | XZPT_ECOLI  |
| 8          | 3     | 25.0        | 13     | 1     | CRBL_VESAN  |
| 9          | 3     | 25.0        | 13     | 1     | CRBL_VESCR  |
| 10         | 3     | 25.0        | 13     | 1     | CRBL_VESLE  |
| 11         | 3     | 25.0        | 13     | 1     | CRBL_VESMA  |
| 12         | 3     | 25.0        | 13     | 1     | CRBL_VESTR  |
| 13         | 3     | 25.0        | 13     | 1     | CRBL_VESXA  |
| 14         | 3     | 25.0        | 13     | 1     | FIBB_RABIT  |
| 15         | 3     | 25.0        | 13     | 1     | FIBB_RANES  |
| 16         | 3     | 25.0        | 13     | 1     | HPB9_RANES  |
| 17         | 3     | 25.0        | 13     | 1     | PEDI_HYDAT  |
| 18         | 3     | 25.0        | 13     | 1     | TEMA_RANTE  |
| 19         | 3     | 25.0        | 13     | 1     | TEME_RANTE  |
| 20         | 3     | 25.0        | 13     | 1     | TEMP_RANTE  |
| 21         | 3     | 25.0        | 13     | 1     | YPNP_PHOLU  |
| 22         | 3     | 25.0        | 14     | 1     | ADFA_TENMO  |
| 23         | 3     | 25.0        | 14     | 1     | CRBL_VESOR  |
| 24         | 3     | 25.0        | 14     | 1     | LPE2_ECOLI  |
| 25         | 3     | 25.0        | 14     | 1     | PHI_FUSE    |
| 26         | 3     | 25.0        | 15     | 1     | CDN4_LITCE  |
| 27         | 3     | 25.0        | 15     | 1     | CKX_WHEAT   |
| 28         | 3     | 25.0        | 15     | 1     | ESTB_SCHGA  |
| 29         | 3     | 25.0        | 15     | 1     | LPP_ECOLI   |
| 30         | 3     | 25.0        | 15     | 1     | PH3_PRUSE   |
| 31         | 3     | 25.0        | 15     | 1     | UC08_MAIZE  |
| 32         | 3     | 25.0        | 15     | 1     | UP01_METAN  |
| 33         | 3     | 25.0        | 16     | 1     | PH2_PRUSE   |

|     |   |      |    |   |            |
|-----|---|------|----|---|------------|
| 34  | 3 | 25.0 | 17 | 1 | BOL5_MEGPE |
| 35  | 3 | 25.0 | 17 | 1 | TPIS_PINPS |
| 36  | 3 | 25.0 | 18 | 1 | A2M_OCTVU  |
| 37  | 3 | 25.0 | 18 | 1 | ALL2_CYPDO |
| 38  | 3 | 25.0 | 18 | 1 | LUXB_KRYAS |
| 39  | 3 | 25.0 | 19 | 1 | COOT_SARBU |
| 40  | 3 | 25.0 | 19 | 1 | MTFH_TRIMR |
| 41  | 3 | 25.0 | 19 | 1 | PSBN_SYNVU |
| 42  | 3 | 25.0 | 19 | 1 | UP25_UPEIN |
| 43  | 3 | 25.0 | 19 | 1 | UP27_UPEMJ |
| 44  | 3 | 25.0 | 19 | 1 | UP28_UPEMJ |
| 45  | 3 | 25.0 | 20 | 1 | CISY_STRHY |
| 46  | 3 | 25.0 | 20 | 1 | COGI_PARM  |
| 47  | 3 | 25.0 | 20 | 1 | EFTU_MYCSI |
| 48  | 3 | 25.0 | 20 | 1 | FLA_VIBAL  |
| 49  | 3 | 25.0 | 20 | 1 | FRE3_LITIN |
| 50  | 3 | 25.0 | 20 | 1 | MDH_KIBAR  |
| 51  | 3 | 25.0 | 20 | 1 | MIF_PIG    |
| 52  | 3 | 25.0 | 20 | 1 | TENB_ACTTE |
| 53  | 2 | 16.7 | 4  | 1 | FFKA_ATEFL |
| 54  | 2 | 16.7 | 4  | 1 | FLRF_HIRME |
| 55  | 2 | 16.7 | 4  | 1 | FLRN_ATEFL |
| 56  | 2 | 16.7 | 5  | 1 | PRCT_PERAM |
| 57  | 2 | 16.7 | 5  | 1 | RE11_LITRU |
| 58  | 2 | 16.7 | 5  | 1 | RE21_LITRU |
| 59  | 2 | 16.7 | 5  | 1 | RE31_LITRU |
| 60  | 2 | 16.7 | 5  | 1 | RE32_LITRU |
| 61  | 2 | 16.7 | 5  | 1 | UC22_MAIZE |
| 62  | 2 | 16.7 | 6  | 1 | ACPH_RABIT |
| 63  | 2 | 16.7 | 6  | 1 | PARP_MONEX |
| 64  | 2 | 16.7 | 6  | 1 | TRPI_PSEPU |
| 65  | 2 | 16.7 | 7  | 1 | PARI_HELTI |
| 66  | 2 | 16.7 | 7  | 1 | PARI_MACRS |
| 67  | 2 | 16.7 | 7  | 1 | PARI_PROCL |
| 68  | 2 | 16.7 | 7  | 1 | PARI_PROCL |
| 69  | 2 | 16.7 | 7  | 1 | PPH2_LYCES |
| 70  | 2 | 16.7 | 7  | 1 | UN05_PINPS |
| 71  | 2 | 16.7 | 8  | 1 | AKHG_GRYBI |
| 72  | 2 | 16.7 | 8  | 1 | AKH_LIABA  |
| 73  | 2 | 16.7 | 8  | 1 | ALL6_CYPDO |
| 74  | 2 | 16.7 | 8  | 1 | CADI_ENTFA |
| 75  | 2 | 16.7 | 8  | 1 | CLP_THICU  |
| 76  | 2 | 16.7 | 8  | 1 | COW2_CONPU |
| 77  | 2 | 16.7 | 8  | 1 | CPDI_ENTFA |
| 78  | 2 | 16.7 | 8  | 1 | FARI_PANRE |
| 79  | 2 | 16.7 | 8  | 1 | FARI_PENMO |
| 80  | 2 | 16.7 | 8  | 1 | FAR2_MACRS |
| 81  | 2 | 16.7 | 8  | 1 | FAR3_HOMAM |
| 82  | 2 | 16.7 | 8  | 1 | FAR3_HOMAM |
| 83  | 2 | 16.7 | 8  | 1 | FUSO_FUSSO |
| 84  | 2 | 16.7 | 8  | 1 | HTFI_PERAM |
| 85  | 2 | 16.7 | 8  | 1 | NPB_BOVIN  |
| 86  | 2 | 16.7 | 8  | 1 | NS3_MYCTU  |
| 87  | 2 | 16.7 | 8  | 1 | PLP_BRANA  |
| 88  | 2 | 16.7 | 8  | 1 | UPAL_HUMAN |
| 89  | 2 | 16.7 | 9  | 1 | BS43_SERPL |
| 90  | 2 | 16.7 | 9  | 1 | FAR2_PANRE |
| 91  | 2 | 16.7 | 9  | 1 | FAR3_MACRS |
| 92  | 2 | 16.7 | 9  | 1 | FAR6_MACRS |
| 93  | 2 | 16.7 | 9  | 1 | FAR8_MACRS |
| 94  | 2 | 16.7 | 9  | 1 | FARP_CALSI |
| 95  | 2 | 16.7 | 9  | 1 | FIBB_EKIPA |
| 96  | 2 | 16.7 | 9  | 1 | FIBB_MACFU |
| 97  | 2 | 16.7 | 9  | 1 | FIBB_PAPAN |
| 98  | 2 | 16.7 | 9  | 1 | FIBB_PAPHA |
| 99  | 2 | 16.7 | 9  | 1 | FIBB_THEGE |
| 100 | 2 | 16.7 | 9  | 1 | MOSF_CLYJA |

ALIGNMENTS

RESULT 1

```

UP36 UPEMJ
ID UP36 UPEMJ STANDARD; PRT; 17 AA.
AC P82043;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 3.6.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1826; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 17
FT SEQUENCE 17 AA; 1778 MW; 784D9BB46263CA3D CRC64;
SQ
Query Match 41.7%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNVL 11
Db 9 VVNVL 13

RESULT 2
UC15 MAIZE
ID UC15 MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON_TER 1
FT NON_TER 14
FT SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;
SQ
Query Match 33.3%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 5 LPVV 8

```

```

Db 5 LPVV 8

RESULT 3
PAP2 PARMA
ID PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
FT SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;
SQ
Query Match 25.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
Db 2 FFF 4

RESULT 4
GRAR RANRU
ID GRAR RANRU STANDARD; PRT; 12 AA.
AC P40754;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Granuliberin-R.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=78062810; PubMed=589733;
RA Nakajima T., Yasuhara T.;
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
RT (Rana rugosa) skin.";
RL Chem. Pharm. Bull. 25:2464-2465(1977).
RN [2]
RP SYNTHESIS.
RX MEDLINE=78189201; PubMed=657408;
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
RA Koyama K., Yajima H.;
RT "Synthesis of the dodecapeptide amide corresponding to the entire
RT amino acid sequence of granuliberin-R, a new frog skin peptide from
RT Rana rugosa.";

```

```

RL Chem. Pharm. Bull. 26:1222-1230(1978).
CC -!- FUNCTION: Mast cell degranulating peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Mast cell degranulation; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1424 MW; 2B974BB9CA1B5047 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 3 FLP 5

RESULT 5
TN2A_METMA STANDARD; PRT; 12 AA.
ID TM2A_METMA
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Go1
RT reconstituted in ether lipid liposomes.";
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 6DB4A5766232D76B CRC64;

Query Match 25.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
DB 7 VLP 9

RESULT 6
UN39_CLOPA STANDARD; PRT; 12 AA.
ID UN39_CLOPA
AC P81359;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 39 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.

```

---

```

OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengstrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 23.5 kDa.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; 940561E66BD2CB01 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 7 VVN 9

RESULT 7
YZPY_ECOLI STANDARD; PRT; 12 AA.
ID YZPY_ECOLI
AC P17776;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Hypothetical PYRE leader peptide.
OS PYRL OR PYRE-LP
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85003586; PubMed=6207018;
RA Poulsen P., Bonnekamp F., Jensen K.F.;
RT "Structure of the Escherichia coli PYRE operon and control of PYRE
RT expression by a UTP modulated intercistronic attenuation.";
RL EMBO J. 3:1783-1790(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83287414; PubMed=6349999;
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
RA Lundberg L.G.;
RT "Nucleotide sequence of the Escherichia coli PYRE gene and of the DNA
RT in front of the protein-coding region.";
RL Eur. J. Biochem. 135:223-229(1983).
CC -!- CAUTION: THIS SEQUENCE, ACCORDING TO THE EMBL DATABASE (K. RUDD)
CC IS PROBABLY NOT A REAL PROTEIN; THEREFORE THIS ENTRY WILL PROBABLY
CC BE DELETED IN FUTURE RELEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/ebis-sib.ch/
CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL; X00781; -; NOT ANNOTATED CDS.
CC DR EMBL; V01578; -; NOT ANNOTATED_CDS.
CC DR PIR; A30400; LFECPF.
KW Hypothetical protein.
SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LFP 3  
Db 4 LFP 6

RESULT 8  
CRBL\_VESAN STANDARD; PRT; 13 AA.  
AC P17233;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide A (VESCP-A).  
OS Vespa analis (Hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7449;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,  
RA Fujino M.;  
RL (In) Murekata E. (eds.);  
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,  
RL Osaka (1984).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils.  
KW Mast cell degranulation; Chemotaxis; Amidation.  
FT MOD RES 13 13  
SQ SEQUENCE 13 AA; 1386 MW; C85554365DF9233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
Db 1 FLP 3

RESULT 9  
CRBL\_VESCR STANDARD; PRT; 13 AA.  
AC P01518;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Crabrolin.  
OS Vespa crabro (European hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7445;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=84289390; PubMed=6206053;  
RA Argiolas A., Pisano J.J.;  
RT "Isolation and characterization of two new peptides, mastoparan C and  
RT crabrolin, from the venom of the European hornet, Vespa crabro.";  
RL J. Biol. Chem. 259:10106-10111(1984).  
RN [2]  
RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
RX MEDLINE=97419326; PubMed=9273892;  
RA Krishnakumari V., Nagaraj R.;  
RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
RT peptide from the venom of the European hornet, Vespa crabro, and its  
RT analogs.";  
RL J. Pept. Res. 50:88-93(1997).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils. Has antimicrobial and hemolytic activity.

DR PIR; A01781; JZVHP1.  
KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.  
FT MOD RES 13 13  
SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
Db 1 FLP 3

RESULT 10  
CRBL\_VESLE STANDARD; PRT; 13 AA.  
AC P17235;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide L (VESCP-L).  
OS Vespa lewisii (Yellow jacket) (Wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7452;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
RL (In) Izumiya N. (eds.);  
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,  
RL Osaka (1985).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils.  
KW Mast cell degranulation; Chemotaxis; Amidation.  
FT MOD RES 13 13  
SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
Db 1 FLP 3

RESULT 11  
CRBL\_VESMA STANDARD; PRT; 13 AA.  
AC P17232;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide M (VESCP-M).  
OS Vespa mandarinia (Hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7446;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,  
RA Fujino M.;  
RL (In) Murekata E. (eds.);  
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,  
RL Osaka (1984).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils.  
KW Mast cell degranulation; Chemotaxis; Amidation.

FT MOD RES 13 13 AMIDATION.  
SQ SEQUENCE 13 AA; 1384 MW; 265040289DF92338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 12

ID\_CRL\_VESX STANDARD; PRT; 13 AA.  
AC P17231;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide T (VESP-T).  
OS Vespa tropica (Hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7450;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Yasuhara T., Nakajima T., Erspaer V.;  
RL (In) Sakakibara S. (eds.);  
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,  
RL Osaka (1983).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils.  
KW Mast cell degranulation; Chemotaxis; Amidation.  
FT MOD RES 13 13  
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 13

ID\_CRL\_VESXA STANDARD; PRT; 13 AA.  
AC P17234;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide X (VESP-X).  
OS Vespa xanthoptera (Japanese hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7448;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;  
RL (In) Izumiya N. (eds.);  
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,  
RL Osaka (1985).  
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
of neutrophils.  
KW Mast cell degranulation; Chemotaxis; Amidation.  
FT MOD RES 13 13  
SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
|||  
Db 1 FLP 3

## RESULT 14

ID\_FIBB\_RABIT STANDARD; PRT; 13 AA.  
AC P14478;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals.";  
RL Acta Chem. Scand. 19:1789-1791(1965).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR InterPro: IPR002181; Fibrinogen C.  
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.  
FT MOD RES 4 4 SULFATION.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12  
|||  
Db 8 VLP 10

## RESULT 15

ID\_HPA1\_RANES STANDARD; PRT; 13 AA.  
AC P32415;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hemolytic protein A1 (Fragment).  
OS Rana esculenta (Edible frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8401;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90198965; PubMed=2317508;  
RA Simmaco M., de Biase D., Severini C., Alta M., Erspaer G.F.,  
RA Barra D., Bossa F.;  
RT "Purification and characterization of bioactive peptides from skin  
extracts of Rana esculenta.";

Query Match 25.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12  
|||  
Db 8 VLP 10

```

RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S09018.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 16
HPB9 RANES
ID HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S09019;
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 17
PEDI_HYDAT
ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;

```

```

RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLP 12
Db 7 VLP 9

RESULT 18
TEMA RANTE
ID TEMA RANTE STANDARD; PRT; 13 AA.
AC P56917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin A.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1398 MW; 2653612B99ECD408 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 19
TEME RANTE
ID TEME RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;

```

```

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RA "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
DB 1 VLP 3

RESULT 20
TEMP_RANGE
ID TEMP_RANGE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RX MEDLINE=9175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
DB 1 FLP 3

RESULT 21
YFNP_PHOLU
ID YFNP_PHOLU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3' region (ORF3) (Fragment).
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.

```

```

OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photorhabdus sp.
RT strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76069; CAAS3672.1; -.
KW Hypothetical protein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFL 5
DB 3 PFL 5

RESULT 22
ADFA_TENMO
ID ADFA_TENMO STANDARD; PRT; 14 AA.
AC P82965;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Head;
RX MEDLINE=21642653; PubMed=11756661;
RA Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
RT "Identification of a potent antidiuretic factor acting on beetle
RT Malpighian tubules.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC -!- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian
CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC PROTEIN LFCP29.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005184; F:neuropeptide hormone activity; NAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Neuropeptide; Hormone.
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 1 VVN 3

```



## RESULT 23

CREL\_VESOR STANDARD; PRT; 14 AA.  
 AC FL236;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histamine releasing peptide II (HR-II).  
 OS Vespa orientalis (Oriental hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 NCBI\_TaxID=7447;  
 RN NCBI  
 [1]  
 RN SEQUENCE.  
 RC TISSUE=Venom;  
 RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,  
 RA Rozynov B.V., Gushchin I.S.;  
 RT "Structure and properties of histamine releasing peptides from the  
 RT venom of Vespa orientalis hornet."  
 RL Bioorg. Khim. 7:1467-1477(1981).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 CC PIR; JN0390; JN0390.  
 KW Mast cell degranulation; Chemotaxis; Amidation.  
 FT MOD RES 14 14  
 SQ SEQUENCE 14 AA; 1524 NW; 22015B4A6CEDFD38 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FLP 6  
 DB 1 FLP 3

## RESULT 24

LPF2\_ECOLI STANDARD; PRT; 14 AA.  
 AC P06985;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phenylalanyl-tRNA synthetase operon leader peptide (PheST attenuator  
 DE peptide).  
 GN PHM OR PHTL OR B1715 OR C5495 OR Z2744 OR ECS2422 OR STY1774 OR T1217  
 GN OR SF1516.  
 OS Escherichia coli,  
 OS Escherichia coli O6,  
 OS Escherichia coli O157:H7,  
 OS Salmonella typhi, and  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NCBI\_TaxID=562, 217992, 83334, 601, 623;  
 RN NCBI  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=E. coli;  
 RX MEDLINE=85210878; PubMed=3158742;  
 RA Springer M., Mayaux J.-F., Fayat G., Plunbridge J.A., Graffe M.,  
 RA Blanquet S., Grunberg-Manago M.;  
 RT "Attenuation control of the Escherichia coli phenylalanyl-tRNA  
 RT synthetase operon."  
 RL J. Mol. Biol. 181:467-478(1985).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=E. coli;  
 RX MEDLINE=84030239; PubMed=6317865;  
 RA Fayat G., Mayaux J.-F., Sacerdot C., Fromant M., Springer M.,  
 RA Grunberg-Manago M., Blanquet S.;

RT "Escherichia coli phenylalanyl-tRNA synthetase operon region.  
 RT Evidence for an attenuation mechanism. Identification of the gene for  
 RT the ribosomal protein L20."  
 RL J. Mol. Biol. 171:239-261(1983).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=E. coli;  
 RC MEDLINE=88163794; PubMed=3126825;  
 RX Springer M., Graffe M., Mayaux J.-F., Dardel F., Fayat G.,  
 RA Blanquet S., Grunberg-Manago M.;  
 RT "Open reading frames in the control regions of the phenylalanyl-tRNA  
 RT synthetase operon of E. coli."  
 RL Biochimie 69:1065-1070(1987).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=E. coli; STRAIN=KL2 / MG1655;  
 RC MEDLINE=97426617; PubMed=9278503;  
 RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12."  
 RL Science 277:12453-12474(1997).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=E. coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;  
 RC MEDLINE=22388234; PubMed=12471157;  
 RX Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic Escherichia coli."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=E. coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RC MEDLINE=21074935; PubMed=11206551;  
 RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
 RL Nature 409:529-533(2001).  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=E. coli; STRAIN=O157:H7 / RIMD 0509952;  
 RC MEDLINE=21156231; PubMed=11258796;  
 RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,  
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12."  
 RL DNA Res. 8:11-22(2001).  
 RN [8]  
 RN SEQUENCE FROM N.A.  
 RP SPECIES=S. typhi; STRAIN=CT18;  
 RC MEDLINE=21534947; PubMed=11677608;  
 RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18."  
 RL Nature 413:848-852(2001).  
 RN [9]

RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative Genomics of Salmonella enterica serovar Typhi strains Ty2  
RT and C718.";  
RL J. Bacteriol. 185:2330-2337(2003).  
RN [10]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
RX MEDLINE=2272406; PubMed=12384590;  
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
RA Yu J.;  
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
RT through comparison with genomes of Escherichia coli K12 and O157.";  
RL Nucleic Acids Res. 30:4432-4441(2002).  
RN -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
RN -----  
DR EMBL; M10423; AAA23961.1; -;  
DR EMBL; V00291; CAA23563.1; -;  
DR EMBL; M13251; AAA24333.1; -;  
DR EMBL; AB000266; AAC74785.1; -;  
DR EMBL; AB016761; AAN80571.1; -;  
DR EMBL; AB005394; AAG56702.1; -;  
DR EMBL; AF002558; BAB35845.1; -;  
DR EMBL; AL627271; CAD02016.1; -;  
DR EMBL; AB016838; AAC66872.1; -;  
DR EMBL; AB015174; AAN43106.1; -;  
DR PIR; B85780; B85780.  
DR PIR; F90931; F90931.  
DR PIR; S11551; LFECPFS.  
DR EcoGene; EGI1272; pHEM.  
KW Leader peptide; Complete proteome.  
SQ SEQUENCE 14 AA; 1762 MW; 7031C48E0060F0D4 CRC64;  
Query Match 25.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FFF 4  
Db 8 FFF 10  
RESULT 25  
PHI\_PRUSE  
ID PHI\_PRUSE STANDARD; PRT; 14 AA.  
AC F29263;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase  
DE isozyme I) (PH I) (Fragment).  
OS Prunus serotina (Black cherry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
RN [1]\_TaxID=23207;  
RP SEQUENCE.  
RC TISSUE=Seed;  
RA Li C.P., Swain E., Poulton J.E.;

RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
RL Plant Physiol. 100:282-290(1992).  
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
CC glucose.  
CC -!- SUBUNIT: Monomer.  
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
CC EMBRYONAL TISSUES.  
CC -!- PTM: GLYCOSYLATED.  
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1575 MW; F83D7F4FB90CA9CA CRC64;  
Query Match 25.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PVV 8  
Db 4 PVV 6  
RESULT 26  
CDNA\_LITCE  
ID CDNA\_LITCE STANDARD; PRT; 15 AA.  
AC F82076;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Caeridin 4  
OS Litoria caerulea (Green tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OC NCBI\_TaxID=30344;  
RN [1]\_TaxID=30344;  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Parotoid gland;  
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. Structures of the caeridins from  
RT Litoria caerulea.";  
RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).  
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
CC glands.  
CC -!- MASS SPECTROMETRY: MW=1504; METHOD=FAB.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 15 15  
SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;  
Query Match 25.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 NVL 11  
Db 8 NVL 10  
RESULT 27  
CKX\_WHEAT  
ID CKX\_WHEAT STANDARD; PRT; 15 AA.  
AC P58763;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (CKX) (Fragment).  
OS Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=cv. Samanthera;  
 RX MEDLINE=21099312; PubMed=11168382;  
 RA Galuszka P., Frebort I., Sebelia M., Sauer P., Jacobsen S., Pec P.;  
 RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin  
 RT degradation in cereals.";  
 RL Eur. J. Biochem. 268:450-461(2001).  
 CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-  
 CC substituted adenine derivatives that are plant hormones, where the  
 CC substituent is an isopentenyl group. Substrate preference is 2-(2-  
 CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>  
 CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>  
 CC zeatin riboside.  
 CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +  
 CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).  
 CC -!- COFACTOR: FAD.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).  
 CC -!- MISCELLANEOUS: Optimal pH is 6.5.  
 CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
 CC oxidoreductase family.  
 KW Oxidoreductase; Flavoprotein; FAD.  
 FT UNSURE 1 1  
 FT UNSURE 13 15  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;  
  
 Query Match 25.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 FLP 6  
 DB 1 FLP 3  
  
 RESULT 28  
 ESTB\_SCHGA  
 ID ESTB\_SCHGA STANDARD; PRT; 15 AA.  
 AC P81011;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Esterase 56 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)  
 DE (Fragment).  
 OS Schizaphis graminum (Aphid).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 CC Aphidoidea; Aphididae; Aphidini; Schizaphis.  
 OX NCBI\_TaxID=13262;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=97468499; PubMed=9327586;  
 RA Siegfried B.D., Ono M., Swanson J.J.;  
 RT "Purification and characterization of a carboxylesterase associated  
 RT with organophosphate resistance in the greenbug, Schizaphis graminum  
 RT (Homoptera: Aphididae).";  
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).  
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; PARTIAL.  
 KW Hydrolase; Serine esterase.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1609 MW; 1208B2BCC969482 CRC64;  
  
 Query Match 25.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 PW 8  
 DB 2 PW 4  
  
 RESULT 29  
 LPP\_ECOLI  
 ID LPP\_ECOLI STANDARD; PRT; 15 AA.  
 AC P03057;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE PHE leader peptide (Attenuator peptide).  
 GN PHE OR PHEAF OR B2598 OR SF2658.  
 CC Escherichia coli, and  
 CC Shigella flexneri.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562, 623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=79033820; PubMed=360214;  
 RA Zurawski G., Brown K., Killingly D., Yanofsky C.;  
 RT "Nucleotide sequence of the leader region of the phenylalanine operon  
 RT of Escherichia coli.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=91072346; PubMed=2254312;  
 RA Gavini N., Davidson B.E.;  
 RT "phea mutants of Escherichia coli have a defective pheA attenuator.";  
 RL J. Biol. Chem. 265:21532-21535(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97428617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1232-1244(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
 RX MEDLINE=22272406; PubMed=12384590;  
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
 RA Yu J.;  
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
 RT through comparison with genomes of Escherichia coli K12 and O157.";  
 RL Nucleic Acids Res. 30:4432-4441(2002).  
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
 CC OF PHENYLALANINE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; V00314; CAA23600.1; -;  
 CC EMBL; M10431; AAA24329.1; -;  
 CC EMBL; M58024; AAA62783.1; -;.

```

DR EMBL; AE000346; AAC75647.1; -.
DR EMBL; AE015281; AAN44154.1; -.
DR PIR; A03593; LFECF.
DR EcoGene; EG11271; pheL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFF 4
DB 6 PFF 8

RESULT 30
PH3_PRUSE
ID PH3_PRUSE STANDARD; PRT; 15 AA.
AC P29265;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme IIB) (PH IIB) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FW NON_TPR 15 15
SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 25.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
DB 5 PVV 7

RESULT 31
UC08_MAIZE
ID UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.

```

```

RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -!- SUBUNIT: Homodimer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4PB90CFE01 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
DB |||
6 PVV 8

RESULT 34
BOL5 MEGPE STANDARD; PRT; 17 AA.
AC P07496;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin V.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Argiolas A., Pisano J.J.;
RT "Bombolitin, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; E22595; E22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1731 MW; B076C091571606A5 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
DB |||
2 NVL 4

RESULT 35
TPIS PINPS STANDARD; PRT; 17 AA.
AC P81656;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragments).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;

```

```

RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- INDUCTION: By water stress.
CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 kDa.
CC -!- SIMILARITY: BELONGS TO THE TRIOSPHOSPHATE ISOMERASE FAMILY.
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_CONS 9 10
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;

Query Match 25.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
DB |||
9 LFF 11

RESULT 36
AZM_OCTVU STANDARD; PRT; 18 AA.
AC P30800;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344633; PubMed=1379044;
RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Engild J.J.;
RT "Purification and characterization of an alpha-macroglobulin
RT proteinase inhibitor from the mollusc Octopus vulgaris.";
RL Biochem. J. 285:521-527(1992).
CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
DR PIR; S23971; S23971.
DR GO; GO:0016575; F.alpha-2 macroglobulin; NAS.
DR InterPro; IPR001599; MacroglobinA2.

```

DR Pfam: PF00207; A2M; 1.  
 DR PROSITE: PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;  
 KW Thioester bond.  
 FT NON TER 1 1  
 FT CROSSLINK 5 8 Isoglutamyl cysteine thioester (Cys-Gln).  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;

Query Match 25.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11  
 ||||  
 DB 16 NVL 18

## RESULT 37

ALL2 CYDPO  
 ID ALL2 CYDPO STANDARD; PRT; 18 AA.  
 AC P82153;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 2.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RA MEDLINE=98054539; PubMed=9392829;  
 RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 18 18  
 SQ SEQUENCE 18 AA; 2169 MW; 8B66679C0C0F175C CRC64;

Query Match 25.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
 ||||  
 DB 11 LPV 13

## RESULT 38

LUXB KRYAS  
 ID LUXB KRYAS STANDARD; PRT; 18 AA.  
 AC P18300;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase  
 DE beta chain) (Fragment).  
 GN LUXB.

OS Kryptophanon alfredi symbiont.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; light emitting symbionts of fish.  
 OX NCBI\_TaxID=28177;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91076680; PubMed=2256783;  
 RA Haygood M.G.;  
 RT "Relationship of the luminous bacterial symbiont of the Caribbean  
 flashlight fish, Kryptophanon alfredi (family Anomalopidae) to

RT other luminous bacteria based on bacterial luciferase (luxA) genes.";  
 RL Arch. Microbiol. 154:496-503(1990).  
 CC -!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE  
 CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY  
 CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.  
 CC -!- CATALYTIC ACTIVITY: RCHO + FMN(2) + O(2) = RCOOH + FMN + H(2)O +  
 CC light.  
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----

DR EMBL: M36597; AAA91214.1;  
 DR InterPro: IPR002103; Bac\_luciferase.  
 DR PROSITE: PS00494; BACTERIAL LUCIFERASE; PARTIAL.  
 KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;  
 KW Flavoprotein; FMN.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;

Query Match 25.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPF 3  
 ||||  
 DB 5 LPF 7

## RESULT 39

COOT SARBU  
 ID COOT SARBU STANDARD; PRT; 19 AA.  
 AC Q09148;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE NEB-collcoostatin (Folliculostatin).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95188911; PubMed=7883009;  
 RA Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,  
 RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;  
 RT "Neb-collcoostatin, a second folliculostatin of the grey fleshfly,  
 RT Neobellieria bullata.";  
 RL Eur. J. Biochem. 228:45-49(1995).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO  
 CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC  
 CC FOLLICLES.

CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.  
 CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM  
 CC COLLAGEN IV.  
 DR PIR; S69153; S69153.  
 SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
 ||||  
 DB 7 LPV 9

```

RESULT 40
MIFP_TRIMR
ID MIFP_TRIMR STANDARD; PRT; 19 AA.
AC P81530;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory
DE factor homolog) (Fragment).
OS Trichuris muris (Mouse whipworm).
OC Eukaryota; Metazoa; Nematoda; Ecnephia; Trichocephalida; Trichuridae;
OC Trichuris.
OX NCBI_TaxID=70415;
RN [1]
RP SEQUENCE.
RX MEDLINE=99013685; PubMed=9794786;
RA Pennock J.L., Behnke J.M., Bickle O.D., Devaney E., Grenier R.K.,
RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT "Rapid purification and characterization of L-dopamine-methyl-ester
RT tautomerase (macrophage migration inhibitory factor) from Trichinella
RT spiralis, Trichuris muris and Brugia pahangi."
RL Biochem. J. 335:495-498(1998).
CC -!- FUNCTION: INHIBITED BY FREE FATTY ACIDS AND HARMATIN.
CC -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR InterPro; IPR001398; MIF.
DR PROSITE; PS01159; MIF; PARTIAL.
KW Cytokine.
FT NON_TER
FT Cytokine.
SQ SEQUENCE 19 AA; 2058 MW; F7D70C81D12F1234 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFL 5
Db 17 FFL 19

RESULT 41
PSBN_SYNNU
ID PSBN_SYNNU STANDARD; PRT; 19 AA.
AC P12313;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem II reaction center N protein (fragment).
GN PSBN.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338735; PubMed=2503398;
RA Ikeuchi M., Koike H., Inoue Y.;
RA "N-terminal sequencing of low-molecular-mass components in
RT cyanobacterial photosystem II core complex. Two components correspond
RT to unidentified open reading frames of plant chloroplast DNA."
RL FEBS Lett. 253:178-182(1989).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: Belongs to the psbN family.
DR HAMAP; MF 00293; -; 1.
KW Photosystem II; Transmembrane.
FT MOD_RES 1 1 BLOCKED.
FT TRANSMEM 6 >19 POTENTIAL.
FT NON_TER 19
FT SEQUENCE 19 AA; 2217 MW; A97C99B523106D14 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LFF 3
Db 16 LFF 18

RESULT 42
UP25_UPEIN
ID UP25_UPEIN STANDARD; PRT; 19 AA.
AC P82031;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.5
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the Australian
RT floodplain toadlet Uperoleia inundata."
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: SHOWS A MEDIUM ANTIBACTERIAL ACTIVITY AGAINST M.LUTEUS,
CC -!- L.MESENTERIOIDES AND S.UBERIS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1940; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 19 AA; 1941 MW; 5E94C6C757B463D9 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11
Db 15 NVL 17

RESULT 43
UP27_UPEMJ
ID UP27_UPEMJ STANDARD; PRT; 19 AA.
AC P82039;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.7
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RT Australian toadlet Uperoleia mjobergii."
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1948; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 19 AA; 1949 MW; 24E4F83A6BA35F21 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 9 NVL 11
 |||
Db 15 NVL 17

RESULT 44
UP28_UPEMJ STANDARD; PRT; 19 AA.
AC P82040;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 2.8.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
RT australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1323-1331(1996).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS
CC S.EPIDERMIS AND S.UBERIS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1978; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 19 AA; 1979 MW; 4E524822C8A340F9 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 9 NVL 11
 |||
Db 15 NVL 17

RESULT 45
CISY_STRHY
ID _CISY_STRHY STANDARD; PRT; 20 AA.
AC P20903;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Citrate synthase (EC 2.3.3.1) (Fragment).
GN GLTA.
DE Streptomyces hygroscopicus.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE.
RC STRAIN=SF1293;
RA MEDLINE=90334852; PubMed=1368511;
RX Shimotohno K.W., Imai S., Murakami T., Seto H.;
RT "Purification and characterization of citrate synthase from
RT Streptomyces hygroscopicus SF-1293 and comparison of its properties
RT with those of 2-phosphomethylmalic acid synthase.";
RL Agric. Biol. Chem. 54:463-470(1990).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
CC CoA.
CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Homohexamer.
CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -!- SIMILARITY: Belongs to the citrate synthase family.
DR PIR; PQ0046; PQ0046.

```



OS Mycoplasma synoviae.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2109;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ULB 925 / Isolate KP9.  
 RX MEDLINE=99237234; PubMed=10220885;  
 RA Bencina D., Narat M., Dovic P., Drobic-Valic M., Habe F., Kleven S.H.;  
 RT "The characterization of Mycoplasma synoviae EF-Tu protein and  
 RT proteins involved in hemagglutination and their N-terminal amino acid  
 RT sequences";  
 RL FEMS Microbiol. Lett. 173:85-94 (1999).  
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
 CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
 CC BIOSYNTHESIS.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-TU/EF-1A SUBFAMILY.  
 DR HAMAP: 00118; -; 1.  
 DR InterPro: IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFATOR\_GTP; PARTIAL.  
 DR Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2222 MW; C3C92564B740ACC6 CRC64;  
 Query Match 25.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 VNV 10  
 Db 12 VNV 14

RESULT 48  
 FLA\_VIBAL  
 ID FLA\_VIBAL STANDARD; PRT; 20 AA.  
 AC P83150;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Flagellin (Outer membrane protein 38Va) (Omp38Va) (Fragment).  
 OS Vibrio alginolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=563;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NCIMB 1903T;  
 RA Onji M., Hirabayashi J., Suzuki S.;  
 RT "Characterization of major outer membrane proteins of Vibrio  
 RT alginolyticus and the stability against proteases";  
 RL Microbes Environ. 0:0-0(2002).  
 CC -1- FUNCTION: Flagellin is the subunit protein which polymerizes to  
 CC form the filaments of bacterial flagella.  
 CC -1- SUBCELLULAR LOCATION: Flagellar.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.  
 KW Flagella; Outer membrane.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2165 MW; 2BF12B5381E6A085 CRC64;  
 Query Match 25.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 VNV 10  
 Db 2 VNV 4

RESULT 49  
 FRE3\_LITIN

ID FRE3\_LITIN STANDARD; PRT; 20 AA.  
 AC P56249;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Frenatin 3  
 OS Litoria infrarenata (Giant tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=61195;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97368637; PubMed=9225251;  
 RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "The structures of the frenatin peptides from the skin secretion of  
 RT the giant tree frog Litoria infrarenata";  
 RL J. Pept. Sci. 2:117-124(1996).  
 CC -1- FUNCTION: Wide spectrum antimicrobial peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
 CC glands.  
 KW Amphibian defense peptide; Antibiotic.  
 SQ SEQUENCE 20 AA; 1956 MW; 7B4ABE30EAL7B20C CRC64;  
 Query Match 25.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 NVL 11  
 Db 12 NVL 14

RESULT 50  
 MDH\_KIBAR  
 ID MDH\_KIBAR STANDARD; PRT; 20 AA.  
 AC P19978;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).  
 OS MDH.  
 GN Kibdelosporangium aridum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Pseudonocardineae; Pseudonocardaceae; Kibdelosporangium.  
 OX NCBI\_TaxID=2030;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=89374824; PubMed=2775496;  
 RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;  
 RT "Purification and N-terminal amino-acid sequences of bacterial malate  
 RT dehydrogenases from six actinomycetales strains and from  
 RT phenyllobacterium immobile, strain E.";  
 RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).  
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.  
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.  
 DR PIR; S04961; S04961.  
 DR InterPro: IPR001252; Mdh.  
 DR PROSITE; PS00068; MDH; PARTIAL.  
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1989 MW; 79587B6F58C00AC9 CRC64;  
 Query Match 25.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 VNV 10  
 Db 5 VNV 7

```

RESULT 51
MIF_PIG
ID MIF_PIG STANDARD; PRT; 20 AA.
AC P80928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE tautomerase) (Glycosylation-inhibiting factor) (GIF) (Fragment).
GN MIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE.
RA Riviere S., Bouet F., Menez A., Galat A.;
RL Submitted (MAR-1997) to the SWISS-PROT data bank.
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR HSP; P14174; IGIF.
DR InterPro: IPR001398; MIF.
DR Pfam; PF01187; MIF; 1.
DR PROSITE; PS01158; MIF; 1.
KW Isomerase; Macrophage; Inflammatory response; Cytokine.
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2147 MW; 3517AF60F3012A61 CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 4 VVN 6

RESULT 52
TENB_ACTTE
ID TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
SEQUENCE.
RA MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa".
RL Toxicol 28:29-41(1990).
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; B34016; B34016.
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 25.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVN 9
DB 4 VVN 6

RESULT 53
FFKA_ANTEL
ID FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-Kamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=61110;
RN [1]
SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RT novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
DR PIR; JQ1273; JQ1273.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339CA00000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
DB 1 FF 2

RESULT 54
FLRF_HIRME
ID FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
SEQUENCE.
RP SPECIES=H.medicalinis;
RC MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Fohl J., Kartsonis M.A., Calabrese R.L.;

```

```

RT "Identification of Rfamidae neuropeptides in the medicinal leech.";
RL Peptides 12:897-908 (1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivoltis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
trivoltis.";
RL Peptides 15:31-36 (1994).
CC -1- SIMILARITY: BELONGS TO THE PARP (FMRFAMIDE RELATED PEPTIDE)
KW Neuropeptide; Amidation.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FL 5
Db 1 FL 2

RESULT 55
FLRN ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid B.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FL 5
Db 1 FL 2

RESULT 56
PRCT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OX Periplaneta americana (American cockroach),

```

```

OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256 (1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569 (1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72 (1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LP 6
Db 3 LP 4

RESULT 57
RE11 LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;

```

```

RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RA "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian defense peptide.
FT MOD RES 5
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 58
RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 59
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

```

```

OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 60
RE32_LITRU
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FF 3
Db 3 FF 4

RESULT 61
UC22_MAIZE
ID UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:1997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.  
 DR Maize-2DPAGE; P80628; COLEOPTILE.  
 DR MaizedB; 123954; -.  
 DR NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C0300000 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FF 3  
 DB ||  
 2 FF 3  
 RESULT 62  
 ACPH RABIT  
 ID ACPH RABIT STANDARD; PRT; 6 AA.  
 AC P25154;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)  
 DE (APH) (Acylaminoacyl-peptidase) (Fragment).  
 GN APEH.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Muscle;  
 RA MEDLINE=32222120; PubMed=1807161;  
 RA Krishna R.G., Chin C.C.Q., Wold F.;  
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
 RT unblocking with N-acylaminoacyl-peptide hydrolase.";  
 RL Anal. Biochem. 199;45-50(1991).  
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
 CC + peptide.  
 CC -!- SUBUNIT: Homotetramer.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.  
 DR PIR; A49792; A49792.  
 DR MEROPS; S09.004; -.  
 DR InterPro; IPR002471; Prol\_endopep\_ser.  
 DR PROSITE; PS00708; PRO\_ENDOPEP\_SER; PARTIAL.  
 KW Hydrolase; Acetylation.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 775 MW; 6732B6C40B16F000 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VL 11  
 DB ||  
 5 VL 6  
 RESULT 63  
 FARP MONEX  
 ID FARP MONEX STANDARD; PRT; 6 AA.  
 AC P41956;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE FMRFamide-like neuropeptide GNFRF-amide.  
 DE FMRFamide-2DPAGE; P80628; COLEOPTILE.  
 OS Moniezia expansa (Sheep tapeworm).  
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.  
 OX NCBI\_TaxID=28841;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=93312289; PubMed=8323531;  
 RA Maule A.G., Shaw C., Halton D.W., Thim L.;  
 RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from  
 RT the sheep tapeworm, Moniezia expansa.";  
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR; A43129; A43129.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FF 3  
 DB ||  
 3 FF 4  
 RESULT 64  
 TRPI\_PSEPU  
 ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TrpBA operon transcriptional activator (Fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PpG1 C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 RT putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING  
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; X13299; CAA31660.1; --  
 DR InterPro; IPR000847; HTH\_LYSR.  
 DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON TER  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LP 6  
 ||  
 Db 5 LP 6

RESULT 65  
 FARI\_HELTI  
 ID FARI\_HELTI STANDARD; PRT; 7 AA.  
 AC P41871;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide GDPFLRF-amide.  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Planorbidae; Helisoma.  
 OX NCBI\_TaxID=27815;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 trivolvis";  
 RL Peptides 15:31-36(1994).  
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
 CC THE KIDNEY, MANTLE AND SKIN.  
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 7  
 FT SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;  
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FL 5  
 ||  
 Db 4 FL 5

RESULT 66  
 FARI\_MACRS  
 ID FARI\_MACRS STANDARD; PRT; 7 AA.  
 AC P83274;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLPI (DRNPLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;

RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=Eyestalk;  
 RC Sithigornkul P., Saraithongkum W., Jaidechoey S., Longyant S.,  
 RA Sithigornkul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
 DR Neuropeptide; Amidation.  
 KW MOD RES 7  
 FT SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;  
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FL 5  
 ||  
 Db 4 FL 5

RESULT 67  
 FARI\_PROCL  
 ID FARI\_PROCL STANDARD; PRT; 7 AA.  
 AC P38499;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRFamide homolog NF1.  
 OS Procambarus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacidea; Cambaridae; Procambarus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebruggge V., Skerrett M.;  
 RT "Isolation of two FMRFamide-related peptides from crayfish  
 RT pericardial organs";  
 RL Peptides 14:137-143(1993).  
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 7  
 FT SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FL 5  
 ||  
 Db 4 FL 5

RESULT 68  
 FARI\_PROCL  
 ID FARI\_PROCL STANDARD; PRT; 7 AA.  
 AC P38498;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRFamide homolog DF2.  
 OS Procambarus clarkii (Red swamp crayfish).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacoidea; Cambaridae; Procambarus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=92248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRFamide-related peptides from crayfish  
 RT pericardial organs.";  
 RL Peptides 14:137-143(1993).  
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 7  
 FT SEQUENCE 7 AA; 967 MW; 69040729C4540AC0 CRC64;  
 SQ SEQUENCE 7 AA; 967 MW; 69040729C4540AC0 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 FL 5  
 Db 4 FL 5  
 RESULT 69  
 PPH2\_LYCES  
 ID \_PPH2\_LYCES STANDARD; PRT; 7 AA.  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).  
 OS Lycopersicon esculentum (tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures.";  
 RL Eur. J. Biochem. 269:6278-6286(2002).  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- FM: Glycosylated.  
 CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of  
 CC purple acid phosphatase.  
 CC Hydrolase; Glycoprotein.  
 KW NON TER 1  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 FL 5  
 Db 1 FL 2

RESULT 70  
 UN06\_PINPS  
 ID UN06\_PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=1647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON TER 1  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;  
 Query Match 16.7%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 LP 6  
 Db 5 LP 6  
 RESULT 71  
 AKHG\_GRYBI  
 ID \_AKHG\_GRYBI STANDARD; PRT; 8 AA.  
 AC P14086;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone G (AKH-G) (RO II).  
 OS Gryllus bimaculatus (Two-spotted cricket), and  
 OS Romalea microptera (Lubber grasshopper).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllinae;  
 OC Gryllus.  
 OX NCBI\_TaxID=6999, 7007;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=88106553; PubMed=3426616;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
 RT of a peptide with adipokinetic activity from the corpora cardiaca of  
 RT the cricket Gryllus bimaculatus.";  
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;  
 RX MEDLINE=89145002; PubMed=3226948;  
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
 RT the lubber grasshopper, Romalea microptera.";  
 RL Peptides 9:681-688(1988).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / RPCH FAMILY.

```
DR PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VN 9
DB 2 VN 3

RESULT 72
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483 (1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VN 9
DB 2 VN 3

RESULT 73
ALL6_CVDPD STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
```

```
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LP 6
DB 1 LP 2

RESULT 74
CADI_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CADI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CADI, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100 (1984).
CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 16.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LF 2
DB 1 LF 2

RESULT 75
CLP_THICU STANDARD; PRT; 8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolithotroph-specific protein (fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
```



CC CHEMOLITHOTROPHICALLY.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;  
Query Match 16.7%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PV 7  
Db 2 PV 3

Search completed: November 25, 2003, 18:17:25  
Job time : 7.80851 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 28.9149 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-4  
Perfect score: 12  
Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

SPTREMBL\_23:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| 1          | 5     | 41.7    | 17           | 11    | Q9ERZ2      |
| 2          | 4     | 33.3    | 9            | 3     | Q9PBE5      |
| 3          | 4     | 33.3    | 13           | 11    | Q9QVK6      |
| 4          | 4     | 33.3    | 15           | 4     | Q9UQUJ2     |
| 5          | 4     | 33.3    | 15           | 7     | Q9TNUQ1     |
| 6          | 4     | 33.3    | 17           | 12    | Q65373      |
| 7          | 4     | 33.3    | 19           | 4     | Q15610      |
| 8          | 4     | 33.3    | 19           | 8     | Q9ZYW7      |
| 9          | 4     | 33.3    | 19           | 12    | O11338      |
| 10         | 4     | 33.3    | 20           | 11    | Q9QUX7      |
| 11         | 3     | 25.0    | 4            | 11    | O08433      |
| 12         | 3     | 25.0    | 7            | 2     | O50556      |
| 13         | 3     | 25.0    | 8            | 3     | O13591      |
| 14         | 3     | 25.0    | 8            | 4     | O15901      |
| 15         | 3     | 25.0    | 8            | 6     | Q9TRX8      |
| 16         | 3     | 25.0    | 8            | 10    | Q40530      |

|    |   |      |    |    |        |
|----|---|------|----|----|--------|
| 17 | 3 | 25.0 | 9  | 2  | P82568 |
| 18 | 3 | 25.0 | 9  | 6  | Q8MJT7 |
| 19 | 3 | 25.0 | 9  | 6  | Q8MJT8 |
| 20 | 3 | 25.0 | 9  | 8  | Q9GD36 |
| 21 | 3 | 25.0 | 9  | 15 | Q64972 |
| 22 | 3 | 25.0 | 10 | 2  | Q9RSN2 |
| 23 | 3 | 25.0 | 10 | 2  | Q9RSN1 |
| 24 | 3 | 25.0 | 10 | 2  | Q9RSN3 |
| 25 | 3 | 25.0 | 10 | 2  | Q9AE19 |
| 26 | 3 | 25.0 | 10 | 4  | Q9H1I5 |
| 27 | 3 | 25.0 | 10 | 5  | P82383 |
| 28 | 3 | 25.0 | 10 | 8  | Q8WBR7 |
| 29 | 3 | 25.0 | 10 | 11 | Q9ESU5 |
| 30 | 3 | 25.0 | 10 | 12 | O39952 |
| 31 | 3 | 25.0 | 10 | 12 | Q9WLE4 |
| 32 | 3 | 25.0 | 10 | 13 | Q8JFE7 |
| 33 | 3 | 25.0 | 10 | 13 | Q8JJ33 |
| 34 | 3 | 25.0 | 11 | 6  | Q9TQSO |
| 35 | 3 | 25.0 | 11 | 12 | O39951 |
| 36 | 3 | 25.0 | 12 | 8  | Q9GI96 |
| 37 | 3 | 25.0 | 12 | 10 | P82329 |
| 38 | 3 | 25.0 | 12 | 11 | Q62966 |
| 39 | 3 | 25.0 | 12 | 13 | P82820 |
| 40 | 3 | 25.0 | 13 | 8  | Q9GCU0 |
| 41 | 3 | 25.0 | 13 | 11 | O88176 |
| 42 | 3 | 25.0 | 13 | 12 | Q9WMG5 |
| 43 | 3 | 25.0 | 13 | 13 | P82880 |
| 44 | 3 | 25.0 | 13 | 13 | P82881 |
| 45 | 3 | 25.0 | 13 | 13 | P82882 |
| 46 | 3 | 25.0 | 13 | 13 | P82883 |
| 47 | 3 | 25.0 | 13 | 13 | P82884 |
| 48 | 3 | 25.0 | 13 | 13 | P82830 |
| 49 | 3 | 25.0 | 13 | 13 | P82848 |
| 50 | 3 | 25.0 | 14 | 2  | Q9R224 |
| 51 | 3 | 25.0 | 14 | 2  | Q45876 |
| 52 | 3 | 25.0 | 14 | 2  | Q9R225 |
| 53 | 3 | 25.0 | 14 | 2  | Q9X715 |
| 54 | 3 | 25.0 | 14 | 2  | Q9WW79 |
| 55 | 3 | 25.0 | 14 | 2  | Q45872 |
| 56 | 3 | 25.0 | 14 | 4  | O95179 |
| 57 | 3 | 25.0 | 14 | 5  | Q9TWW0 |
| 58 | 3 | 25.0 | 14 | 5  | P82216 |
| 59 | 3 | 25.0 | 14 | 8  | Q8M099 |
| 60 | 3 | 25.0 | 14 | 10 | Q9S8X6 |
| 61 | 3 | 25.0 | 14 | 10 | P82340 |
| 62 | 3 | 25.0 | 14 | 11 | Q9QVF3 |
| 63 | 3 | 25.0 | 14 | 11 | O70599 |
| 64 | 3 | 25.0 | 14 | 13 | P82832 |
| 65 | 3 | 25.0 | 14 | 16 | Q8ZDW9 |
| 66 | 3 | 25.0 | 15 | 2  | Q8RKN0 |
| 67 | 3 | 25.0 | 15 | 2  | O68425 |
| 68 | 3 | 25.0 | 15 | 4  | Q9UCH4 |
| 69 | 3 | 25.0 | 15 | 6  | Q9TRA6 |
| 70 | 3 | 25.0 | 15 | 7  | Q9TNO5 |
| 71 | 3 | 25.0 | 15 | 8  | O78794 |
| 72 | 3 | 25.0 | 15 | 8  | Q8HIF8 |
| 73 | 3 | 25.0 | 15 | 8  | Q8HIF6 |
| 74 | 3 | 25.0 | 15 | 16 | Q8XF44 |
| 75 | 3 | 25.0 | 15 | 16 | Q8X2E0 |
| 76 | 3 | 25.0 | 15 | 16 | Q8FEZ7 |
| 77 | 3 | 25.0 | 16 | 2  | Q44610 |
| 78 | 3 | 25.0 | 16 | 2  | Q44610 |
| 79 | 3 | 25.0 | 16 | 4  | Q9VNS8 |
| 80 | 3 | 25.0 | 16 | 4  | Q9UC52 |
| 81 | 3 | 25.0 | 16 | 9  | Q37853 |
| 82 | 3 | 25.0 | 16 | 12 | Q9WMG6 |
| 83 | 3 | 25.0 | 16 | 13 | Q9PT90 |
| 84 | 3 | 25.0 | 16 | 16 | Q8D183 |
| 85 | 3 | 25.0 | 17 | 2  | Q9R4C4 |
| 86 | 3 | 25.0 | 17 | 2  | Q93UW3 |
| 87 | 3 | 25.0 | 17 | 4  | Q6800  |
| 88 | 3 | 25.0 | 17 | 4  | Q9UML8 |
| 89 | 3 | 25.0 | 17 | 4  | O95794 |

P82568 streptococc  
Q8mj77 eulemur ful  
Q8mj78 eulemur ful  
Q9gd36 juncus effu  
Q64972 avian rous-  
Q9rsn2 clostridium  
Q9rsn1 clostridium  
Q9rsn3 clostridium  
Q9ae19 streptococc  
Q9h1i5 homo sapien  
P82383 drosophila  
Q8wbr7 chaitophoru  
Q9esu5 mus musculu  
Q39952 hepatitis g  
Q9wle4 hepatitis g  
Q8jfe7 ficedula al  
Q8jj33 ficedula hy  
Q9tqso bos taurus  
Q39951 hepatitis g  
Q9g196 sargassum p  
P82329 pisum sativ  
Q62966 rattus norv  
P82820 rana catesb  
Q9gcu0 xyris sp. c  
O88176 mus musculu  
Q9wmg5 sigma virus  
P82880 rana clamit  
P82881 rana clamit  
P82882 rana clamit  
P82883 rana clamit  
P82884 rana clamit  
P82830 rana luteiv  
P82848 rana pipien  
Q9r224 campylobact  
Q45876 clostridium  
Q9r225 campylobact  
Q9x715 campylobact  
Q9ww79 campylobact  
Q45872 clostridium  
Q95179 homo sapien  
Q9ttw0 trypanosoma  
P82216 bombyx mori  
Q8m099 tockus nasu  
Q9s8x6 glycine max  
P82340 pisum sativ  
Q9gvf3 rattus sp.  
O70599 rattus norv  
P82832 rana luteiv  
Q8xdw9 yersinia pe  
Q8rkn0 escherichia  
O68425 buchnera ap  
Q9uch4 homo sapien  
Q9tra6 bos taurus  
Q9tng5 mus sp. maj  
O78794 pylaiaella l  
Q8hif8 arthroderma  
Q8hif6 trichophyto  
Q8xf44 salmonella  
Q8xe20 escherichia  
Q8fez7 escherichia  
Q44610 buchnera ap  
Q8vns8 escherichia  
Q9uc52 homo sapien  
Q9tr60 bos taurus  
Q37853 bacterioph  
Q9wmg6 sigma virus  
Q9pt90 gallus gall  
Q8d183 yersinia pe  
Q9r4c4 agrobacteri  
Q93uw3 agrobacteri  
Q6800 saccharomyc  
Q9uml8 homo sapien  
O95794 homo sapien

90 3 25.0 17 4 Q95795 O95795 homo sapien  
 91 3 25.0 17 5 Q9TW16 Q9TW16 ceratitidis c  
 92 3 25.0 17 5 Q17203 Q17203 bombyx mori  
 93 3 25.0 17 6 Q9TRY8 Q9TRY8 sus sp. ins  
 94 3 25.0 17 6 Q9TRU8 Q9TRU8 bos taurus  
 95 3 25.0 17 8 Q95F78 Q95F78 hizikia fus  
 96 3 25.0 17 8 Q8HKH3 Q8HKH3 boophilus a  
 97 3 25.0 17 8 Q8HKH2 Q8HKH2 boophilus d  
 98 3 25.0 17 11 Q62547 Q62547 mus spretus  
 99 3 25.0 17 12 Q8V9K6 Q8V9K6 human papil  
 100 3 25.0 18 3 Q9P897 Q9P897 emericella

## ALIGNMENTS

## RESULT 1

Q9ERZ2 ID Q9ERZ2 PRELIMINARY; PRT; 17 AA.  
 AC Q9ERZ2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Protein tyrosine phosphatase RPTP-GMC1 (Fragment).  
 GN PTPRO.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Wright M.B., Foerzler D., Pech M.;  
 RT "Organization of the mouse Ptpq gene encoding protein-tyrosine  
 phosphatase RPTP-GMC1";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF265561; AAG22700.1; -.  
 FT NON TER 17  
 FT SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;

Query Match 41.7%; Score 5; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5  
 |||||  
 Db 4 LFFFL 8

## RESULT 2

Q9P8E5 ID Q9P8E5 PRELIMINARY; PRT; 9 AA.  
 AC Q9P8E5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE HIS4 protein (Fragment).  
 GN HIS4.  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL-Y1140;  
 RX MEDLINE=99448382; PubMed=10518937;  
 RA Lamas-Maceiras M., Esperanza Cardan E., Freire-Picos M.A.;  
 RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities  
 and differences to Saccharomyces cerevisiae HIS4 gene.";  
 RL FEBS Lett. 458:72-76 (1999).  
 DR EMBL; AJ238494; CAB87125.1; -.  
 FT NON TER 9  
 FT SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 33.3%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
 |||||  
 Db 2 LPVV 5

## RESULT 3

Q9QVK6 ID Q9QVK6 PRELIMINARY; PRT; 13 AA.  
 AC Q9QVK6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373341; PubMed=1832670;  
 RA Hoppner W., Becker L., Buck F., Seitz H.J.;  
 RT "Is the p29 protein involved in the rapid regulation of  
 phosphoenolpyruvate carboxykinase (GTP)?";  
 RL J. Biol. Chem. 266:17257-17260 (1991).  
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBBA6D2D7 CRC64;

Query Match 33.3%; Score 4; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
 |||||  
 Db 5 LPVV 8

## RESULT 4

Q9UQJ2 ID Q9UQJ2 PRELIMINARY; PRT; 15 AA.  
 AC Q9UQJ2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Prorelaxin H2 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Garibay-Tupas J.;  
 RT "Characterization of the human relaxins H1 and H2 5'-flanking  
 regions";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF104935; AAD21961.1; -.  
 FT NON TER 15  
 FT SEQUENCE 15 AA; 1806 MW; E9AFA622F3A86818 CRC64;

Query Match 33.3%; Score 4; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4  
 |||||  
 Db 4 LFFF 7

## RESULT 5

Q9TNTQ1

|                       |                                                                       |                                         |      |        |                                                    |
|-----------------------|-----------------------------------------------------------------------|-----------------------------------------|------|--------|----------------------------------------------------|
| ID                    | Q9TNQ1                                                                | PRELIMINARY;                            | PRT; | 15 AA. |                                                    |
| AC                    | Q9TNQ1;                                                               |                                         |      |        |                                                    |
| DT                    | 01-MAY-2000                                                           | (TrEMBLrel. 13, Created)                |      |        |                                                    |
| DT                    | 01-MAY-2000                                                           | (TrEMBLrel. 13, Last sequence update)   |      |        |                                                    |
| DT                    | 01-OCT-2002                                                           | (TrEMBLrel. 22, Last annotation update) |      |        |                                                    |
| DE                    | Beta 2M- class I-binding PEPTIDE=MAJOR histocompatibility complex     |                                         |      |        |                                                    |
| DE                    | H-2KB-specific molecule POORLY associated with beta 2-microglobulin   |                                         |      |        |                                                    |
| DE                    | (Fragment).                                                           |                                         |      |        |                                                    |
| OS                    | Mus sp.                                                               |                                         |      |        |                                                    |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                         |      |        |                                                    |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |                                         |      |        |                                                    |
| OX                    | NCBI_TaxID=10095;                                                     |                                         |      |        |                                                    |
| RN                    | [1]                                                                   |                                         |      |        |                                                    |
| RP                    | SEQUENCE                                                              |                                         |      |        |                                                    |
| RX                    | MEDLINE=94240094; PubMed=8193884;                                     |                                         |      |        |                                                    |
| RA                    | Joyce S., Kuzushima K., Kepes G., Angeletti R.H., Nathenson S.G.;     |                                         |      |        |                                                    |
| RT                    | "Characterization of an incompletely assembled major                  |                                         |      |        |                                                    |
| RT                    | histocompatibility class I molecule (H-2Kb) associated with unusually |                                         |      |        |                                                    |
| RT                    | long peptides: implications for antigen processing and presentation." |                                         |      |        |                                                    |
| RL                    | Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).                     |                                         |      |        |                                                    |
| KW                    | MHC                                                                   |                                         |      |        |                                                    |
| FT                    | NON_TER                                                               | 1                                       |      |        |                                                    |
| FT                    | NON_TER                                                               | 15                                      |      |        |                                                    |
| SQ                    | SEQUENCE                                                              | 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64; |      |        |                                                    |
| Query Match           |                                                                       |                                         |      |        | 33.3%; Score 4; DB 7; Length 15;                   |
| Best Local Similarity |                                                                       |                                         |      |        | 100.0%; Pred. No. 1.1e+03;                         |
| Matches               |                                                                       |                                         |      |        | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 5 LPVW 8                                                              |                                         |      |        |                                                    |
| Db                    |                                                                       |                                         |      |        |                                                    |
|                       | 7 LPVW 10                                                             |                                         |      |        |                                                    |
| RESULT 6              |                                                                       |                                         |      |        |                                                    |
| Q65373                |                                                                       |                                         |      |        |                                                    |
| ID                    | Q65373                                                                | PRELIMINARY;                            | PRT; | 17 AA. |                                                    |
| AC                    | Q65373;                                                               |                                         |      |        |                                                    |
| DT                    | 01-NOV-1996                                                           | (TrEMBLrel. 01, Created)                |      |        |                                                    |
| DT                    | 01-NOV-1996                                                           | (TrEMBLrel. 01, Last sequence update)   |      |        |                                                    |
| DT                    | 01-OCT-2001                                                           | (TrEMBLrel. 18, Last annotation update) |      |        |                                                    |
| DE                    | ORF 2 minigene.                                                       |                                         |      |        |                                                    |
| OS                    | Orgyia pseudotsugata single capsid nuclear polyhedrosis virus         |                                         |      |        |                                                    |
| OS                    | (OpsNPV). dsDNA viruses, no RNA stage; Baculoviridae;                 |                                         |      |        |                                                    |
| OC                    | Nucleopolyhedrovirus.                                                 |                                         |      |        |                                                    |
| OX                    | NCBI_TaxID=10450;                                                     |                                         |      |        |                                                    |
| RN                    | [1]                                                                   |                                         |      |        |                                                    |
| RP                    | SEQUENCE FROM N.A.                                                    |                                         |      |        |                                                    |
| RX                    | MEDLINE=93286576; PubMed=8389803;                                     |                                         |      |        |                                                    |
| RA                    | Russell R.L., Rohrmann G.F.;                                          |                                         |      |        |                                                    |
| RT                    | "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia |                                         |      |        |                                                    |
| RT                    | pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."   |                                         |      |        |                                                    |
| RL                    | J. Gen. Virol. 74:1191-1195(1993).                                    |                                         |      |        |                                                    |
| DR                    | EMBL; D13375; BAA02640.1; --                                          |                                         |      |        |                                                    |
| SQ                    | SEQUENCE                                                              | 17 AA; 1882 MW; BFECA959495FE6A CRC64;  |      |        |                                                    |
| Query Match           |                                                                       |                                         |      |        | 33.3%; Score 4; DB 12; Length 17;                  |
| Best Local Similarity |                                                                       |                                         |      |        | 100.0%; Pred. No. 1.2e+03;                         |
| Matches               |                                                                       |                                         |      |        | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 8 VNVL 11                                                             |                                         |      |        |                                                    |
| Db                    |                                                                       |                                         |      |        |                                                    |
|                       | 5 VNVL 8                                                              |                                         |      |        |                                                    |
| RESULT 7              |                                                                       |                                         |      |        |                                                    |
| Q15610                |                                                                       |                                         |      |        |                                                    |
| ID                    | Q15610                                                                | PRELIMINARY;                            | PRT; | 19 AA. |                                                    |
| AC                    | Q15610;                                                               |                                         |      |        |                                                    |
| DT                    | 01-NOV-1996                                                           | (TrEMBLrel. 01, Created)                |      |        |                                                    |
| DT                    | 01-JUL-1997                                                           | (TrEMBLrel. 04, Last sequence update)   |      |        |                                                    |
| DT                    | 01-DEC-2001                                                           | (TrEMBLrel. 19, Last annotation update) |      |        |                                                    |

|                       |                                                                       |                                         |      |        |                                                    |
|-----------------------|-----------------------------------------------------------------------|-----------------------------------------|------|--------|----------------------------------------------------|
| DE                    | Topoisomerase I (Fragment).                                           |                                         |      |        |                                                    |
| GN                    | TOP1.                                                                 |                                         |      |        |                                                    |
| OS                    | Homo sapiens (Human).                                                 |                                         |      |        |                                                    |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                         |      |        |                                                    |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.            |                                         |      |        |                                                    |
| OX                    | NCBI_TaxID=9606;                                                      |                                         |      |        |                                                    |
| RN                    | [1]                                                                   |                                         |      |        |                                                    |
| RP                    | SEQUENCE FROM N.A.                                                    |                                         |      |        |                                                    |
| RX                    | MEDLINE=91099302; PubMed=2176592;                                     |                                         |      |        |                                                    |
| RA                    | Kunze N., Klein M., Richter A., Knippers R.;                          |                                         |      |        |                                                    |
| RT                    | "Structural characterisation of the human DNA topoisomerase I gene    |                                         |      |        |                                                    |
| RT                    | promoter."                                                            |                                         |      |        |                                                    |
| RL                    | Eur. J. Biochem. 194:323-330(1990).                                   |                                         |      |        |                                                    |
| DR                    | EMBL; X52601; CAA36834.1; --                                          |                                         |      |        |                                                    |
| KW                    | Isomerase.                                                            |                                         |      |        |                                                    |
| FT                    | NON_TER                                                               | 19                                      |      |        |                                                    |
| SQ                    | SEQUENCE                                                              | 19 AA; 2236 MW; 47BDB36F44FFEEFB CRC64; |      |        |                                                    |
| Query Match           |                                                                       |                                         |      |        | 33.3%; Score 4; DB 4; Length 19;                   |
| Best Local Similarity |                                                                       |                                         |      |        | 100.0%; Pred. No. 1.3e+03;                         |
| Matches               |                                                                       |                                         |      |        | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 1 LFFF 4                                                              |                                         |      |        |                                                    |
| Db                    |                                                                       |                                         |      |        |                                                    |
|                       | 12 LFFF 15                                                            |                                         |      |        |                                                    |
| RESULT 8              |                                                                       |                                         |      |        |                                                    |
| Q9ZYW7                |                                                                       |                                         |      |        |                                                    |
| ID                    | Q9ZYW7                                                                | PRELIMINARY;                            | PRT; | 19 AA. |                                                    |
| AC                    | Q9ZYW7;                                                               |                                         |      |        |                                                    |
| DT                    | 01-MAY-1999                                                           | (TrEMBLrel. 10, Created)                |      |        |                                                    |
| DT                    | 01-MAY-1999                                                           | (TrEMBLrel. 10, Last sequence update)   |      |        |                                                    |
| DT                    | 01-MAY-1999                                                           | (TrEMBLrel. 10, Last annotation update) |      |        |                                                    |
| DE                    | Cytochrome oxidase II (Fragment).                                     |                                         |      |        |                                                    |
| OS                    | Aphidius rosae.                                                       |                                         |      |        |                                                    |
| OC                    | Mitochondrion.                                                        |                                         |      |        |                                                    |
| OC                    | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;         |                                         |      |        |                                                    |
| OC                    | Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;        |                                         |      |        |                                                    |
| OC                    | Braconidae; Aphidinae; Aphidius.                                      |                                         |      |        |                                                    |
| OX                    | NCBI_TaxID=64817;                                                     |                                         |      |        |                                                    |
| RN                    | [1]                                                                   |                                         |      |        |                                                    |
| RP                    | SEQUENCE FROM N.A.                                                    |                                         |      |        |                                                    |
| RX                    | MEDLINE=99152621; PubMed=10028295;                                    |                                         |      |        |                                                    |
| RA                    | Dowton M., Austin A.D.;                                               |                                         |      |        |                                                    |
| RT                    | "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in |                                         |      |        |                                                    |
| RT                    | the hymenoptera."                                                     |                                         |      |        |                                                    |
| RL                    | Mol. Biol. Evol. 16:298-309(1999).                                    |                                         |      |        |                                                    |
| DR                    | EMBL; AF034594; AAC79742.1; --                                        |                                         |      |        |                                                    |
| KW                    | Mitochondrion.                                                        |                                         |      |        |                                                    |
| FT                    | NON_TER                                                               | 1                                       |      |        |                                                    |
| SQ                    | SEQUENCE                                                              | 19 AA; 2361 MW; B624CD9DF26536C3 CRC64; |      |        |                                                    |
| Query Match           |                                                                       |                                         |      |        | 33.3%; Score 4; DB 8; Length 19;                   |
| Best Local Similarity |                                                                       |                                         |      |        | 100.0%; Pred. No. 1.3e+03;                         |
| Matches               |                                                                       |                                         |      |        | 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 1 LFFF 4                                                              |                                         |      |        |                                                    |
| Db                    |                                                                       |                                         |      |        |                                                    |
|                       | 9 LFFF 12                                                             |                                         |      |        |                                                    |
| RESULT 9              |                                                                       |                                         |      |        |                                                    |
| O11338                |                                                                       |                                         |      |        |                                                    |
| ID                    | O11338                                                                | PRELIMINARY;                            | PRT; | 19 AA. |                                                    |
| AC                    | O11338;                                                               |                                         |      |        |                                                    |
| DT                    | 01-JUL-1997                                                           | (TrEMBLrel. 04, Created)                |      |        |                                                    |
| DT                    | 01-JUL-1997                                                           | (TrEMBLrel. 04, Last sequence update)   |      |        |                                                    |
| DT                    | 01-JUN-2002                                                           | (TrEMBLrel. 21, Last annotation update) |      |        |                                                    |
| DE                    | H1-7-1 protein (Fragment).                                            |                                         |      |        |                                                    |
| GN                    | H1-7-1.                                                               |                                         |      |        |                                                    |
| OS                    | Molluscum contagiosum virus subtype 1 (MCV1).                         |                                         |      |        |                                                    |
| OC                    | Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;   |                                         |      |        |                                                    |

OC Molluscipoxvirus.  
 OX NCBI\_TaxID=10280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,  
 RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.,  
 RT "A Random DNA Sequencing, Computer-Based Approach for the Generation  
 RT of a Gene Map of Molluscum Contagiosum Virus.",  
 RL Virus Genes 0:0-0(1997).  
 DR EMBL; U86916; AAB57971.1; -.  
 DR InterPro; IPR004900; Pox\_P35.  
 DR Pfam; PF03213; Pox\_P35; I.  
 FT NON TER 19  
 SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;  
 Query Match 33.3%; Score 4; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LPVV 8  
 DB 13 LPVV 16  
 RESULT 10  
 O9QUX7 PRELIMINARY; PRT; 20 AA.  
 AC O9QUX7  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Carboxylesterase isozyme (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96170127; PubMed=8597091;  
 RA Satoh T., Hosokawa M.;  
 RT "Molecular aspects of carboxylesterase isoforms in comparison with  
 RT other esterases.",  
 RL Toxicol. Lett. 82:439-445(1995).  
 SQ SEQUENCE 20 AA; 2133 MW; 435160FFA80E086D CRC64;  
 Query Match 33.3%; Score 4; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PVVN 9  
 DB 6 PVVN 9  
 RESULT 11  
 Q08433 PRELIMINARY; PRT; 4 AA.  
 AC Q08433  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gunn;  
 RX MEDLINE=91282758; PubMed=1840486;  
 RA Sato H., Aono S., Kashiwamata S., Koizumi O.;  
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 RT hyperbilirubinemic Gunn rat.",

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).  
 DR EMBL; S38636; AAB19259.1; -.  
 KW Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;  
 Query Match 25.0%; Score 3; DB 11; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 NVL 11  
 DB 1 NVL 3  
 RESULT 12  
 O50556 PRELIMINARY; PRT; 7 AA.  
 AC O50556  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE GlyA (Fragment).  
 GN GLYA.  
 OS Actinobacillus actinomycetemcomitans (Haemophilus  
 OS actinomycetemcomitans).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33384;  
 RX MEDLINE=96355846; PubMed=8751884;  
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
 RA Kraig E.;  
 RT "cis Elements and trans factors are both important in strain-specific  
 RT regulation of the leukotoxin gene in Actinobacillus  
 RT actinomycetemcomitans.",  
 RL Infect. Immun. 64:3451-3460(1996).  
 DR EMBL; U51862; AAB88721.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;  
 Query Match 25.0%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LPV 7  
 DB 3 LPV 5  
 RESULT 13  
 O13591 PRELIMINARY; PRT; 8 AA.  
 AC O13591  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE ORF YNL337W (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obermaier B., Piravandi E., Rinke M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z71612; CAA96271.2; -.

FT NON TER 1 1  
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;  
Query Match 25.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3  
Db 2 LFF 4

## RESULT 14

Q15901 ID Q15901 PRELIMINARY; PRT; 8 AA.  
AC Q15901;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE (Clone XP7B11B) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32080; AAA73891.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 860 MW; 37D72878676729CB CRC64;

Query Match 25.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
Db 2 FLP 4

## RESULT 15

Q9TRX8 ID Q9TRX8 PRELIMINARY; PRT; 8 AA.  
AC Q9TRX8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Osteopontin (fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91282766; PubMed=1676261;  
RA Prince C.W., Dickie D., Krumdieck C.L.;  
RT "Osteopontin, a substrate for transglutaminase and factor XIII  
RT activity."  
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 LPV 7  
Db 1 LPV 3

## RESULT 16

Q40530 ID Q40530 PRELIMINARY; PRT; 8 AA.  
AC Q40530;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE P20 n with a leader peptide.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87089808; PubMed=3540612;  
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;  
RT "Isolation of tobacco DNA segments with plant promoter activity."  
RL Mol. Cell. Biol. 6:4486-4492(1986).  
DR EMBL; M14685; AAA34090.1; -.  
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C6 CRC64;

Query Match 25.0%; Score 3; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
Db 2 FFF 4

## RESULT 17

P82568 ID P82568 PRELIMINARY; PRT; 9 AA.  
AC P82568;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page (Fragment).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=13114;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC STRAIN=JRS4;  
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,  
RA VanSogelen R.A.;  
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
RT proteins."  
RL Submitted (MAY-2000) to the SWISS-PROT data bank.  
CC -!- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7  
Db 1 LPV 3

## RESULT 18

Q8MJT7  
ID Q8MJT7 PRELIMINARY; PRT; 9 AA.  
AC Q8MJT7  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hemopexin (fragment).  
OS Eulemur fulvus (brown lemur).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.  
OX NCBI\_TaxID=13515;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;  
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid  
zone at Andringitra, Madagascar."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF258049; AAM43870.1; -.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;  
Query Match 25.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFF 3  
Db 6 LFF 8  
RESULT 19  
Q8MJT8  
ID Q8MJT8 PRELIMINARY; PRT; 9 AA.  
AC Q8MJT8  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hemopexin (fragment).  
OS Eulemur fulvus albocollaris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.  
OX NCBI\_TaxID=122224;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;  
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid  
zone at Andringitra, Madagascar."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF258028; AAM43849.1; -.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;  
Query Match 25.0%; Score 3; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFF 3  
Db 6 LFF 8  
RESULT 20  
Q9GD36  
ID Q9GD36 PRELIMINARY; PRT; 9 AA.  
AC Q9GD36  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Ribosomal protein S16 (fragment).  
GN RPS16.  
OS Juncus effusus (Soft rush).

OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.  
OX NCBI\_TaxID=13579;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Asmussen C.B., Chase M.W.;  
RT "Coding and noncoding plastid DNA in palm systematics."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ404962; CAC17904.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;  
Query Match 25.0%; Score 3; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FFF 4  
Db 7 FFF 9  
RESULT 21  
Q64972  
ID Q64972 PRELIMINARY; PRT; 9 AA.  
AC Q64972  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env  
protein (fragment).  
OS Avian rous-associated virus type 1.  
OC Viruses; Retroviridae; Alpharetrovirus.  
OX NCBI\_TaxID=11950;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89037349; PubMed=2846875;  
RA Marx M., Crisanti P., Eychene A., Bechade C., Laugier D.,  
RA Gydaedal J., Peseac B., Calothy G.;  
RT "Activation and transduction of c-mil sequences in chicken neuroretina  
cells induced to proliferate by infection with avian lymphomatosis  
virus."  
RL J. Virol. 62:4627-4633(1998).  
DR EMBL; M25399; AAA42548.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;  
Query Match 25.0%; Score 3; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 LPV 7  
Db 6 LPV 8  
RESULT 22  
Q9RSN2  
ID Q9RSN2 PRELIMINARY; PRT; 10 AA.  
AC Q9RSN2  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Neurotoxin type A HN+ 57 kDa SUBUNIT=SAMPLE 2 (fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.

```

RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1225 MW; EC3DBE932D366C1BA CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 23
Q9R5N1 PRELIMINARY; PRT; 10 AA.
AC Q9R5N1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Neurotoxin type A HN+ 57 kDa subunit (Fragment)
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1172 MW; E5DAE932D416C1BA CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 24
Q9R5N3 PRELIMINARY; PRT; 10 AA.
AC Q9R5N3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Neurotoxin type B HN+ 57 kDa subunit (Fragment)
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1225 MW; EC3DBE932D366C1BA CRC64;

```

```

FT NON TER 10 10
SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 25
Q9AE19 PRELIMINARY; PRT; 10 AA.
AC Q9AE19;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Laminin-binding surface protein (Fragment)
GN LMB.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5;
RX MEDLINE=21172873; PubMed=11274116;
RA Granlund M., Michel F., Norgren M.;
RT "Mutually exclusive distribution of IS1548 and GBS11, an active group
RT II intron identified in human isolates of group b streptococci.";
RL J. Bacteriol. 183:2560-2569(2001).
DR EMBL; AJ290953; CAC35987.1; -.
FT NON TER 10 10
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1204 MW; 4965EF9729C9C873 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFL 5
Db 5 FFL 7

RESULT 26
Q9H1I5 PRELIMINARY; PRT; 10 AA.
AC Q9H1I5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Mutant beta-globin (Fragment)
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.;
RT "Molecular characterization of beta thalassemia in Yunnan, China.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013300; AAG46183.1; -.
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 2210B2A2C732C448 CRC64;

Query Match 25.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 9 NVL 11
Db 4 NVL 6

RESULT 27
P82383 PRELIMINARY; PRT; 10 AA.
ID P82383
AC P82383;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Larval cuticle LCP2A protein (Minor band protein) (Fragment).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE
RC STRAIN=OREGON-R; TISSUE=LARVA;
RA Chihara C.J.;
RT "Third instar cuticle proteins.";
RL DIS 83:0-0(2000).
CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
DR FlyBase; FBgn0061208; Lcp2a.
DR InterPro; IPR000618; Insect_cuticle.
DR PROSITE; PS00233; CUTICLE; PARTIAL.
KW Cuticle; Structural protein.
FT NON TER 10
SQ SEQUENCE 10 AA; 1100 MW; 9DCF320732C44DDA CRC64;

Query Match 25.0%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
Db 5 NVL 7

RESULT 28
Q8WBK7 PRELIMINARY; PRT; 10 AA.
ID Q8WBK7
AC Q8WBK7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN COI
OS Chaitophorus leucomelas.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Drepanosiphidae; Chaitophorus.
OX NCBI_TaxID=136351;
RN [1]
RP SEQUENCE FROM N.A.
RA Shingleton A.W.; Stern D.L.;
RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
RT within the aphid genus Chaitophorus.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF44288; AAL38565.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 25.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
Db 1

```

---

```

Db 4 LPV 6

RESULT 29
Q9ESU5 PRELIMINARY; PRT; 10 AA.
ID Q9ESU5
AC Q9ESU5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127859; PubMed=10660538;
RA Munsch D.; Watanabe-Fukunaga R.; Bourdon J.C.; Nagata S.; May E.;
RA Yonish-Rouach E.; Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
RT p53-responsive element that is activated by p53 mutants unable to
RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 25.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 7 VLP 9

RESULT 30
Q39952 PRELIMINARY; PRT; 10 AA.
ID Q39952
AC Q39952;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=39839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B.; Cuceanu N.; Davidson P.; Jarvis L.M.; Mokili J.L.;
RA Hamid S.; Ludlam C.A.; Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
DR EMBL; AF003170; AAC57981.1; -.
KW NON TER 10
SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 25.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
Db 6 LFF 8

```

```

RESULT 31
ID Q9WLE4 PRELIMINARY; PRT; 10 AA.
AC Q9WLE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAM22902.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 25.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
Db 6 LFF 8

RESULT 32
ID Q8JFE7 PRELIMINARY; PRT; 10 AA.
AC Q8JFE7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bc5, and Bc8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAM22903.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 25.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 5 VLP 7

RESULT 33
ID Q8JUJ3 PRELIMINARY; PRT; 10 AA.
AC Q8JUJ3;

```

```

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAM22902.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 25.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db 5 VLP 7

RESULT 34
ID Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8
Db 5 PVV 7

RESULT 35
ID O39951 PRELIMINARY; PRT; 11 AA.
AC O39951;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).

```

```

OS Hepatitis GB virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV Group.
OX NCBI_TaxID=39839;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Edinburgh haemophilic;
RX MEDLINE=97368412; PubMed=9225026;
RA Smith D.B., Cuccaneu N., Davidson P., Jarvis L.M., Mokili J.L.,
RA Hamid S., Ludlam C.A., Simmonds P.;
RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
RT analysis of the 5' non-coding region.";
RL J. Gen. Virol. 78:1533-1542(1997).
DR EMBL; AF003169; AAC57980.1; -.
FT NON TER 11
FT SEQUENCE 11 AA; 1281 MW; 45DC88F0C9C72727 CRC64;
SQ

Query Match 25.0%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
Db 6 LFF 8

RESULT 36
Q9GI96 PRELIMINARY; PRT; 12 AA.
ID Q9GI96
AC Q9GI96
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN RBCS
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=nepl27;
RA Phillips N.E.;
RA "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=nepl27;
RA Phillips N.E., Smith C.M., Morden C.W.;
RA "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
FT NON TER 12
FT SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;
SQ

Query Match 25.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 10 FLP 12

RESULT 37
P82329 PRELIMINARY; PRT; 12 AA.
ID P82329
AC P82329;

```

```

DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT111) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3886;
RN [1]
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Paltier J.-B., Friiso G., Kalume D.E., Roepstorff P., Nilsson P.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON TER 12
FT SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;
SQ

Query Match 25.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 8 FLP 10

RESULT 38
Q62966 PRELIMINARY; PRT; 12 AA.
ID Q62966
AC Q62966
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interstitial collagenase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96408720; PubMed=9813727;
RA Rajakumar R.A., Quinn C.O.;
RT "Parathyroid hormone induction of rat interstitial collagenase mRNA in
RT osteosarcoma cells is mediated through an AP-1-binding site.";
RL Mol. Endocrinol. 10:867-878(1996).
DR EMBL; U53605; AAB47407.1; -.
KW Collagen.
FT NON TER 12
FT SEQUENCE 12 AA; 1432 MW; 148A4DFEE8ADD720 CRC64;
SQ

Query Match 25.0%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
Db 9 FFF 11

RESULT 39
P82820 PRELIMINARY; PRT; 12 AA.
ID P82820
AC P82820;

```

DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE RANATUERIN 5.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SKIN;  
 RX MEDLINE=98422096; PubMed=9751476;  
 RA Goraya J., Knoop F.C., Conlon J.M.;  
 RT "Ranaturins: antimicrobial peptides isolated from the skin of the  
 RT American bullfrog, Rana catesbeiana."  
 RL Biochem. Biophys. Res. Commun. 250:589-592(1998).  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;  
 Query Match 25.0%; Score 3; DB 13; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FLP 6  
 Db |||  
 1 FLP 3  
 RESULT 40  
 Q9GCU0 PRELIMINARY; PRT; 13 AA.  
 ID Q9GCU0  
 AC Q9GCU0  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Xyris sp. Chase 154.  
 OS Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Xyridaceae; Xyris.  
 OX NCBI\_TaxID=120079;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Kasmussen C.B., Chase M.W.;  
 RT "Coding and noncoding plastid DNA in palm systematics."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ404965; CAC18098.1;  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1593 MW; 6F79408FB7A55EA4 CRC64;  
 Query Match 25.0%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFF 4  
 Db |||  
 10 FFF 12  
 RESULT 41  
 O88176 PRELIMINARY; PRT; 13 AA.  
 ID O88176  
 AC O88176  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM1 OR NCAM.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb-C; TISSUE=Liver;  
 RX MEDLINE=98250618; PubMed=9582442;  
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
 RT "A cis-acting regulatory element that affects the alternative splicing  
 RT of a muscle-specific exon in the mouse NCAM gene."  
 RL Biochim. Biophys. Acta 1397:305-315(1998).  
 DR EMBL; AB001873; BAA31275.1;  
 DR MGI; MGI:97281; Ncam1.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;  
 Query Match 25.0%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LPV 7  
 Db |||  
 4 LPV 6  
 RESULT 42  
 Q9WMG5 PRELIMINARY; PRT; 13 AA.  
 ID Q9WMG5  
 AC Q9WMG5  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
 DE 3 protein (Fragment).  
 GN GENE 3.  
 OS Sigma virus.  
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; unclassified Rhabdoviridae.  
 OX NCBI\_TaxID=11301;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212481; PubMed=8384742;  
 RA Teninges D., Bras F., Dezelee S.;  
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
 RT overlap."  
 RL Virology 193:1018-1023(1993).  
 DR EMBL; S57850; AAD40700.1;  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;  
 Query Match 25.0%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VLP 12  
 Db |||  
 7 VLP 9  
 RESULT 43  
 P82880 PRELIMINARY; PRT; 13 AA.  
 ID P82880  
 AC P82880  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE Temporin-1CA.  
 OS Rana clamitans (green frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=145282;  
 RN [1]  
 RP SEQUENCE.

```

RC TISSUE=Skin;
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC Antibiotic; Amidation.
KW MOD RES 13 13
SQ SEQUENCE 13 AA; 1432 MW; CC18532F8DFE533D CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 44
P82881 ID P82881 PRELIMINARY; PRT; 13 AA.
AC P82881;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Tempurin-1CB.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC Antibiotic; Amidation.
KW MOD RES 13 13
SQ SEQUENCE 13 AA; 1432 MW; CAA71A765A8935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 45
P82882 ID P82882 PRELIMINARY; PRT; 13 AA.
AC P82882;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Tempurin-1CC.
OS Rana clamitans (green frog).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1461.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC Antibiotic; Amidation.
KW MOD RES 13 13
SQ SEQUENCE 13 AA; 1462 MW; CC18586F8DF935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 46
P82883 ID P82883 PRELIMINARY; PRT; 13 AA.
AC P82883;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Tempurin-1CD.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RL skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1447.0; MW ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC Antibiotic; Amidation.
KW MOD RES 13 13
SQ SEQUENCE 13 AA; 1448 MW; CC18586B9DF935BD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
Db 1 FLP 3

RESULT 47
P82884 ID P82884 PRELIMINARY; PRT; 13 AA.
AC P82884;

```

```

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1CB.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
[1]
RN SEQUENCE.
RP TISSUE=Skin;
RC MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RT skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1461.0; MW_ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1482 MW; CC18568B9DF931AD CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db |||
1 FLP 3

RESULT 48
P82830 PRELIMINARY; PRT; 13 AA.
ID P82830;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1LA.
OS Rana luteiventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=58176;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=SKIN;
RC MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- MASS SPECTROMETRY: MW=1366.8; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1368 MW; 92541A7649A3D685 CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12
Db |||
1 VLP 3

```

```

RESULT 49
P82848 PRELIMINARY; PRT; 13 AA.
ID P82848;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Temporin-1P.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=SKIN;
RC MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RT Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1370 MW; 3EF3402B9DF92338 CRC64;

Query Match 25.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
Db |||
1 FLP 3

RESULT 50
Q9R2Z4 PRELIMINARY; PRT; 14 AA.
ID Q9R2Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Flagellin A (fragment).
GN FLAA.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
[1]
RN SEQUENCE FROM N.A.
RP Studer E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Studer E., Dohnke M., Wegmueller B., Luethy J., Schmid S.,
RA Candrian U.;
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter
RT coli PCR products amplified directly from environmental samples.";
RL Food Sci. Technol. 31:337-345(1998).
DR EMBL; AJ133577; CAB39387.1; -.
DR EMBL; AJ133572; CAB39382.1; -.
DR EMBL; AJ133573; CAB39383.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1599 MW; C7C4BBB7A1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;

```

Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
Db 8 NVL 10

RESULT 51  
Q45876 PRELIMINARY; PRT; 14 AA.  
AC Q45876;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HA-II protein (Fragment).  
GN HA-II.  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OC Clostridium.  
CN NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCTC 7273;  
RA East A.K., Stacey J.M., Collins M.D.;  
RT "Cloning and sequencing of a hemagglutinin component of the botulinum  
neurotoxin complex encoded by Clostridium botulinum types A and B.";  
RL Syst. Appl. Microbiol. 17:306-312(1994).  
DR EMBL; X79102; CAA55711.1; -.  
FT NON TER 14  
RN 14  
SQ SEQUENCE 14 AA; 1628 MW; CD689B0937D75E29 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6  
Db 7 FLP 9

RESULT 52  
Q9R2Z5 PRELIMINARY; PRT; 14 AA.  
AC Q9R2Z5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Flagellin A (Fragment).  
GN FLAA.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
CN NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Studer E.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,  
RA Candrian U.;  
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter  
coli PCR products amplified directly from environmental samples.";  
RL Food Sci. Technol. 31:337-345(1998).  
DR EMBL; AJ133567; CAB55353.1; -.  
DR EMBL; AJ133568; CAB39378.1; -.  
DR EMBL; AJ133569; CAB39379.1; -.  
DR EMBL; AJ133570; CAB39380.1; -.  
DR EMBL; AJ133571; CAB39381.1; -.  
DR EMBL; AJ133574; CAB39384.1; -.  
DR EMBL; AJ133575; CAB39385.1; -.  
DR EMBL; AJ133576; CAB39386.1; -.

FT NON TER 1 1  
SQ SEQUENCE 14 AA; 1611 MW; C7C0EFB7A1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
Db 8 NVL 10

RESULT 53  
Q9X715 PRELIMINARY; PRT; 14 AA.  
AC Q9X715;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Flagellin A (Fragment).  
GN FLAA.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
CN NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Studer E.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,  
RA Candrian U.;  
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter  
coli PCR products amplified directly from environmental samples.";  
RL Food Sci. Technol. 31:337-345(1998).  
DR EMBL; AJ133578; CAB39388.1; -.  
FT NON TER 1  
RN 1  
SQ SEQUENCE 14 AA; 1595 MW; C7C0F96DA1739156 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVL 11  
Db 8 NVL 10

RESULT 54  
Q9WW79 PRELIMINARY; PRT; 14 AA.  
AC Q9WW79;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Flagellin A (Fragment).  
GN FLAA.  
OS Campylobacter coli.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
CN NCBI\_TaxID=195;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Studer E.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S.,  
RA Candrian U.;  
RT "RFLP and sequence analysis of Campylobacter jejuni and Campylobacter  
coli PCR products amplified directly from environmental samples.";  
RL Food Sci. Technol. 31:337-345(1998).

DR EMBL; AJ133579; CAB39377.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1611 MW; C7C0EPB7A1739156 CRC64;  
 Query Match 25.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11  
 ||||  
 Db 8 NVL 10

RESULT 55  
 Q45872 PRELIMINARY; PRT; 14 AA.  
 AC Q45872; Q45869;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last annotation update)  
 DE (NCTC 7272 type A) HA-33 and P-21 genes (Fragment).  
 GN HA-II.  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 7272, TYPE A, and 178;  
 RA East A.K., Stacey J.W., Collins M.D.;  
 RL Syst. Appl. Microbiol. 17:306-312(1994).  
 DR EMBL; X79104; CAA55719.1; -.  
 DR EMBL; X79103; CAA55715.1; -.  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1656 MW; CD689B1BBCD75E29 CRC64;

Query Match 25.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6  
 ||||  
 Db 7 FLP 9

RESULT 56  
 Q95179 PRELIMINARY; PRT; 14 AA.  
 AC Q95179;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Glucose-6-phosphatase hydrolytic subunit (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99156747; PubMed=10024523;  
 RA Schmolli D., Washer C., Hinds C.J., Allan B.B., Walther R.,  
 RA Burchell A.;  
 RT "Identification of a cAMP response element within the glucose-6-phosphatase hydrolytic subunit gene promoter which is involved in the transcriptional regulation by cAMP and glucocorticoids in H4IIE hepatoma cells";  
 RT Biochem. J. 338:457-463(1999).  
 DR EMBL; AF051355; AAD11621.1; -.  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1666 MW; A6B78EEF99F7FD46 CRC64;

Query Match 25.0%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11  
 ||||  
 Db 8 NVL 10

RESULT 57  
 Q9TWW0 PRELIMINARY; PRT; 14 AA.  
 AC Q9TWW0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Histone C (Fragment).  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5691;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93064852; PubMed=1437281;  
 RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;  
 RT "Sequence differences between histones of procyclic Trypanosoma brucei and higher eukaryotes.";  
 RL Parasitology 105:97-104(1992).  
 SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 25.0%; Score 3; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLP 12  
 ||||  
 Db 8 VLP 10

RESULT 58  
 P82216 PRELIMINARY; PRT; 14 AA.  
 AC P82216;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;  
 RX MEDLINE=21177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of silkworm.";  
 RL I Chuan Hsueh Pao 28:217-224(2001).  
 CC -I- SIMILARITY: TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1619 MW; 86C63995B983BC45 CRC64;

Query Match 25.0%; Score 3; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVV 8  
 ||||  
 Db 4 PVV 6

RESULT 59  
 Q8M099 PRELIMINARY; PRT; 14 AA.  
 ID Q8M099



```

AC Q8M099;
DE 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
OS Tokus nasutus (African grey hornbill).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Bucerotiformes; Bucerotidae; Tockus.
OX NCBI_TaxID=118205;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2024936; PubMed=12029361;
RA Delport W., Ferguson J.W.H., Bloomer P.;
RT "Characterization and evolution of the mitochondrial DNA control
RT region in hornbills (Bucerotiformes).";
RL J. Mol. Evol. 54:794-806(2002).
DR EMBL; AY027933; AAK31783.1; -.
KW Mitochondrion.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1638 MW; DFAE115DFA724E29 CRC64;

Query Match 25.0%; Score 3; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFL 5
DB 6 FFL 8

RESULT 60
Q9S8X6 PRELIMINARY; PRT; 14 AA.
ID Q9S8X6
AC Q9S8X6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Vegetative storage protein 94 peptide 1, VS994=LIPOXYGENASE
DE (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE.
RX MEDLINE=92361246; PubMed=1822994;
RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
RT "The soybean 94-kilodalton vegetative storage protein is a
RT lipoxigenase that is localized in paraveinal mesophyll cell
RT vacuoles.";
RL Plant Cell 3:973-987(1991).
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 98EB730EA6AE785A CRC64;

Query Match 25.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVL 11
DB 4 NVL 6

RESULT 61
P82340 PRELIMINARY; PRT; 14 AA.
ID P82340
AC P82340;
DT 01-JUN-2000 (TReMBLrel. 14, Created)
DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

```

```

DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;

Query Match 25.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVW 8
DB 7 PVW 9

RESULT 62
Q9QVF3 PRELIMINARY; PRT; 14 AA.
ID Q9QVF3
AC Q9QVF3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE TRANSFERRIN=PEPTIDE 35 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin, 1.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1499 MW; 01ABE89E54E3224 CRC64;

Query Match 25.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVW 8
DB 10 PVW 12

RESULT 63
O70599 PRELIMINARY; PRT; 14 AA.
ID O70599
AC O70599;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Sauer M.;  
 RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.  
 DR EMBL; AJ006455; CAA07030.1; -.  
 KW Kinase; Transferase.  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;  
 25.0%; Score 3; DB 11; Length 14;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 10 VLP 12  
 |||  
 9 VLP 11  
 |||  
 RESULT 64  
 P82832  
 ID P82832 PRELIMINARY; PRT; 14 AA.  
 AC P82832;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Temporin-ILC.  
 OS Rana luteiventris.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=58176;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN;  
 RX MEDLINE=20117700; PubMed=10651828;  
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,  
 RA Conlon J.M.;  
 RT "Peptides with antimicrobial activity from four different families  
 RT isolated from the skins of the North American frogs *Rana luteiventris*,  
 RT *Rana berlandieri* and *Rana pipiens*.";  
 RL Eur. J. Biochem. 267:894-900(2000).  
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM  
 CC S.AUREUS. WEAK ACTIVITY AGAINST GRAM-NEGATIVE BACTERIUM E.COLI AND  
 CC THE YEAST C.ALBICANS.  
 CC -!- MASS SPECTROMETRY: MW=1603.1; METHOD=ELECTROSPRAY.  
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN  
 CC FAMILY.  
 KW Antibiotic; Amidation; Fungicide.  
 FT MOD RES 14 14  
 FT SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;  
 25.0%; Score 3; DB 13; Length 14;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 4 FLP 6  
 |||  
 1 FLP 3  
 |||  
 RESULT 65  
 Q8ZDW9  
 ID Q8ZDW9 PRELIMINARY; PRT; 14 AA.  
 AC Q8ZDW9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Phenylalanyl-tRNA synthetase operon leader peptide (Phenylalanyl-tRNA  
 DE synthetase (pheST) operon leader peptide).  
 GN PHEW OR YF02429A OR Y1906.

OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Peltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whithead S., Barrall B.G.;  
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";  
 RL Nature 413:523-527(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of *Yersinia pestis* KIM.";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 DR EMBL; AJ414152; CAC91234.1; -.  
 DR EMBL; AE013793; AAM85473.1; -.  
 KW Aminoacyl-tRNA synthetase; Complete proteome.  
 SQ SEQUENCE 14 AA; 1813 MW; 6141D61508FEF0D4 CRC64;  
 25.0%; Score 3; DB 16; Length 14;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 2 FFF 4  
 |||  
 8 FFF 10  
 |||  
 RESULT 66  
 Q8RKN0  
 ID Q8RKN0 PRELIMINARY; PRT; 15 AA.  
 AC Q8RKN0;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative transposase ORF1005 (Fragment).  
 GN ORF1005.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=743-D;  
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,  
 RA Prats G.;  
 RT "A novel complex sul1-type integron in *Escherichia coli* carrying the  
 RT bla(CTX-M-9) gene.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY092058; AAM15719.1; -.  
 FT NON TER 1  
 FT SEQUENCE 15 AA; 1751 MW; 2D706E3A12001249 CRC64;  
 25.0%; Score 3; DB 2; Length 15;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 5 LPV 7  
 |||

```

Db 10 LPV 12

RESULT 67
O68425 PRELIMINARY; PRT; 15 AA.
AC O68425;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.8 kDa protein (Fragment).
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98290710; PubMed=9625791;
RA Baumann L., Baumann P., Moran N.A.;
RT "News & notes: the endosymbiont (Buchnera) of the aphid diuraphis
RT noxia contains all the genes of the cryptophan biosynthetic pathway.";
RL Curr. Microbiol. 37:59-59(1998).
DR EMBL; AF038565; AAC27732.1; -.
KW Hypothetical protein.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1795 MW; 54A3D5B40D326E1E CRC64;

Query Match 25.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFF 3
 |||
Db 9 LFF 11

RESULT 68
Q9UCH4
ID Q9UCH4 PRELIMINARY; PRT; 15 AA.
AC Q9UCH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Natural killer enhancing factor, NKEF (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93215001; PubMed=8462106;
RA Shau H., Gupta R.K., Golub S.H.;
RT "Identification of a natural killer enhancing factor (NKEF) from human
RT erythroid cells.";
RL Cell. Immunol. 147:1-11(1993).
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1738 MW; 4909D4A793D382BF CRC64;

Query Match 25.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNV 10
 |||
Db 9 VNV 11

RESULT 69
Q9TRA6
ID Q9TRA6 PRELIMINARY; PRT; 15 AA.
AC Q9TRA6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PA700 subunit P31=ATP-dependent 20 S proteasome activator
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=94342244; PubMed=8063704;
RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,
RA Afendis S.J., Swaffield J.C., Slaughter C.A.;
RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an
RT ATPase containing multiple members of a nucleotide-binding protein
RT family.";
RL J. Biol. Chem. 269:20878-20884(1994).
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1659 MW; D189812B9389B755 CRC64;

Query Match 25.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLP 6
 |||
Db 8 FLP 10

RESULT 70
Q9TNQ5
ID Q9TNQ5 PRELIMINARY; PRT; 15 AA.
AC Q9TNQ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major histocompatibility complex class II bound peptide
DE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=94082939; PubMed=8260091;
RA Freed J.H., Marrack P.;
RT "Tissue-specific expression of self peptides bound by major
RT histocompatibility complex class II molecules.";
RL Chem. Immunol. 57:88-112(1993).
KW MHC.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1607 MW; CBE93F7B8C5E7425 CRC64;

Query Match 25.0%; Score 3; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPV 7
 |||
Db 10 LPV 12

RESULT 71
O78794
ID O78794 PRELIMINARY; PRT; 15 AA.
AC O78794;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial ribosomal protein S14 (Fragment).

```

GN RPS14  
OS *Pyralia littoralis*.  
OG Mitochondrion.  
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;  
OC Acinetosporaceae; *Pyralia*.  
OX NCBI\_TaxID=2885;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=ROSCOFF;  
RX MEDLINE=98239704; PubMed=9571021;  
RA Rousvoal S., Oudot M.-P., Fontaine J.-M., Kloareg B.,  
Loiseaux-De Goer S.L.;  
RT "Witnessing the evolution of transcription in mitochondria: the  
mitochondrial genomes of the primitive brown alga *Pyralia littoralis*  
(L.) Kjellm. encodes a T7-like RNA polymerase.";  
RL J. Mol. Biol. 277:1047-1057(1998).  
CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
CC -|- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
DR EMBL; AF034976; AAC23952.1; -.  
DR InterPro; IPR001209; Ribosomal\_S14.  
DR PROSITE; PS00527; RIBOSOMAL\_S14; PARTIAL.  
KW Ribosomal protein; Mitochondrion; Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1599 MW; 2D406410C588731B CRC64;  
  
Query Match 25.0%; Score 3; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 VLP 12  
DB 6 VLP 8  
|||  
|||  
|||  
  
RESULT 72  
Q8HIF8 PRELIMINARY; PRT; 15 AA.  
ID Q8HIF8  
AC Q8HIF8  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
OS *Pyralia littoralis*.  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Onygenales; Arthrodermataceae; Arthroderma.  
OX NCBI\_TaxID=63400;  
[1]  
RN SEQUENCE FROM N.A.  
RP Probst S., Polyakov I., Ivanova L., Graeser Y.;  
RT "Development of DNA markers to explore the genetic relatedness of  
strains of the two dermatophyte species causing Favus of human and  
mouse.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ430624; CAD23371.1; -.  
DR EMBL; AJ430624; CAD23371.1; -.  
KW Mitochondrion.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1766 MW; 2AF79998CD0C9B5E CRC64;  
  
Query Match 25.0%; Score 3; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LFF 3  
DB 11 LFF 13  
|||  
|||  
|||  
  
RESULT 73  
Q8HIF6 PRELIMINARY; PRT; 15 AA.  
ID Q8HIF6  
AC Q8HIF6

DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
OS *Pyralia littoralis*.  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;  
OC Trichophyton.  
OX NCBI\_TaxID=34386;  
[1]  
RN SEQUENCE FROM N.A.  
RP Probst S., Polyakov I., Ivanova L., Graeser Y.;  
RT "Development of DNA markers to explore the genetic relatedness of  
strains of the two dermatophyte species causing Favus of human and  
mouse.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ430625; CAD23373.1; -.  
DR EMBL; AJ430625; CAD23373.1; -.  
KW Mitochondrion.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1766 MW; 2AF79998CD0C9B5E CRC64;  
  
Query Match 25.0%; Score 3; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LFF 3  
DB 11 LFF 13  
|||  
|||  
|||  
  
RESULT 74  
Q8XF44 PRELIMINARY; PRT; 15 AA.  
ID Q8XF44  
AC Q8XF44  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein STM2666 (Phe leader peptide).  
GN STM2666 OR STY2853A.  
OS *Salmonella typhimurium*, and  
OS *Salmonella typhi*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Salmonella*.  
OX NCBI\_TaxID=602, 601;  
[1]  
RN SEQUENCE FROM N.A.  
RP SPECIES=*S. typhimurium*; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,  
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
Waterston R., Wilson R.K.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
LT2.";  
RL Nature 413:852-856 (2001).  
[2]  
RN SEQUENCE FROM N.A.  
RP SPECIES=*S. typhi*; STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
Churcher C., Mungall K.L., Bentley S.D., Bentley S.D., Sebaihia M.,  
Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,  
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
Whitehead S., Barrall B.G.;  
RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
*enterica* serovar Typhi CT18.";  
RL Nature 413:848-852 (2001).

DR EMBL; AE008821; AAL21555.1; -.  
DR EMBL; AL627276; CAD05845.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 15 AA; 1959 MW; CFE1598393ED35E0 CRC64;

Query Match 25.0%; Score 3; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
|||  
Db 6 FFF 8

RESULT 75

Q8X2E0 PRELIMINARY; PRT; 15 AA.  
AC Q8X2E0;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Leader peptide of chorismate mutase-P-prephenate  
DE dehydratase.  
GN ECS3461.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H;  
RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
DR EMBL; AP002562; BAB36884.1; -.  
SQ SEQUENCE 15 AA; 1912 MW; CFE14AF996F935E0 CRC64;

Query Match 25.0%; Score 3; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFF 4  
|||  
Db 6 FFF 8

Search completed: November 25, 2003, 18:25:17  
Job time : 31.9649 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 38.8723 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFFFLPVNVLP 12

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

A\_Geneseq\_19Jun03:\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 12    | 100.0       | 12     | 22    | Colostrinin derive |
| 2          | 12    | 100.0       | 12     | 22    | Colostrinin peptid |
| 3          | 12    | 100.0       | 12     | 22    | Colostrinin peptid |
| 4          | 12    | 100.0       | 12     | 22    | Ewe colostrinin pe |
| 5          | 12    | 100.0       | 12     | 23    | Colostrinin consti |
| 6          | 12    | 100.0       | 12     | 23    | Colostrinin consti |
| 7          | 12    | 100.0       | 12     | 23    | Neural cell regula |
| 8          | 12    | 100.0       | 14     | 22    | Ewe colostrinin pe |
| 9          | 6     | 50.0        | 6      | 22    | Colostrinin peptid |

|    |   |      |    |    |          |                     |
|----|---|------|----|----|----------|---------------------|
| 10 | 6 | 50.0 | 7  | 22 | AAE07196 | Modified colostrin  |
| 11 | 6 | 50.0 | 9  | 19 | AAZ21194 | Human bcl2 proto-o  |
| 12 | 5 | 41.7 | 5  | 19 | AAW51338 | Peptide #21 useful  |
| 13 | 5 | 41.7 | 5  | 19 | AAW51344 | Peptide #27 useful  |
| 14 | 5 | 41.7 | 5  | 21 | AAV49996 | Natural beta amyl   |
| 15 | 5 | 41.7 | 5  | 22 | AAE12536 | APP70 abeta peptid  |
| 16 | 5 | 41.7 | 5  | 24 | ABG73485 | Natural beta-amyl   |
| 17 | 5 | 41.7 | 9  | 21 | AAE61675 | Arabidopsis thalia  |
| 18 | 5 | 41.7 | 11 | 19 | AAW69637 | Peptide SEQ ID No:  |
| 19 | 5 | 41.7 | 11 | 20 | AAW74434 | Ste2 agonist pepti  |
| 20 | 5 | 41.7 | 11 | 21 | AAE20744 | MF-alpha-1 express  |
| 21 | 5 | 41.7 | 11 | 21 | AAV93630 | Peptide encoded by  |
| 22 | 5 | 41.7 | 11 | 22 | AAV79162 | Amino acid sequenc  |
| 23 | 5 | 41.7 | 11 | 22 | AAE84510 | Amino acid sequenc  |
| 24 | 5 | 41.7 | 14 | 22 | AAW96786 | Human peptide #61   |
| 25 | 5 | 41.7 | 14 | 22 | AAW98289 | Human peptide #156  |
| 26 | 5 | 41.7 | 14 | 22 | AAW98290 | Human peptide #156  |
| 27 | 5 | 41.7 | 15 | 22 | AAE64341 | Ribosomal protein   |
| 28 | 5 | 41.7 | 15 | 22 | AAE01592 | Human gene 11 enco  |
| 29 | 5 | 41.7 | 17 | 23 | ABG63823 | Human albumin fusi  |
| 30 | 5 | 41.7 | 19 | 22 | AAE91942 | Complement inhibit  |
| 31 | 5 | 41.7 | 19 | 23 | AAO17268 | A thaliana recepto  |
| 32 | 5 | 41.7 | 20 | 19 | AAW47343 | Apolipoprotein B t  |
| 33 | 5 | 41.7 | 20 | 20 | AAV55885 | Apolipoprotein fra  |
| 34 | 5 | 41.7 | 20 | 20 | AAV33110 | Alipoprotein B try  |
| 35 | 4 | 33.3 | 4  | 21 | AAV96713 | Human E3 ubiquitin  |
| 36 | 4 | 33.3 | 5  | 19 | AAW51334 | Peptide #17 useful  |
| 37 | 4 | 33.3 | 5  | 19 | AAW51332 | Peptide #15 useful  |
| 38 | 4 | 33.3 | 5  | 19 | AAW51333 | Peptide #16 useful  |
| 39 | 4 | 33.3 | 5  | 21 | AAV49991 | Natural beta amyl   |
| 40 | 4 | 33.3 | 5  | 21 | AAV49992 | Natural beta amyl   |
| 41 | 4 | 33.3 | 5  | 21 | AAV49993 | Natural beta amyl   |
| 42 | 4 | 33.3 | 5  | 22 | AAE12530 | APP70 abeta peptid  |
| 43 | 4 | 33.3 | 5  | 22 | AAE12531 | APP70 abeta peptid  |
| 44 | 4 | 33.3 | 5  | 22 | AAE12532 | APP70 abeta peptid  |
| 45 | 4 | 33.3 | 5  | 22 | AAE10004 | Beta-amylloid pepti |
| 46 | 4 | 33.3 | 5  | 22 | AAE10005 | Beta-amylloid pepti |
| 47 | 4 | 33.3 | 5  | 22 | AAE10006 | Beta-amylloid pepti |
| 48 | 4 | 33.3 | 5  | 23 | AAE26294 | Peptide #16 capabl  |
| 49 | 4 | 33.3 | 5  | 23 | AAE26295 | Peptide #17 capabl  |
| 50 | 4 | 33.3 | 5  | 23 | AAE26296 | Peptide #18 capabl  |
| 51 | 4 | 33.3 | 5  | 23 | AAE15197 | Human HGF receptor  |
| 52 | 4 | 33.3 | 5  | 23 | AAE15232 | Human HGF receptor  |
| 53 | 4 | 33.3 | 5  | 23 | AAE15324 | Peptide #5 related  |
| 54 | 4 | 33.3 | 5  | 24 | ABG73479 | Natural beta-amyl   |
| 55 | 4 | 33.3 | 5  | 24 | ABG73480 | Natural beta-amyl   |
| 56 | 4 | 33.3 | 5  | 24 | ABG73481 | Natural beta-amyl   |
| 57 | 4 | 33.3 | 5  | 24 | ABG73481 | Sequence of substa  |
| 58 | 4 | 33.3 | 6  | 5  | AAE40527 | Sequence of substa  |
| 59 | 4 | 33.3 | 6  | 19 | AAW31486 | Transcriptional ac  |
| 60 | 4 | 33.3 | 6  | 21 | AAE27043 | Beta-amylloid pepti |
| 61 | 4 | 33.3 | 6  | 21 | AAE27045 | Beta-amylloid pepti |
| 62 | 4 | 33.3 | 6  | 21 | AAE28963 | Peptide encoded by  |
| 63 | 4 | 33.3 | 6  | 21 | AAE87707 | Feline human TRFP   |
| 64 | 4 | 33.3 | 6  | 21 | AAV90133 | TRFP derived pepti  |
| 65 | 4 | 33.3 | 6  | 21 | AAV51504 | Human TRFP derived  |
| 66 | 4 | 33.3 | 7  | 16 | AAE64963 | Peralkylated oligo  |
| 67 | 4 | 33.3 | 7  | 16 | AAE64963 | Peralkylated oligo  |
| 68 | 4 | 33.3 | 7  | 16 | AAE64968 | Peralkylated oligo  |
| 69 | 4 | 33.3 | 7  | 21 | AAE23226 | Hsp47-binding phag  |
| 70 | 4 | 33.3 | 8  | 15 | AAE61722 | PLP peptide 74, po  |
| 71 | 4 | 33.3 | 8  | 18 | AAW35337 | HIV-1 pol peptide   |
| 72 | 4 | 33.3 | 8  | 21 | AAE37338 | Peptide linker #23  |
| 73 | 4 | 33.3 | 8  | 22 | ABP14646 | HIV A03 super moti  |
| 74 | 4 | 33.3 | 8  | 22 | ABP21858 | HIV A03 motif pol   |
| 75 | 4 | 33.3 | 8  | 22 | ABP23685 | HIV A11 motif pol   |
| 76 | 4 | 33.3 | 8  | 22 | ABE56001 | Vascular dementia-  |
| 77 | 4 | 33.3 | 8  | 23 | AAU77974 | Cleavable peptide   |
| 78 | 4 | 33.3 | 9  | 15 | AAE67113 | Anti-contraction p  |
| 79 | 4 | 33.3 | 9  | 15 | AAE61774 | PLP peptide 76, po  |
| 80 | 4 | 33.3 | 9  | 15 | AAE61780 | PLP peptide 78, po  |
| 81 | 4 | 33.3 | 9  | 15 | AAE61794 | PLP peptide 73, po  |
| 82 | 4 | 33.3 | 9  | 15 | AAE61818 | PLP peptide 74, po  |

83 4 33.3 9 18 AAW43839 Specific human leu  
84 4 33.3 9 20 AAY06041 Human cancer antig  
85 4 33.3 9 21 AAB23686 Cytotoxic T lympho  
86 4 33.3 9 22 ABP15973 HIV A24 super moti  
87 4 33.3 9 22 ABP23687 HIV A11 motif pol  
88 4 33.3 9 22 ABP24323 HIV A24 motif pol  
89 4 33.3 9 22 AAM99552 Vaccine related MH  
90 4 33.3 9 22 AAG67192 Cancer testis tumo  
91 4 33.3 9 22 AAB69924 Human NY-ESO-1 HLA  
92 4 33.3 9 23 AAE31375 Human MUC1 peptide  
93 4 33.3 9 23 ABG79052 Human Gp100 class  
94 4 33.3 9 23 ABG66788 Tumour antigen Gp1  
95 4 33.3 9 23 AAU94300 Human novel protei  
96 4 33.3 9 23 AAU94307 Human novel protei  
97 4 33.3 9 23 AAU94469 Human novel protei  
98 4 33.3 9 23 AAU94507 Human novel protei  
99 4 33.3 9 23 AAU94677 Human novel protei  
100 4 33.3 9 23 AAU94712 Human novel protei

## ALIGNMENTS

RESULT 1  
AAB72249  
XX ID AAB72249 standard; peptide; 12 AA.  
XX AC AAB72249;  
XX DT 14-MAY-2001 (first entry)  
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 4.  
XX KW Colostrinin; immune response; cytokine; blood cell proliferation;  
XX KW central nervous system disorder; neurological disorder; mental disorder;  
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
XX KW neurosis; infection.  
XX OS Synthetic.  
XX PN WO200111937-A2.  
XX XX 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22818.  
XX PR 17-AUG-1999; 99US-0149311.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PA (REGG-) REGEN THERAPEUTICS PLC.  
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2001-202804/20.  
XX DR  
XX PT Inducing a cytokine and modulating an immune response, useful for  
XX PT treating central nervous system diseases and bacterial and viral  
XX PT infections, comprises administering colostrinin as an immunological  
XX PT regulator -  
XX PS Claim 1; Page 34; 50pp; English.  
XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
XX CC a proline rich polypeptide aggregate contained in colostrinum. The  
XX CC peptides have immune response modulatory activity, and are capable of  
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for  
XX CC inducing cytokine production, for modulating an immunological response  
XX CC and for inducing blood cell proliferation. The peptides are useful in the  
XX CC treatment of disorders of the central nervous system, neurological  
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,  
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
XX CC disorders of the immune system, bacterial and viral infections and  
XX CC acquired immunological deficiencies.

XX SQ Sequence 12 AA;  
XX Query Match 100.0%; Score 12; DB 22; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 1 LFFFLPVNVLP 12  
XX Db 1 LFFFLPVNVLP 12  
XX RESULT 2  
XX ID AAB72503 standard; Peptide; 12 AA.  
XX AC AAB72503;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #4.  
XX KW Dermatological; oxidative stress regulator; colostrinin.  
XX OS Unidentified.  
XX PN WO200112650-A2.  
XX XX 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22665.  
XX PR 17-AUG-1999; 99US-0149310.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.  
XX PT Modulating oxidative stress level in a cell, involves contacting the  
XX PT cell with an oxidative stress regulator selected from colostrinin, its  
XX PT constituent peptide, analog or their combinations -  
XX PS Claim 6; Page 25; 48pp; English.  
XX CC The present invention relates to a method for modulating the oxidative  
XX CC stress level in a cell or a patient, comprising contacting the cell with,  
XX CC or administering to the patient, an oxidative stress regulator selected  
XX CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
XX CC to change the level of an oxidising species in the cell. The method can  
XX CC be used to treat oxidative damage to skin, by decreasing or preventing an  
XX CC increase in the level of damage to a biomolecule of the patient.  
XX SQ Sequence 12 AA;  
XX Query Match 100.0%; Score 12; DB 22; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 1 LFFFLPVNVLP 12  
XX Db 1 LFFFLPVNVLP 12  
XX RESULT 3  
XX ID AAB72535 standard; Peptide; 12 AA.  
XX AC AAB72535;  
XX DT 09-MAY-2001 (first entry)  
XX





CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 12 AA;

Query Match 100.0%; Score 12; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLPVNVLP 12  
 |||||  
 Db 1 LFFFLPVNVLP 12

#### RESULT 6

AA014580  
 ID AAM51039 standard; Peptide; 12 AA.

XX AAM51039;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 12 /note= "optional C-terminal amidation"

PN WO200213849-A1.

XX 21-FEB-2002.

PR 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

PR (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

DR Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10.

XX Sequence 12 AA;

Query Match 100.0%; Score 12; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLPVNVLP 12  
 |||||  
 Db 1 LFFFLPVNVLP 12

#### RESULT 7

AA014580  
 ID AA014580 standard; peptide; 12 AA.

XX AA014580;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 4.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 12 /note= "Optional C-terminal amide"

PN WO200213851-A1.

XX 21-FEB-2002.

PR 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

DR Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention.

XX SQ Sequence 12 AA;

Query Match  
Best Local Similarity 100.0%; Score 12; DB 23; Length 12;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVNLP 12  
|||||

Db 1 LFFFLPVNVNLP 12

RESULT 8  
AAB59353  
ID AAB59353 standard; Peptide; 14 AA.  
XX AC AAB59353;  
XX DT 21-MAR-2001 (first entry)  
DE Ewe colostrinin peptide fragment derived sequence #13.  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX Ovis sp.  
OS WO200075173-A2.  
PN 14-DEC-2000.  
PD 02-JUN-2000; 2000WO-GB02128.  
PF 02-JUN-1999; 99GB-0012852.  
PR (REGE-) REGEN THERAPEUTICS PLC.  
PA Georgiades JA;  
PI WPI; 2001-071058/08.  
DR Peptides having an N-terminal amino acid sequence isolated from  
XX colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 14 AA;

Query Match  
Best Local Similarity 100.0%; Score 12; DB 22; Length 14;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVNLP 12  
|||||

Db 2 LFFFLPVNVNLP 13

RESULT 9  
AAE07186

ID AAE07186 standard; peptide; 6 AA.  
XX AC AAE07186;  
XX DT 06-NOV-2001 (first entry)  
XX Colostrinin peptide 2.  
DE Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
KW central nervous system disorder; neurodegenerative disorder; weight loss;  
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
KW acquired immunological deficiency; neurological disorder; dementia;  
KW antiviral.  
XX Unidentified.  
OS WO200155199-A1.  
PN 02-AUG-2001.  
PD 26-JAN-2001; 2001WO-GB00329.  
PF 26-JAN-2000; 2000GB-0001825.  
PR (REGE-) REGEN THERAPEUTICS PLC.  
XX Georgiades JA;  
PI WPI; 2001-488775/53.  
DR Peptide useful as an inter alia in the treatment of e.g. disorders of  
XX the immune system and the central nervous system comprises ten  
PT amino-terminal amino acid sequence derived from peptides present in  
PT colostrinin -  
XX Claim 1; Page 15; 40pp; English.

CC The invention relates to colostrinin peptide fragments which are useful,  
CC inter alia, in the treatment of chronic disorders of the immune system  
CC and the central nervous system. Colostrinin peptides are used as a  
CC medicament in the treatment of neurological disorders e.g., dementia,  
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
CC viral infections and diseases characterised by the presence of beta-  
CC amyloid plaques and as a dietary supplement for babies, small children,  
CC adults and senile persons, who have been subjected to chemotherapy or  
CC have suffered from cachexia or weight loss due to the chronic disease.  
CC Colostrinin peptides are also used as food additives and as an auxiliary  
CC withdrawal treatment for drug addicts, after a period of detoxification  
CC and in persons dependent on stimulants. Colostrinin peptides are used to  
CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
CC disturbances of psychiatric patients in a state of depression. These  
CC colostrinin peptides improves the development of immune system in a new  
CC born child and to correct the immunological deficiencies in a child.  
CC The present sequence is colostrinin peptide 2 related to the invention.

XX SQ Sequence 6 AA;

Query Match  
Best Local Similarity 50.0%; Score 6; DB 22; Length 6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPVVN 9  
|||||

Db 1 FLPVVN 6

RESULT 10  
AAE07196  
ID AAE07196 standard; peptide; 7 AA.  
XX

AAE07196;  
 06-NOV-2001 (first entry)  
 Modified colostrinin cyclic peptide #2.  
 Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 central nervous system disorder; neurodegenerative disorder; weight loss;  
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 acquired immunological deficiency; neurological disorder; dementia;  
 antiviral; cyclic.  
 Synthetic.  
 Key Location/Qualifiers  
 Modified-site 1  
 /note= "N-terminal acetyl; this residue forms a cyclic  
 linkage with Asn found at the C-terminal end"  
 WO200155199-A1.  
 02-AUG-2001.  
 26-JAN-2001; 2001WO-GB00329.  
 26-JAN-2000; 2000GB-0001825.  
 (REG-) REGEN THERAPEUTICS PLC.  
 Georgiades JA;  
 WPI; 2001-488775/53.  
 Peptide useful as an inter alia in the treatment of e.g. disorders of  
 the immune system and the central nervous system comprises ten  
 amino-terminal amino acid sequence derived from peptides present in  
 colostrinin -  
 Example 2; Page 8; 40pp; English.  
 The invention relates to colostrinin peptide fragments which are useful,  
 inter alia, in the treatment of chronic disorders of the immune system  
 and the central nervous system. Colostrinin peptides are used as a  
 medicament in the treatment of neurological disorders e.g., dementia,  
 neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 neurosis, in acquired immunological deficiencies, chronic bacterial and  
 viral infections and diseases characterised by the presence of beta-  
 amyloid plaques and as a dietary supplement for babies, small children,  
 adults and senile persons, who have been subjected to chemotherapy or  
 have suffered from cachexia or weight loss due to the chronic disease.  
 Colostrinin peptides are also used as food additives and as an auxiliary  
 withdrawal treatment for drug addicts, after a period of detoxification  
 and in persons dependent on stimulants. Colostrinin peptides are used to  
 prepare antibodies and to treat emotional disturbances e.g. emotional  
 disturbances of psychiatric patients in a state of depression. These  
 colostrinin peptides improves the development of immune system in a new  
 born child and to correct the immunological deficiencies in a child.  
 The present sequence is modified colostrinin cyclic peptide #2 related to  
 the invention.  
 Sequence 7 AA;  
 Query Match 50.0%; Score 6; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 11

AAZ21194  
 ID AAZ21194 standard; Protein; 9 AA.  
 XX  
 AC AAZ21194;  
 XX  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human bcl2 proto-oncogene mutant protein fragment 42.  
 XX  
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 frameshift mutation; age-related disease; neurodegenerative disorder;  
 Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 high mobility group protein-C; neuroendocrine specific protein A.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9845322-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 02-APR-1998; 98WO-IB00705.  
 XX  
 PR 10-APR-1997; 97US-0043163.  
 XX  
 PA (UYUT-) RIJKSUNIV UTRECHT.  
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
 XX  
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;  
 XX  
 DR WPI; 1998-609901/51.  
 DR N-PSDB; AAX75766.  
 XX  
 PT Diagnosing disease by detecting frameshift mutations in RNA or  
 corresponding protein mutations - used to diagnose cancer and  
 neurological diseases, particularly Alzheimer's disease, and also  
 for treatment and prevention with specific ribozymes or wild-type  
 RNA  
 XX  
 PS Disclosure; Figure 15; 258pp; English.  
 XX  
 CC This invention describes a novel method for the diagnosis of a disease  
 caused by, or associated with, an RNA molecule that has a frameshift  
 mutation. The method is used to diagnose age-related diseases, especially  
 cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 and many others listed) or susceptibility to these disorders. The method  
 allows a definitive diagnosis of Alzheimer's disease in living patients,  
 at an early stage. It is based on the observation that disease may be  
 caused by mutations in RNA rather than DNA. The invention describes the  
 use of neuronal system RNA molecules, specifically proteins including  
 beta-amyloid precursor protein (beta-APP), the microtubule associated  
 proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 protein-C (HMGP-C) and neuroendocrine specific protein A.  
 XX  
 SQ Sequence 9 AA;

Query Match

50.0%; Score 6; DB 19; Length 9;

Best Local Similarity

100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPLPV 7  
 Db 4 FFPLPV 9

RESULT 12  
 AAW51338  
 ID AAW51338 standard; peptide; 5 AA.  
 AC AAW51338;  
 XX  
 DT 14-AUG-1998 (first entry)  
 DE Peptide #21 useful as modulator of beta-amyloid peptide aggregation.  
 KW Natural beta-amyloid peptide; aggregation; D-amino acid;  
 KW Alzheimer's disease; beta-amyloidosis.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Modified-site /note= "D-form residue, C-terminal amide"  
 FT  
 XX  
 PN WO9808868-A1.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 27-AUG-1997; 97WO-US15166.  
 XX  
 PR 21-JUL-1997; 97US-0897342.  
 PR 27-AUG-1996; 96US-0703675.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PI Arico-muendel CC, Chin J, Findeis MA, Gefter ML;  
 PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;  
 PI Musso G, Phillips K, Signer ER, Wakefield J;  
 XX WPI; 1998-216936/19.  
 DR  
 XX  
 PT Peptide compounds which are preferably based on beta-amyloid  
 PT peptide(s) - are useful in treatment of disorders related to  
 PT beta-amyloidosis, especially Alzheimer's disease  
 XX  
 PS Claim 8; Page 78; 92pp; English.  
 CC The invention relates to peptides that modulate natural beta-amyloid  
 CC peptide aggregation. The modulators of the invention comprise a peptide  
 CC preferably based on a beta-amyloid peptide, that is comprised entirely  
 CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid  
 CC residues and includes at least two D-amino acid residues independently  
 CC selected from the group consisting of D-leucine, D-phenylalanine and  
 CC D-valine. Preferred amino-terminal modifying groups include cyclic,  
 CC heterocyclic, polycyclic and branched alkyl groups. Preferred  
 CC carboxy-terminal modifying groups include an amide group, an alkyl amide  
 CC group, an aryl amide group or a hydroxy group. The peptides may be used  
 CC to treat disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease. They may also be used in methods for detecting the  
 CC presence of beta-amyloid peptides in biological samples. The present  
 CC sequence represents a specifically claimed peptide.  
 XX  
 SQ Sequence 5 AA;

Query Match 41.7%; Score 5; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
 Db 1 LFFFL 5

RESULT 13  
 AAW51344  
 ID AAW51344 standard; peptide; 5 AA.  
 XX  
 AC AAW51344;  
 XX  
 DT 14-AUG-1998 (first entry)  
 DE Peptide #27 useful as modulator of beta-amyloid peptide aggregation.  
 KW Natural beta-amyloid peptide; aggregation; D-amino acid;  
 KW Alzheimer's disease; beta-amyloidosis.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "D-form residue, N-terminal acetyl"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Modified-site /note= "D-form residue, C-terminal amide"  
 FT  
 XX  
 PN WO9808868-A1.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 27-AUG-1997; 97WO-US15166.  
 XX  
 PR 21-JUL-1997; 97US-0897342.  
 PR 27-AUG-1996; 96US-0703675.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PI Arico-muendel CC, Chin J, Findeis MA, Gefter ML;  
 PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;  
 PI Musso G, Phillips K, Signer ER, Wakefield J;  
 XX WPI; 1998-216936/19.  
 DR  
 XX  
 PT Peptide compounds which are preferably based on beta-amyloid  
 PT peptide(s) - are useful in treatment of disorders related to  
 PT beta-amyloidosis, especially Alzheimer's disease  
 XX  
 PS Claim 8; Page 80; 92pp; English.  
 CC The invention relates to peptides that modulate natural beta-amyloid  
 CC peptide aggregation. The modulators of the invention comprise a peptide  
 CC preferably based on a beta-amyloid peptide, that is comprised entirely  
 CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid  
 CC residues and includes at least two D-amino acid residues independently  
 CC selected from the group consisting of D-leucine, D-phenylalanine and  
 CC D-valine. Preferred amino-terminal modifying groups include cyclic,  
 CC heterocyclic, polycyclic and branched alkyl groups. Preferred  
 CC carboxy-terminal modifying groups include an amide group, an alkyl amide  
 CC group, an aryl amide group or a hydroxy group. The peptides may be used  
 CC to treat disorders associated with beta-amyloidosis, especially  
 CC Alzheimer's disease. They may also be used in methods for detecting the

CC presence of beta-amyloid peptides in biological samples. The present  
 CC sequence represents a specifically claimed peptide.

XX  
 SQ Sequence 5 AA;

Query Match 41.7%; Score 5; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LFFFL 5  
 Db 1 LFFFL 5

RESULT 14  
 AAY49996  
 ID AAY49996 standard; peptide; 5 AA.  
 XX AAY49996;  
 AC  
 XX  
 DT 04-FEB-2000 (first entry)  
 XX  
 DE Natural beta amyloid peptide aggregation modulating compound #3.  
 XX  
 DE Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;  
 KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;  
 KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;  
 KW amyloidosis-Dutch-type.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..5  
 FT Modified-site 5 /note= "D-form residues"  
 FT /note= "amidated"  
 XX  
 XX US5985242-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 XX 27-AUG-1997; 97US-0920162.  
 XX  
 XX 27-OCT-1995; 95US-0548998.  
 XX 14-MAR-1996; 96US-0616081.  
 PR 27-AUG-1996; 96US-0703675.  
 PR 21-JUL-1997; 97US-0897342.  
 XX  
 XX (PRAE-) PRACIS PHARM INC.  
 PA  
 XX Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;  
 PI Musso G, Phillips K, Hayward NJ, Gefter ML, Findels MA, Lee J;  
 PI Arico-Muendel CC, Chin J;  
 XX  
 DR WPI; 2000-022266/02.  
 XX  
 XX Compound comprising a peptidic structure, an amino-terminal modifying  
 PT group and a carboxy-terminal modifying group, useful for treating  
 PT Alzheimer's disease -  
 XX  
 XX Claim 8; Column 63; 40pp; English.  
 PS  
 XX The present invention describes a compound of formula A-(Xaa)-B,  
 CC comprising a peptidic structure (Xaa), an amino-terminal modifying  
 CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to  
 CC AAY49994 represent specifically claimed examples of (Xaa). Also  
 CC described is a method for inhibiting aggregation of natural beta-amyloid  
 CC peptides and treating Alzheimer's disease, comprising contacting the  
 CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence  
 CC of natural beta-amyloid peptides in a biological sample by contacting  
 CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease  
 CC and for detecting the presence of natural beta-amyloid peptides in a

CC biological sample. The compound can also be used prophylactically or  
 CC therapeutically to treat other clinical occurrences of beta-amyloid  
 CC deposition, such as in Down's syndrome individuals and in patients with  
 CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).  
 CC The present sequence represents an example of the compound from the  
 CC present invention.

XX  
 SQ Sequence 5 AA;

Query Match 41.7%; Score 5; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LFFFL 5  
 Db 1 LFFFL 5

RESULT 15  
 AAE12536  
 ID AAE12536 standard; peptide; 5 AA.  
 XX AAE12536;  
 AC  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE APP70 abeta peptide (residues 17-21) inverso isomer mutant (V18F; A21L).  
 XX  
 KW Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis;  
 KW Alzheimer's disease; neuroprotective; beta-amyloid precursor protein;  
 KW APP-770; nootropic; mutant; mutain.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..5  
 FT Modified-site 1 /note= "D-form residues"  
 FT /note= "Optionally modified with 4-hydroxy benzoyl  
 FT or acetyl"  
 FT Misc-difference 2 /note= "Wild-type Val substituted with Phe; corresponds  
 FT to position 18 of natural Abeta peptide"  
 FT Misc-difference 5 /note= "Wild-type Ala substituted with Leu; corresponds  
 FT to position 21 of natural Abeta peptide; Optionally  
 FT C-terminal amide"  
 XX  
 XX US6277826-B1.  
 XX  
 PD 21-AUG-2001.  
 XX  
 XX 19-JUL-1999; 99US-0356931.  
 XX  
 XX 27-AUG-1997; 97US-0920162.  
 PR 27-AUG-1996; 96US-0703675.  
 XX  
 XX (PRAE-) PRACIS PHARM INC.  
 PA  
 XX Findels MA, Gefter ML, Musso G, Signer ER, Wakefield J;  
 PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;  
 PI Arico-Muendel CC, Phillips K, Hayward NJ;  
 XX  
 DR WPI; 2001-637856/73.  
 XX  
 XX Modulator compound for treating disorders associated with  
 PT beta-amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid  
 PT peptide containing D-amino acids -  
 XX  
 XX Example 11; Column 48; 41pp; English.  
 PS  
 XX The patent discloses compounds and pharmaceutical compositions thereof,  
 CC that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide),

CC modulate the aggregation of natural beta-AP and/or inhibit the cyto-  
CC toxicity of natural beta-APs. The beta-amyloid modulator compounds of  
CC the invention comprise a peptide, preferably based on beta-AP, that is  
CC composed entirely of D-amino acids. The modulators of the invention are  
CC useful for treating a disorder associated with beta-amyloidosis such as  
CC Alzheimer's disease. The present sequence is an inversed isomer mutant  
CC (W18F; A41L) of Abeta peptide. Beta AP is a cleavage product of beta  
CC amyloid precursor protein (APP-770; residues 17-21).

XX Sequence 5 AA;

Query Match 41.7%; Score 5; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred.No. 9.3e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LFFFL 5  
|  
|  
|  
|  
Db 1 LFFFL 5

RESULT 16  
ABG73485  
ID ABG73485 standard; Peptide; 5 AA.

XX ABG73485;

AC ABG73485;

XX 10-MAY-2003 (first entry)

XX Natural beta-amyloid peptide modulator compound #28.

XX Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;  
KW Alzheimer's disease; beta-amyloid deposition; Down's syndrome;  
KW hereditary cerebral haemorrhage with amyloidosis-dutch-type; HCHWA-D;  
KW neurological impairment; neuroprotective; nootropic.

XX Synthetic.

XX US2002103134-A1.

XX 01-AUG-2002.

XX 29-JUN-2001; 2001US-0895443.

XX 27-AUG-1997; 97US-0920162.

XX 19-JUL-1999; 99US-0356931.

XX 27-OCT-1995; 95US-0548998.

XX 14-MAR-1996; 96US-0616081.

XX 27-AUG-1996; 96US-0703675.

XX 21-JUL-1997; 97US-0897342.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;

XX Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;

XX Arico-Muendel CC, Phillips K, Hayward NJ;

XX WPI; 2003-298609/29.

XX Novel compound that modulate natural beta-amyloid peptide aggregation,  
XX is useful for treating amyloidogenic diseases e.g. Alzheimer's disease  
XX  
XX Claim 8; Page 36; 42pp; English.  
XX  
XX The invention relates to a compound that modulates natural beta-amyloid  
XX peptide aggregation. The peptide is useful for inhibiting aggregation of  
XX natural beta-amyloid peptides and for treating a disorder associated with  
XX beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful  
XX for detecting the presence or absence of natural beta-amyloid peptides in  
XX a biological sample, by contacting the biological sample with the  
XX compound in vitro, where the compound is labelled with a detectable  
XX substance and detecting the compound bound to natural beta-amyloid  
XX peptides to thus detect the presence or absence of natural beta-amyloid

CC peptides. The compound is preferably labelled with radioactive technetium  
CC or radioactive iodine and is administered to the subject. The compound is  
CC also useful for prophylactically or therapeutically treating other  
CC clinical occurrences of beta-amyloid deposition such as in Down's  
CC syndrome individuals and in patients with hereditary cerebral haemorrhage  
CC with amyloidosis-dutch-type (HCHWA-D), and for therapeutically allowing  
CC for the sequestration of beta-amyloid proteins at sites that do not lead  
CC to neurological impairment. This sequence represents a natural  
CC beta-amyloid peptide modulator compound of the invention.

XX Sequence 5 AA;

Query Match 41.7%; Score 5; DB 24; Length 5;  
Best Local Similarity 100.0%; Pred.No. 9.3e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 LFFFL 5  
|  
|  
|  
|  
Db 1 LFFFL 5

RESULT 17  
AAG61675  
ID AAG61675 standard; Protein; 9 AA.

XX AAG61675;

AC AAG61675;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 80031.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 18-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130891.

XX 28-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 06-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144634.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 05-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 5; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
 Db 1 FFFLP 5

## RESULT 18

AAW69637  
 ID AAW69637 standard; peptide; 11 AA.

AC AAW69637;

XX DT 19-OCT-1998 (first entry)

DE Peptide SEQ ID NO:57 from US5789184 Example 5.

XX Yeast; Saccharomyces cerevisiae; pheromone; alpha factor; receptor;  
 KW surrogate; screening; selection.

XX OS Synthetic.

XX PN US5789184-A.

XX PD 04-AUG-1998.

XX PF 05-JUN-1995; 95US-0464531.

XX PR 05-JUN-1995; 95US-0464531.

XX PR 31-MAR-1993; 93US-0041431.

XX PR 31-JAN-1994; 94US-0190328.

XX PR 20-SEP-1994; 94US-0309313.

XX PR 13-OCT-1994; 94US-0322137.

XX (CADU-) CADUS PHARM CORP.

XX PI Broach J, Fowlkes DM, Klein C, Manfredi J, Murphy AJ;

XX PI Paul J, Trueheart J;

XX DR WPI; 1998-446076/38.

XX DR N-PSDB; AAV50008.

XX PT Recombinant yeast cells - containing gene encoding yeast pheromone  
 PT system protein surrogate and gene encoding peptide modulator

XX PS Example 5; Column 125; 93pp; English.

XX CC The present invention describes a yeast cell having a pheromone system,  
 CC in which the cell comprises: (a) a first heterologous gene encoding a  
 CC heterologous surrogate of a yeast pheromone system protein, the surrogate  
 CC being a kinase and performing in the pheromone system of the yeast cell  
 CC a function naturally performed by the corresponding yeast pheromone  
 CC system protein; and (b) a second heterologous gene encoding a  
 CC heterologous peptide, where the heterologous peptide modulates the  
 CC interaction of the surrogate with the pheromone system in the yeast cell,  
 CC and the modulation is a selectable or screenable event. The yeast cells  
 CC are used in assaying a peptide for modulation of the activity of a non-  
 CC yeast surrogate for a pheromone system protein and determining by  
 CC detecting a change in the selectable or screenable event whether the  
 CC pheromone signal pathway is activated or inhibited by the interaction of  
 CC the surrogate and the peptide. The present sequence represents a  
 XX peptide which is used in an example of the present invention.

XX SQ Sequence 11 AA;

Query Match 41.7%; Score 5; DB 19; Length 11;

Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
 Db 6 FFFLP 10

## RESULT 19

AAW74434  
 ID AAW74434 standard; peptide; 11 AA.

XX AC AAW74434;

XX DT 20-MAR-2003 (updated)

XX DT 10-MAY-1999 (first entry)

XX DE Ste2 agonist peptide sequence.

XX KW Yeast pheromone; Ste2 agonist; cognate yeast pheromone system protein;

XX KW farnesyl transferase; anticancer therapy.

XX OS Synthetic.

XX PN US5876951-A.

XX PD 02-MAR-1999.

XX PF 05-JUN-1995; 95US-0461598.

XX PR 05-JUN-1995; 95US-0461598.

XX PR 31-MAR-1993; 93US-0041431.

XX PR 31-JAN-1994; 94US-0190328.

XX PR 20-SEP-1994; 94US-0309313.

XX PR 13-OCT-1994; 94US-0322137.

XX (CADU-) CADUS PHARM CORP.

XX PI Broach J, Fowlkes DM, Klein C, Manfredi J, Murphy AJ;

XX PI Paul J, Trueheart J;

XX DR WPI; 1999-189631/16.

XX DR N-PSDB; AAX18224.

XX PT Yeast cells having an engineered pheromone system - useful for

PT identifying drugs which can inhibit or activate pheromone system

PT protein, e.g. to develop anti-cancer therapies

XX PS Example 5; Column 61; 93pp; English.

XX CC This sequence represents an Ste2 agonist peptide sequence.

XX CC The invention relates to Yeast cells engineered to express an exogenous  
 CC protein capable of substituting for a yeast protein involved in the  
 CC post-translational modification, transport, recognition or signal  
 CC transduction of a yeast pheromone. The system can be used to identify  
 CC drugs which inhibit or activate the ability of the surrogate to  
 CC substitute for the cognate yeast pheromone system protein. Inhibitors of  
 CC farnesyl transferase identified can be used for anticancer therapies.  
 CC (Updated on 20-MAR-2003 to correct PF field.)

XX SQ Sequence 11 AA;

Query Match 41.7%; Score 5; DB 20; Length 11;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
 Db 6 FFFLP 10

## RESULT 20

AAW20744



```
ID XX AAB20744 standard; Peptide; 11 AA.
AC XX AAB20744;
DT DT 21-DEC-2000 (first entry)
XX XX
DE DE MF-alpha-1 expression construct peptide SEQ ID NO:57.
XX XX
KW Yeast; pheromone; alpha-factor; transporter; pheromone receptor;
KW G alpha subunit; MF alpha 1; Mfal; STE2; STE3; C5a receptor; GPAl;
KW G protein coupled receptor; mutagenesis; amplification; screening;
KW hybrid; agonist; antagonist; signal transduction; detection;
KW identification.
XX XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX XX
PN PN US6100042-A.
XX XX
PD PD 08-AUG-2000.
XX XX
PF PF 13-OCT-1994; 94US-0322137.
XX XX
PR PR 31-MAR-1993; 93US-0041431.
XX XX
PR PR 31-JAN-1994; 94US-0190328.
XX XX
PR PR 20-SEP-1994; 94US-0309313.
XX XX
PA (CADU-) CADUS PHARM CORP.
XX XX
PI Fowlkes DM, Broach J, Klein C, Murphy AJ, Paul J, Trueheart J;
PI Manfredi J;
XX XX
DR WPI; 2000-531665/48.
XX XX
XX Mixture of recombinant yeast cells comprising a heterologous G protein
FT coupled receptor whose signal transduction activity is modulated by a
FT heterologous polypeptide which provides a detectable signal on
FT modulation.
XX XX
PS Example 5; Column 63; 95pp; English.
XX XX
CC The present invention describes recombinant yeast cell mixtures (I).
CC Each (I) has a heterologous G protein coupled receptor (GPCR) expressed
CC in the cell membrane such that signal transduction (ST) activity via
CC GPCR is modulated by interaction of extracellular region (ER) of GPCR
CC with a heterologous polypeptide (P) which interacts with ER of GPCR.
CC Modulation of the ST activity by (P) provides a detectable signal.
CC Also described is a recombinant yeast cell (II) that has a cell membrane
CC which comprises a GPCR such that ST activity via GPCR is modulated by
CC interaction of an ER of GPCR with an extracellular signal, and a (P)
CC which is transported to a location allowing interaction with ER of GPCR.
CC (I) is used for identifying a modulator of (P) expressed by the yeast
CC cell which involves providing (I) which comprises heterologous GPCR and
CC a heterologous test polypeptide, allowing the cells within the mixture
CC to generate a detectable signal and then identifying the heterologous
CC test peptide as a modulator of the heterologous receptor protein
CC expressed by the yeast cell. The yeast cells may be used to identify
CC drugs which inhibit or activate, to a detectable degree, the ability of
CC the surrogate to substitute for the cognate yeast pheromone system
CC proteins. The yeast cell is also used to screen agonists and
CC antagonists. The present sequence is used in the exemplification of
CC the present invention.
XX XX
SQ Sequence 11 AA;
Query Match 41.7%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFFLP 6
Db 6 FFFLP 10
```

```
RESULT 21
AAY93630
ID ID AAY93630 standard; peptide; 11 AA.
XX XX
AC AC AAY93630;
XX XX
DT DT 25-SEP-2000 (first entry)
XX XX
DE Peptide encoded by the insert of an a-factor variant.
XX XX
KW Surrogate ligand; formyl peptide receptor like-1 receptor;
KW FPRL-1 receptor; signal transduction; cellular receptor; a-factor;
KW ABC transporter; ion channel.
XX XX
OS Synthetic.
XX XX
PN WO200031261-A2.
XX XX
PD 02-JUN-2000.
XX XX
PF 24-NOV-1999; 99WO-US27909.
XX XX
PR 25-NOV-1998; 98US-0109902.
XX XX
PR 30-NOV-1998; 98US-0201396.
XX XX
PA (CADU-) CADUS PHARM CORP.
XX XX
PI Klein CA, Murphy AJ, Paul J;
XX XX
DR WPI; 2000-400071/34.
XX XX
XX Recombinant cell used to identify modulators of heterologous formyl
FT peptide receptor like-1 (FPRL-1) receptor, comprising FPRL-1 receptor
FT expressed in the cell membrane, and a FPRL-1 receptor ligand agonist -
XX Example 5; Page 88; 156pp; English.
XX XX
CC AAY93628-31 represent peptides encoded by the inserts of a-factor
CC variants identified from random peptide libraries. These variants have
CC utility as improved substrates of ABC transporters expressed in yeast.
CC The specification describes a method for screening and identifying
CC pharmacologically effective compounds which specifically interact with
CC and modulate the activity of a cellular receptor or ion channel. The
CC method uses a cells which expresses a heterologous formyl peptide
CC receptor like-1 (FPRL-1) receptor in the cell membrane, so
CC that extracellular signal interaction with the receptors extracellular
CC region modulates signal transduction via the receptor. The cell is
CC used in a method to screen and identify pharmaceutically effective
CC compounds which specifically interact with and modulate the activity
CC of a cellular receptor or ion channel, especially the FPRL-1 receptor.
XX XX
SQ Sequence 11 AA;
Query Match 41.7%; Score 5; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFFLP 6
Db 6 FFFLP 10
```

```
RESULT 22
AAG79162
ID ID AAG79162 standard; peptide; 11 AA.
XX XX
AC AAG79162;
XX XX
DT 03-JAN-2002 (first entry)
XX XX
DE Amino acid sequence of an improved a-factor variant.
XX XX
```



PN WO200147944-A2.  
 XX 05-JUL-2001.  
 XX 28-DEC-2000; 2000WO-US35498.  
 XX 28-DEC-1999; 99US-0173419.  
 XX 27-DEC-2000; 2000US-0173419.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 XX WPI; 2001-465210/50.  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 XX oncogenes and histones, useful for diagnosing and treating, e.g.  
 XX cancer, autoimmune diseases and infections -  
 XX Disclosure; Page 3681; 4143pp; English.  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 XX encoding polymorphic variants of proteins related to amylases, amyloid  
 XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 XX polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 XX complement related proteins, cytochromes, kinesins, cytokines,  
 XX interferons, interleukins, G-protein coupled receptors and thioesterases.  
 XX The present sequence is a peptide encoded by one such oligonucleotide.  
 XX The oligonucleotides and the peptides encoded by them may be used in the  
 XX prevention, diagnosis and treatment of diseases associated with  
 XX inappropriate expression of the proteins listed above. Disorders that may  
 XX be prevented, diagnosed and/or treated include multifactorial diseases  
 XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 XX brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 XX system and an infection of pathogenic organisms.  
 XX Sequence 14 AA;  
 SQ Query Match 41.7%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PVNVV 10  
 |||||  
 Db 6 PVNVV 10  
 |||||  
 RESULT 25  
 AAM98289  
 ID AAM98289 standard; Peptide; 14 AA.  
 AC AAM98289;  
 XX 24-JAN-2002 (first entry)  
 DT Human peptide #1564 encoded by a SNP oligonucleotide.  
 DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX Homo sapiens.  
 OS WO200147944-A2.  
 XX 05-JUL-2001.  
 XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-2000; 2000WO-US35498.  
 XX 28-DEC-1999; 99US-0173419.  
 XX 27-DEC-2000; 2000US-0173419.  
 XX (CURA-) CURAGEN CORP.  
 XX Shimkets RA, Leach M;  
 XX WPI; 2001-465210/50.  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 XX oncogenes and histones, useful for diagnosing and treating, e.g.  
 XX cancer, autoimmune diseases and infections -  
 XX Disclosure; Page 4011; 4143pp; English.  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 XX encoding polymorphic variants of proteins related to amylases, amyloid  
 XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 XX polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 XX complement related proteins, cytochromes, kinesins, cytokines,  
 XX interferons, interleukins, G-protein coupled receptors and thioesterases.  
 XX The present sequence is a peptide encoded by one such oligonucleotide.  
 XX The oligonucleotides and the peptides encoded by them may be used in the  
 XX prevention, diagnosis and treatment of diseases associated with  
 XX inappropriate expression of the proteins listed above. Disorders that may  
 XX be prevented, diagnosed and/or treated include multifactorial diseases  
 XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 XX brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 XX system and an infection of pathogenic organisms.  
 XX Sequence 14 AA;  
 SQ Query Match 41.7%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFFL 5  
 |||||  
 Db 4 LFFFL 8  
 |||||  
 RESULT 26  
 AAM98290  
 ID AAM98290 standard; Peptide; 14 AA.  
 AC AAM98290;  
 XX 24-JAN-2002 (first entry)  
 DT Human peptide #1565 encoded by a SNP oligonucleotide.  
 DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX Homo sapiens.  
 OS WO200147944-A2.  
 XX 05-JUL-2001.  
 XX 28-DEC-2000; 2000WO-US35498.

```

PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-465210/50.
DR
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
XX Disclosure; Page 4011; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinases, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
XX Sequence 14 AA;
SQ
Query Match 41.7%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LFFFL 5
DB 6 LFFFL 10
RESULT 27
AAG64341
ID AAG64341 standard; Peptide; 15 AA.
AC
XX AAG64341;
XX
XX 24-SEP-2001 (first entry)
DT
XX
DE Ribosomal protein L2-11 peptide fragment.
XX
XX Ribosomal protein L2-11; cytosolic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation.
XX
XX Unidentified.
OS
XX
XX WO200147990-A1.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 18-DEC-2000; 2000WO-CN00630.
PF
XX
XX 24-DEC-1999; 99CN-0125768.
PR
XX (BIOW-) BIOWINDOW GENE DEV INC.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2001-425641/45.
DR
XX
XX

```

---

```

PT Ribosomal protein L2-11 and encoded polynucleotide, used in diagnosis
PT and treatment of malignant tumors, hemopathy, human immunodeficiency
PT virus infection, immunological diseases and inflammation -
XX
XX Example 6; Page 14; 35pp; Chinese.
XX
XX The present invention relates to ribosomal protein L2-11 and its coding
XX sequence (see AAH49665 and AAG64340). The ribosomal protein and its
XX coding sequence are useful in the diagnosis and treatment of malignant
XX tumour, haemopathy, HIV infection, immunological diseases and various
XX inflammations. The present sequence is a N-terminal peptide fragment of
XX the ribosomal protein, which was used in an example from the present
XX invention.
XX
XX Sequence 15 AA;
SQ
Query Match 41.7%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 FFLPV 7
DB 4 FFLPV 8
RESULT 28
AAE01592
ID AAE01592 standard; peptide; 17 AA.
XX
XX AAE01592;
XX
XX 17-JUL-2001 (first entry)
DT
XX
DE Human gene 11 encoded secreted protein fragment HMVDP35, SEQ ID NO:142.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerability;
KW cell culture; chemotaxis; food additive;
KW binding partner identification; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200134623-A1.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 01-NOV-2000; 2000WO-US30037.
PF
XX
XX 05-NOV-1999; 99US-0163577.
PR
XX 30-JUN-2000; 2000US-0215137.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Komatsoulis GA, Moore PA;
PI
XX WPI; 2001-316490/33.
DR
XX N-PSDB; AAD05435.
DR
XX
XX Nucleic acids encoding 29 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX
XX Claim 11; Page 495-496; 535pp; English.
PS
XX
XX AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted
CC protein genes, and AAE01546-AAE01630 represent the proteins they encode.
CC

```

CC AAE01631-AAE01660 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 29 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC cardiovascular disorders, angogenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment of the invention.  
 XX  
 SQ Sequence 17 AA;

Query Match 41.7%; Score 5; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5  
 |||||  
 Db 5 LFFFL 9

RESULT 29  
 ABG63823

ID ABG63823 standard; Protein; 17 AA.

AC ABG63823;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #498.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytosolic; antifertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.

XX Homo sapiens.  
 OS Synthetic.

XX WO200177137-A1.

PD 18-OCT-2001.

XX 12-APR-2001; 2001WO-US11988.

XX 12-APR-2000; 2000US-229359P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Haseltine WA;

DR WPI; 2002-010886/01.

XX  
 PT New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -

XX Claim 1; Page 848; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.

XX Sequence 17 AA;

Query Match 41.7%; Score 5; DB 23; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5  
 |||||  
 Db 5 LFFFL 9

RESULT 30  
 AAB91942

ID AAB91942 standard; Peptide; 19 AA.

AC AAB91942;

DT 22-JUN-2001 (first entry)

XX Complement inhibitor peptide SEQ ID NO:1118.

DE Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

PD 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

XX

PS Disclosure; Page 561; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX

SQ Sequence 19 AA;  
 Query Match 41.7%; Score 5; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVLP 12  
 Db 15 VNVLP 19  
 |||||

RESULT 31  
 AAO17268  
 ID AAO17268 standard; Protein; 19 AA.  
 AC AAO17268;  
 DT 08-JUL-2002 (first entry)  
 XX  
 DE A thaliana receptor kinase RKX8 peptide fragment.  
 XX  
 KW Vegetative propagation; plant; phytochrome; receptor kinase-like SERK;  
 KW RKS.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1094113-A1.  
 XX  
 PD 25-APR-2001.  
 XX  
 PF 22-OCT-1999; 99EP-0203480.  
 XX  
 PR 22-OCT-1999; 99EP-0203480.  
 XX  
 PA (GENE-) GENETWISTER TECHNOLOGIES BV.  
 XX  
 PI Schmidt BDL, Van Der Kop DAM, De Boer AD;  
 XX  
 DR WPI; 2002-228902/29.  
 XX  
 PT In vitro culture propagation of a plant from plant starting material,  
 PT comprises stimulating root/shoot initiation by introducing a  
 PT recombinant gene product into the starting material, thus reducing  
 PT phytochrome addition to culture -  
 XX  
 PS Disclosure; Page 86; 171pp; English.  
 XX  
 CC The present invention relates to a culture method for propagating a plant  
 CC from a plant starting material, where root or shoot initiation is  
 CC stimulated by introducing a gene into the starting material which allows  
 CC the reduction or absence of phytochrome addition to the culture. The  
 CC method is used for the propagation (preferably, seedless propagation) of  
 CC a plant from a plant starting material in an in vitro culture method.  
 CC Nucleic acids encoding receptor-like kinases are useful in the method.

CC The present sequence is a receptor-like kinase protein.  
 XX

SQ Sequence 19 AA;  
 Query Match 41.7%; Score 5; DB 23; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFELP 6  
 Db 2 FFELP 6  
 |||||

RESULT 32  
 AAW47343  
 ID AAW47343 standard; peptide; 20 AA.  
 AC AAW47343;  
 XX  
 DT 01-JUN-1998 (first entry)  
 XX  
 DE Apolipoprotein B tryptic peptide.  
 XX  
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;  
 KW vascular injury; elastin; collagen; prevention; treatment;  
 KW vascular disease; atherosclerosis; apolipoprotein B; apoB;  
 KW tryptic peptide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5726153-A.  
 XX  
 PD 10-MAR-1998.  
 XX  
 PF 06-JUN-1995; 95US-0468543.  
 XX  
 PR 06-JUN-1995; 95US-0469692.  
 PR 02-MAY-1988; 88US-0189130.  
 PR 03-MAY-1990; 90US-0518142.  
 PR 03-MAY-1990; 90US-0518215.  
 PR 02-MAY-1991; 91US-0694929.  
 PR 16-APR-1993; 93US-0048569.  
 PR 24-FEB-1994; 94US-0201057.  
 PR 28-FEB-1995; 95US-0398046.  
 PR 06-JUN-1995; 95US-0468543.  
 XX  
 PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.  
 XX  
 PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;  
 XX  
 DR WPI; 1998-192802/17.  
 XX  
 PT Inhibiting binding of low-density lipoprotein to vascular walls - by  
 PT administering peptide with affinity for vascular injury sites  
 XX  
 PS Disclosure; Column 10; 31pp; English.  
 XX  
 CC A novel method for inhibiting the binding of a low-density  
 CC lipoprotein (LDL) to vascular walls in vivo, comprises  
 CC administering a synthetic water soluble peptide containing an  
 CC amphiphilic domain and having affinity for sites of vascular  
 CC injury, e.g. derived from the present peptide.  
 CC The peptide inhibits the binding of LDL to vascular wall  
 CC components, e.g. elastin and collagen, and so can be used to  
 CC prevent or treat vascular diseases, e.g. atherosclerosis.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 41.7%; Score 5; DB 19; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVNVV 10

```

Db 11 PVNV 15
|||||
RESULT 33
AAV5885
ID AAV5885 standard; peptide; 20 AA.
XX
AC AAV5885;
XX
DT 01-FEB-2000 (first entry)
XX
DE Apolipoprotein fragment peptide #35 for vascular disease imaging.
XX
KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;
KW detection; imaging; disease; atherosclerosis; apolipoprotein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5972890-A.
XX
PD 26-OCT-1999.
XX
PF 28-FEB-1995; 95US-0398046.
XX
PR 02-MAY-1991; 91US-0694929.
PR 16-APR-1993; 93US-0048569.
PR 24-FEB-1994; 94US-0201057.
PR 02-MAY-1988; 88US-0189130.
PR 03-MAY-1990; 90US-0518142.
PR 03-MAY-1990; 90US-0518142.
XX
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;
XX
DR WPI; 1999-632641/54.
XX
PT New diagnostic synthetic peptides which have affinity for and
PT accumulate at a site of vascular injury useful for detection and
PT imaging of vascular disease such as atherosclerosis -
XX
PS Disclosure; Column 10; 30pp; English.
XX
CC The peptides AAV5851-Y5889 represent examples of diagnostic, synthetic
CC peptides which carry a detectable label, contain 30 or fewer amino
CC acids, are water soluble, contain an amphiphilic domain and have affinity
CC for, and propensity to accumulate at, a site of vascular injury. They
CC are preferably derived from the amino acid sequence of apolipoprotein.
CC The peptides can be used for the detection or imaging of a vascular
CC injury or disease, e.g. atherosclerosis.
XX
SQ Sequence 20 AA;
Query Match 41.7%; Score 5; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10
|||||
Db 11 PVNV 15

RESULT 34
AAV33110
ID AAV33110 standard; peptide; 20 AA.
XX
AC AAV33110;
XX
DT 15-NOV-1999 (first entry)
XX
DE Alipoprotein B tryptic peptide 6.

```

```

XX Alipoprotein B; alipoprotein A; elastin; vascular imaging; detection;
KW injury; vascular system; atherosclerosis; re-endothelializing; noninvasive;
KW aortic lesion; trauma; lipoprotein accumulation.
XX
OS Synthetic.
XX
PN US5955055-A.
XX
PD 21-SEP-1999.
XX
PF 06-JUN-1995; 95US-0469692.
XX
PR 02-MAY-1991; 91US-0694929.
PR 02-MAY-1988; 88US-0189130.
PR 03-MAY-1990; 90US-0518142.
PR 03-MAY-1990; 90US-0518215.
PR 16-APR-1993; 93US-0048569.
PR 24-FEB-1994; 94US-0201057.
PR 28-FEB-1995; 95US-0398046.
PR 06-JUN-1995; 95US-0469692.
XX
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
XX
DR WPI; 1999-539543/45.
XX
PT Detecting vascular injuries using a labeled peptide useful for the
PT diagnosis and monitoring of atherosclerosis
XX
PS Disclosure; Column 31-32; 31pp; English.
XX
CC This invention describes a novel method (I) for detecting injuries in a
CC vascular system using a labeled synthetic peptide with an affinity for,
CC and propensity to accumulate at, a site of vascular injury. The method
CC is particularly suitable for detecting and monitoring atherosclerosis.
CC It has been found that the synthetic peptide accumulates at the healing
CC (re-endothelializing) edge of aortic lesions produced by trauma. These
CC lesions resemble human atherosclerosis in many important respects
CC (including accumulation of lipoproteins and other pathological changes).
CC The ability of the synthetic peptides to localize at the trauma site,
CC and to permit imaging, may be used to visualize vascular lesions
CC method is noninvasive and the peptides used to target vascular lesions
CC may be produced inexpensively, quickly and in large quantities.
CC AAV3088-Y33114 represent synthetic peptides derived from alipoprotein B,
CC alipoprotein A1 and elastin which are used in the method of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 41.7%; Score 5; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10
|||||
Db 11 PVNV 15

RESULT 35
AAV96713
ID AAV96713 standard; peptide; 4 AA.
XX
AC AAV96713;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human E3 ubiquitin ligase peptide sequence tag.
XX
E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytostatic.

```

XX OS Homo sapiens.  
 XX PN WO200034447-A2.  
 XX PD 15-JUN-2000.  
 XX PF 10-DEC-1999; 99WO-US29371.  
 XX PR 10-DEC-1998; 98US-0210060.  
 XX PA (SIGN-) SIGNAL PHARM INC.  
 XX PA (YISS ) YISSUM RES & DEV CO.  
 XX Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubai A;  
 XX Lavon I, Yaron A;  
 XX WPI; 2000-431294/37.  
 XX Polypeptide enhancing phosphorylated lkappaB ubiquitination useful for  
 XX treating disorder associated with NF-kappaB activation e.g. cancer,  
 XX comprising amino acid sequence of human E3 ubiquitin ligase or its  
 XX variant  
 XX Example 5; Page 33; 77pp; English.  
 XX This peptide sequence tag was derived from fragmentation spectra of  
 XX trypsin digested human E3 ubiquitin ligase (E3). Further spectra  
 XX identified peptides shown in AAY96714-18, of which the first four are  
 XX also present within human F-box/WD protein beta-TrCP. The fifth peptide  
 XX matches that of a peptide from the brospahla Slimb protein, which is  
 XX highly homologous to the human beta-TrCP. E3 enhances ubiquitination  
 XX of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor  
 XX kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the  
 XX ubiquitin pathway is useful for identifying modulators of this process  
 XX for use in treating diseases associated with activation of NF-kappa-B.  
 XX In vitro analysis suggests that deletion of the F-box results in a  
 XX protein that functions as a dominant negative molecule in vivo.  
 XX Transient over-expression of delta-beta-TrCP (a deletion mutant)  
 XX inhibited the degradation of endogenous I-kappa-B-alpha in stimulated  
 XX Jurkat cells, resulting in accumulation of phosphorylated  
 XX I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B  
 XX activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat  
 XX inflammatory diseases, autoimmune diseases, cancer and viral  
 XX infections.  
 XX Sequence 4 AA;  
 XX Query Match 33.3%; Score 4; DB 21; Length 4;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 VVNV 10  
 DB |||||  
 1 VVNV 4  
 RESULT 36  
 AAW51334  
 ID AAW51334 standard; peptide; 5 AA.  
 XX AAW51334;  
 XX 14-AUG-1998 (first entry)  
 XX Peptide #17 useful as modulator of beta-amyloid peptide aggregation.  
 XX Natural beta-amyloid peptide; aggregation; D-amino acid;  
 XX Alzheimer's disease; beta-amyloidosis.  
 XX Synthetic.  
 XX Homo sapiens.  
 XX

PH Key Location/Qualifiers  
 FT Modified-site 1 /note= "D-form residue, N-terminal modifying group"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue"  
 FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"  
 XX WO9808868-A1.  
 XX 05-MAR-1998. 97WO-US15166.  
 XX 27-AUG-1997; 97WO-US15166.  
 XX 21-JUL-1997; 97US-0897342.  
 XX 27-AUG-1996; 96US-0703675.  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX Arico-muendel CC, Chin J, Pindeis MA, Geftter ML;  
 XX Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;  
 XX Musso G, Phillips K, Signer ER, Wakefield J;  
 XX WPI; 1998-216936/19.  
 XX Peptide compounds which are preferably based on beta-amyloid  
 XX peptide(s) - are useful in treatment of disorders related to  
 XX beta-amyloidosis, especially Alzheimer's disease  
 XX Claim 1; Page 76; 92pp; English.  
 XX The invention relates to peptides that modulate natural beta-amyloid  
 XX peptide aggregation. The modulators of the invention comprise a peptide  
 XX preferably based on a beta-amyloid peptide, that is comprised entirely  
 XX of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid  
 XX residues and includes at least two D-amino acid residues independently  
 XX selected from the group consisting of D-leucine, D-phenylalanine and  
 XX D-valine. Preferred amino-terminal modifying groups include cyclic,  
 XX heterocyclic, polycyclic and branched alkyl groups. Preferred  
 XX carboxy-terminal modifying groups include an amide group, an alkyl amide  
 XX group, an aryl amide group or a hydroxy group. The peptides may be used  
 XX to treat disorders associated with beta-amyloidosis, especially  
 XX Alzheimer's disease. They may also be used in methods for detecting the  
 XX presence of beta-amyloid peptides in biological samples. The present  
 XX sequence represents a specifically claimed peptide.  
 XX Sequence 5 AA;  
 XX Query Match 33.3%; Score 4; DB 19; Length 5;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFEL 5  
 DB |||||  
 2 FFEL 5  
 RESULT 37  
 AAW51332  
 ID AAW51332 standard; peptide; 5 AA.  
 XX AAW51332;  
 XX 14-AUG-1998 (first entry)  
 XX Peptide #15 useful as modulator of beta-amyloid peptide aggregation.  
 XX Natural beta-amyloid peptide; aggregation; D-amino acid;  
 XX Alzheimer's disease; beta-amyloidosis.  
 XX



```

XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Modified-site 1 /note= "D-form residue, N-terminal modifying group"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"
XX FT
XX PN WO9808868-A1.
XX XX
XX PD 05-MAR-1998.
XX PF 27-AUG-1997; 97WO-US15166.
XX XX
XX PR 21-JUL-1997; 97US-0897342.
XX PR 27-AUG-1996; 96US-0703675.
XX XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX XX
XX PI Arico-muendel CC, Chin J, Findeis MA, Geftter ML;
XX PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
XX PI Musso G, Phillips K, Signer ER, Wakefield J;
XX XX
XX DR WPI; 1998-216936/19.
XX XX
XX PS Claim 1; Page 76; 92pp; English.
XX CC The invention relates to peptides that modulate natural beta-amyloid
XX CC peptide aggregation. The modulators of the invention comprise a peptide
XX CC preferably based on a beta-amyloid peptide, that is comprised entirely
XX CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
XX CC residues and includes at least two D-amino acid residues independently
XX CC selected from the group consisting of D-leucine, D-phenylalanine and
XX CC D-valine. Preferred amino-terminal modifying groups include cyclic,
XX CC heterocyclic, polycyclic and branched alkyl groups. Preferred
XX CC carboxy-terminal modifying groups include an amide group, an alkyl amide
XX CC group, an aryl amide group or a hydroxy group. The peptides may be used
XX CC to treat disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease. They may also be used in methods for detecting the
XX CC presence of beta-amyloid peptides in biological samples. The present
XX CC sequence represents a specifically claimed peptide.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 33.3%; Score 4; DB 19; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 FFPL 5
XX DB 1 FFPL 4
XX
XX RESULT 38
XX AAWS1333
XX ID AAWS1333 standard; peptide; 5 AA.
XX AC AAWS1333;
XX XX
XX DT 14-AUG-1998 (first entry)
XX XX

```

```

DE Peptide #16 useful as modulator of beta-amyloid peptide aggregation.
XX Natural beta-amyloid peptide; aggregation; D-amino acid;
XX Alzheimer's disease; beta-amyloidosis.
XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Modified-site 1 /note= "D-form residue, N-terminal modifying group"
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT Modified-site 5 /note= "D-form residue, C-terminal modifying group"
XX FT
XX PN WO9808868-A1.
XX XX
XX PD 05-MAR-1998.
XX PF 27-AUG-1997; 97WO-US15166.
XX XX
XX PR 21-JUL-1997; 97US-0897342.
XX PR 27-AUG-1996; 96US-0703675.
XX XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX XX
XX PI Arico-muendel CC, Chin J, Findeis MA, Geftter ML;
XX PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
XX PI Musso G, Phillips K, Signer ER, Wakefield J;
XX XX
XX DR WPI; 1998-216936/19.
XX XX
XX PS Claim 1; Page 76; 92pp; English.
XX CC The invention relates to peptides that modulate natural beta-amyloid
XX CC peptide aggregation. The modulators of the invention comprise a peptide
XX CC preferably based on a beta-amyloid peptide, that is comprised entirely
XX CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
XX CC residues and includes at least two D-amino acid residues independently
XX CC selected from the group consisting of D-leucine, D-phenylalanine and
XX CC D-valine. Preferred amino-terminal modifying groups include cyclic,
XX CC heterocyclic, polycyclic and branched alkyl groups. Preferred
XX CC carboxy-terminal modifying groups include an amide group, an alkyl amide
XX CC group, an aryl amide group or a hydroxy group. The peptides may be used
XX CC to treat disorders associated with beta-amyloidosis, especially
XX CC Alzheimer's disease. They may also be used in methods for detecting the
XX CC presence of beta-amyloid peptides in biological samples. The present
XX CC sequence represents a specifically claimed peptide.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 33.3%; Score 4; DB 19; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 FFPL 5
XX DB 2 FFPL 5
XX
XX RESULT 39
XX AAY49991
XX ID AAY49991 standard; peptide; 5 AA.
XX XX

```

```

AC AAY49991;
XX
DT 04-FEB-2000 (first entry)
XX
DE Natural beta amyloid peptide aggregation modulating peptide #19.
XX
KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
KW amyloidosis-Dutch-type.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..5 /note= "D-form residues"
XX
XX US5985242-A.
XX
PD 16-NOV-1999.
XX
XX 27-AUG-1997; 97US-0920162.
XX
XX 27-OCT-1995; 95US-0548998.
XX 14-MAR-1996; 96US-0616081.
XX 27-AUG-1996; 96US-0703675.
XX 21-JUL-1997; 97US-0897342.
XX
(PRAE-) PRAECIS PHARM INC.
XX
PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
PI Musso G, Phillips K, Hayward NJ, Geftter ML, Findeis MA, Lee J;
PI Arico-Muendel CC, Chin J;
XX
XX WPI; 2000-022266/02.
XX
XX Compound comprising a peptidic structure, an amino-terminal modifying
XX group and a carboxy-terminal modifying group, useful for treating
XX Alzheimer's disease -
XX
XX Claim 1; Column 61; 40pp; English.
XX
CC The present invention describes a compound of formula A-(Xaa)-B,
CC comprising a peptidic structure (Xaa), an amino-terminal modifying
CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
CC AAY49994 represent specifically claimed examples of (Xaa). Also
CC described is a method for inhibiting aggregation of natural beta-amyloid
CC peptides and treating Alzheimer's disease, comprising contacting the
CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence
CC of natural beta-amyloid peptides in a biological sample by contacting
CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
CC and for detecting the presence of natural beta-amyloid peptides in a
CC biological sample. The compound can also be used prophylactically or
CC therapeutically to treat other clinical occurrences of beta-amyloid
CC deposition, such as in Down's syndrome individuals and in patients with
CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
XX
SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFPL 5
Db 1 FFPL 4
RESULT 40
AAY49992
ID AAY49992 standard; peptide; 5 AA.
XX

```

```

AC AAY49992;
XX
DT 04-FEB-2000 (first entry)
XX
DE Natural beta amyloid peptide aggregation modulating peptide #20.
XX
KW Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;
KW retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;
KW Down's syndrome; hereditary cerebral haemorrhage; HCHWA-D;
KW amyloidosis-Dutch-type.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..5 /note= "D-form residues"
XX
XX US5985242-A.
XX
PD 16-NOV-1999.
XX
XX 27-AUG-1997; 97US-0920162.
XX
XX 27-OCT-1995; 95US-0548998.
XX 14-MAR-1996; 96US-0616081.
XX 27-AUG-1996; 96US-0703675.
XX 21-JUL-1997; 97US-0897342.
XX
(PRAE-) PRAECIS PHARM INC.
XX
PI Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;
PI Musso G, Phillips K, Hayward NJ, Geftter ML, Findeis MA, Lee J;
PI Arico-Muendel CC, Chin J;
XX
XX WPI; 2000-022266/02.
XX
XX Compound comprising a peptidic structure, an amino-terminal modifying
XX group and a carboxy-terminal modifying group, useful for treating
XX Alzheimer's disease -
XX
XX Claim 1; Column 61; 40pp; English.
XX
CC The present invention describes a compound of formula A-(Xaa)-B,
CC comprising a peptidic structure (Xaa), an amino-terminal modifying
CC group (A), and a carboxy-terminal modifying group (B). AAY49973 to
CC AAY49994 represent specifically claimed examples of (Xaa). Also
CC described is a method for inhibiting aggregation of natural beta-amyloid
CC peptides and treating Alzheimer's disease, comprising contacting the
CC amyloid peptides with A-(Xaa)-B; and a method for detecting the presence
CC of natural beta-amyloid peptides in a biological sample by contacting
CC with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease
CC and for detecting the presence of natural beta-amyloid peptides in a
CC biological sample. The compound can also be used prophylactically or
CC therapeutically to treat other clinical occurrences of beta-amyloid
CC deposition, such as in Down's syndrome individuals and in patients with
CC hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).
XX
SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFPL 5
Db 2 FFPL 5
RESULT 41
AAY49993
ID AAY49993 standard; peptide; 5 AA.
XX

```

AA49993;  
 04-FEB-2000 (first entry)  
 Natural beta amyloid peptide aggregation modulating peptide #21.  
 Beta amyloid peptide aggregation; modulation; D-amino acid; diagnosis;  
 retro-inverso isomer; amyloidogenic disease; Alzheimer's disease;  
 Down's syndrome; hereditary cerebral haemorrhage; HCHWA-B;  
 amyloidosis-Dutch-type.  
 Synthetic.  
 Homo sapiens.  
 Key Location/Qualifiers  
 Misc-difference 1..5 /note= "D-form residues"  
 US5985242-A.  
 16-NOV-1999.  
 27-AUG-1997; 97US-0920162.  
 27-OCT-1995; 95US-0548998.  
 14-MAR-1996; 96US-0616081.  
 27-AUG-1996; 96US-0703675.  
 21-JUL-1997; 97US-0897342.  
 (PRAE-) PRAECIS PHARM INC.  
 Wakefield J, Molineaux S, Signer ER, Kelley M, Komar-Panicucci S;  
 Musso G, Phillips K, Hayward NJ, Gefter ML, Findeis MA, Lee J;  
 Arico-Muendel CC, Chin J;  
 MPI; 2000-022266/02.  
 Compound comprising a peptidic structure, an amino-terminal modifying  
 group and a carboxy-terminal modifying group, useful for treating  
 Alzheimer's disease -  
 Claim 1; Column 61; 40pp; English.  
 The present invention describes a compound of formula A-(Xaa)-B  
 comprising a peptidic structure (Xaa), an amino-terminal modifying  
 group (A), and a carboxy-terminal modifying group (B). AA49993 to  
 AA49994 represent specifically claimed examples of (Xaa). Also  
 described is a method for inhibiting aggregation of natural beta-amyloid  
 peptides and treating Alzheimer's disease, comprising contacting the  
 amyloid peptides with A-(Xaa)-B; and a method for detecting the presence  
 of natural beta-amyloid peptides in a biological sample by contacting  
 with A-(Xaa)-B. The compound is useful for treating Alzheimer's disease  
 and for detecting the presence of natural beta-amyloid peptides in a  
 biological sample. The compound can also be used prophylactically or  
 therapeutically to treat other clinical occurrences of beta-amyloid  
 deposition, such as in Down's syndrome individuals and in patients with  
 hereditary cerebral haemorrhage with amyloidosis-Dutch-type (HCHWA-D).  
 Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFPL 5  
 Db 2 FFPL 5  
 RESULT 42  
 AA49993  
 ID AA49993 standard; peptide; 5 AA.  
 XX

AA12530;  
 03-JAN-2002 (first entry)  
 APP70 abeta peptide (residues 17-21) inverso isomer mutant.  
 Beta-amyloid peptide; beta-AP; Abeta peptide; therapy; beta-amyloidosis;  
 Alzheimer's disease; neuroprotective; beta-amyloid precursor protein;  
 APP-770; nootropic; mutant; mutein.  
 Unidentified.  
 Key Location/Qualifiers  
 Misc-difference 1..5 /note= "D-form residues"  
 Misc-difference 1 /note= "Wild-type Ala substituted with Phe; corresponds  
 to position 21 of natural Abeta peptide"  
 Misc-difference 4 /note= "Wild-type Val substituted with Leu; corresponds  
 to position 18 of natural Abeta peptide"  
 Misc-difference 5 /note= "Wild-type Leu substituted with Val; corresponds  
 to position 17 of natural Abeta peptide; Optionally  
 C-terminal amide"  
 US6277826-B1.  
 21-AUG-2001.  
 19-JUL-1999; 99US-0356931.  
 27-AUG-1997; 97US-0920162.  
 27-AUG-1996; 96US-0703675.  
 (PRAE-) PRAECIS PHARM INC.  
 Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;  
 Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;  
 Arico-Muendel CC, Phillips K, Hayward NJ;  
 MPI; 2001-637856/73.  
 Modulator compound for treating disorders associated with  
 beta-amyloidosis e.g. Alzheimer's disease, comprises a beta-amyloid  
 peptide containing D-amino acids -  
 Example 11; Column 48; 41pp; English.  
 The patent discloses compounds and pharmaceutical compositions thereof,  
 that can bind to natural beta amyloid peptide (beta-AP; Abeta peptide),  
 modulate the aggregation of natural beta-AP and/or inhibit the cyto-  
 toxicity of natural beta-APs. The beta-amyloid modulator compounds of  
 the invention comprise a peptide, preferably based on beta-AP, that is  
 composed entirely of D-amino acids. The modulators of the invention are  
 useful for treating a disorder associated with beta-amyloidosis such as  
 Alzheimer's disease. The present sequence is an inverso isomer mutant  
 (L17V; V18L; A21F) of Abeta peptide. Beta AP is a cleavage product of  
 beta amyloid precursor protein (APP-770; residues 17-21).  
 Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFPL 5  
 Db 1 FFPL 4  
 RESULT 43  
 AA12531



|    |                                                                           |                          |  |
|----|---------------------------------------------------------------------------|--------------------------|--|
| XX | 29-NOV-2001                                                               | (first entry)            |  |
| XX | Beta-amyloid peptide derivative #19.                                      |                          |  |
| XX | Drug bioavailability; beta-amyloid peptide derivative; CNS disorder;      |                          |  |
| XX | central nervous system; multidrug resistance; liver cirrhosis;            |                          |  |
| XX | cardiovascular disorder; neuromuscular disorder; Parkinson's disease;     |                          |  |
| XX | neurodegenerative disorder; Alzheimer's disease; multiple sclerosis;      |                          |  |
| XX | cancer; glioblastoma; stroke; traumatic brain injury; hepatic injury;     |                          |  |
| XX | psychiatric disorder; P-glycoprotein inhibitor; hepatic fibrosis.         |                          |  |
| XX | Synthetic.                                                                |                          |  |
| XX | Key                                                                       | Location/Qualifiers      |  |
| XX | Misc-difference 1.1.4                                                     | /note= "D-form residues" |  |
| XX | Modified-site 5                                                           |                          |  |
| XX | /note= "D-form residue; optionally C-terminal amide                       |                          |  |
| XX | which is particularly preferred"                                          |                          |  |
| XX | W0200158470-A2.                                                           |                          |  |
| XX | 16-AUG-2001.                                                              |                          |  |
| XX | 09-FEB-2001; 2001WO-US04178.                                              |                          |  |
| XX | 11-FEB-2000; 2000US-0181833.                                              |                          |  |
| XX | 11-FEB-2000; 2000US-0181943.                                              |                          |  |
| XX | (PRAE-) PRACIS PHARM INC.                                                 |                          |  |
| XX | Hayward NJ, Geffer MD;                                                    |                          |  |
| XX | WPI; 2001-557599/62.                                                      |                          |  |
| XX | Enhancing the bioavailability of a drug, for e.g. in the brain of a       |                          |  |
| XX | subject suffering from Alzheimer's disease, comprising administering a    |                          |  |
| XX | hydrophobic peptide (e.g. a beta-amyloid peptide derivative) with the     |                          |  |
| XX | drug -                                                                    |                          |  |
| XX | Disclosure; Page 27; 86pp; English.                                       |                          |  |
| XX | The invention relates to a method for enhancing bioavailability           |                          |  |
| XX | of a drug in a subject, comprising administering the drug with a          |                          |  |
| XX | hydrophobic peptide e.g. a beta-amyloid peptide derivative. The method    |                          |  |
| XX | is useful for enhancing bioavailability of a drug in subjects suffering   |                          |  |
| XX | from central nervous system (CNS) disorder, disorder characterised by     |                          |  |
| XX | multidrug resistance, cardiovascular disorder and neuromuscular disorder. |                          |  |
| XX | The CNS disorder includes neurodegenerative disorder (e.g. Alzheimer's    |                          |  |
| XX | disease, Parkinson's disease, multiple sclerosis), cancer (e.g.           |                          |  |
| XX | glioblastoma), stroke, traumatic brain injury, and psychiatric disorder.  |                          |  |
| XX | The invention also relates to a method for treating or preventing hepatic |                          |  |
| XX | injury using P-glycoprotein inhibitor. Examples of hepatic injury include |                          |  |
| XX | hepatic fibrosis, cirrhosis, hepatic injury caused by a drug, injury due  |                          |  |
| XX | to prolonged ethanol uptake or due to carbon tetrachloride exposure.      |                          |  |
| XX | The present sequence is a beta-amyloid peptide derivative useful for      |                          |  |
| XX | enhancing bioavailability of a drug in a subject. The peptide is          |                          |  |
| XX | designed based on retro-inverso isomer of Abeta aggregation core domain   |                          |  |
| XX | (ACD, residues 17-21) of the beta-amyloid peptide.                        |                          |  |
| XX | Sequence 5 AA;                                                            |                          |  |
| XX | Query Watch                                                               |                          |  |
| XX | Best Local Similarity 33.3%; Score 4; DB 22; Length 5;                    |                          |  |
| XX | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps                   |                          |  |

|          |    |                                                                           |
|----------|----|---------------------------------------------------------------------------|
| AAE10005 | ID | AAE10005 standard; peptide; 5 AA.                                         |
| XX       | AC | AAE10005;                                                                 |
| XX       | DT | 29-NOV-2001 (first entry)                                                 |
| XX       | DE | Beta-amyloid peptide derivative #20.                                      |
| XX       | KW | Drug bioavailability; beta-amyloid peptide derivative; CNS disorder;      |
| XX       | KW | central nervous system; multidrug resistance; liver cirrhosis;            |
| XX       | KW | cardiovascular disorder; neuromuscular disorder; Parkinson's disease;     |
| XX       | KW | neurodegenerative disorder; Alzheimer's disease; multiple sclerosis;      |
| XX       | KW | cancer; glioblastoma; stroke; traumatic brain injury; hepatic injury;     |
| XX       | KW | psychiatric disorder; P-glycoprotein inhibitor; hepatic fibrosis.         |
| XX       | OS | Synthetic.                                                                |
| XX       | XX |                                                                           |
| XX       | FH | Key Location/Qualifiers                                                   |
| XX       | FT | Misc-difference 1..4                                                      |
| XX       | FT | /note= "D-form residues"                                                  |
| XX       | FT | Modified-site 5                                                           |
| XX       | FT | /note= "D-form residue; optionally C-terminal amide                       |
| XX       | FT | which is particularly preferred"                                          |
| XX       | XX |                                                                           |
| XX       | FN | WO200158470-A2.                                                           |
| XX       | XX |                                                                           |
| XX       | PD | 16-AUG-2001.                                                              |
| XX       | XX |                                                                           |
| XX       | PF | 09-FEB-2001; 2001WO-US04178.                                              |
| XX       | XX |                                                                           |
| XX       | PR | 11-FEB-2000; 2000US-0181833.                                              |
| XX       | PR | 11-FEB-2000; 2000US-0181943.                                              |
| XX       | XX |                                                                           |
| XX       | PA | (PRAE-) PRAECIS PHARM INC.                                                |
| XX       | XX |                                                                           |
| XX       | PI | Hayward NJ, Gefter ML;                                                    |
| XX       | XX |                                                                           |
| XX       | DR | WPI; 2001-557599/62.                                                      |
| XX       | XX |                                                                           |
| XX       | PT | Enhancing the bioavailability of a drug, for e.g. in the brain of a       |
| XX       | PT | subject suffering from Alzheimer's disease, comprising administering a    |
| XX       | PT | hydrophobic peptide (e.g. a beta-amyloid peptide derivative) with the     |
| XX       | PT | drug -                                                                    |
| XX       | PS | Disclosure; Page 27; 86pp; English.                                       |
| XX       | XX |                                                                           |
| XX       | CC | The invention relates to a method for enhancing bioavailability           |
| XX       | CC | of a drug in a subject, comprising administering the drug with a          |
| XX       | CC | hydrophobic peptide e.g. a beta-amyloid peptide derivative. The method    |
| XX       | CC | is useful for enhancing bioavailability of a drug in subjects suffering   |
| XX       | CC | from central nervous system (CNS) disorder, disorder characterised by     |
| XX       | CC | multidrug resistance, cardiovascular disorder and neuromuscular disorder. |
| XX       | CC | The CNS disorder includes neurodegenerative disorder (e.g. Alzheimer's    |
| XX       | CC | disease, Parkinson's disease, multiple sclerosis), cancer (e.g.           |
| XX       | CC | glioblastoma), stroke, traumatic brain injury, and psychiatric disorder.  |
| XX       | CC | The invention also relates to a method for treating or preventing hepatic |
| XX       | CC | injury using P-glycoprotein inhibitor. Examples of hepatic injury include |
| XX       | CC | to prolonged ethanol uptake or due to carbon tetrachloride exposure.      |
| XX       | CC | The present sequence is a beta-amyloid peptide derivative useful for      |
| XX       | CC | enhancing bioavailability of a drug in a subject. The peptide is          |
| XX       | CC | designed based on retro-inverso isomer of Abeta aggregation core domain   |
| XX       | CC | (ACD, residues 17-21) of the beta-amyloid peptide.                        |
| XX       | XX |                                                                           |
| XX       | SQ | Sequence 5 AA;                                                            |
| XX       | XX |                                                                           |
| XX       | XX | Query Match 33.3%; Score 4; DB 22; Length 5;                              |
| XX       | XX | Best Local Similarity 100.0%; Pred.No.9.3e+05;                            |
| XX       | XX | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0                 |
| XX       | XX |                                                                           |
| XX       | XX | 2 FFFL 5                                                                  |
| XX       | XX |                                                                           |

Query Match 33.3%; Score 4; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

CC examples of amyloidogenic disorders include Huntington's disease and  
 CC inclusion body myocytis. The present sequence is a peptide capable of  
 CC binding an amyloidogenic protein.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFFL 5  
 DB 1 FFFL 4  
 RESULT 49  
 AAE26295  
 ID AAE26295 standard; peptide; 5 AA.  
 AC  
 XX AAE26295;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE Peptide #17 capable of binding an amyloidogenic protein.  
 XX  
 KW Amyloidogenic protein; Alzheimer's disease; Huntington's disease;  
 KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;  
 KW Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS;  
 KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;  
 KW CJ.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..5 /note= "D-form residues"  
 FT  
 XX WO200242462-A2.  
 PN  
 XX 30-MAY-2002.  
 XX  
 XX 27-NOV-2001; 2001WO-US44581.  
 XX  
 XX 27-NOV-2000; 2000US-253302P.  
 PR  
 XX 29-NOV-2000; 2000US-250198P.  
 PR  
 XX 20-DEC-2000; 2000US-257186P.  
 XX  
 XX (PRAE-) PRAECTIS PHARM INC.  
 PA  
 XX Geffer ML, Israel DI, Joyal JL, Gosselin M;  
 PI WPI; 2002-636427/68.  
 XX  
 DR Novel therapeutic agent useful for treating an amyloidogenic disorder,  
 XX e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain  
 PT constant region linked to a peptide capable of binding amyloidogenic  
 PT protein -  
 XX  
 XX Claim 18; Page 54; 79pp; English.  
 PS  
 CC The invention relates to a compound comprising an immunoglobulin (Ig)  
 CC heavy chain constant region or its fragment that retains the ability  
 CC to bind an FC receptor linked by a linker group or a direct bond to a  
 CC peptide capable of binding an amyloidogenic protein. The invention is  
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,  
 CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide  
 CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda  
 CC light chain, amyloid A, procainitonin, cystatin C, beta2-microglobulin,  
 CC ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein  
 CC and lysozyme from a subject and for treating an amyloidogenic disorder  
 CC such as Alzheimer's disease and spongiform encephalopathy. Disorders  
 CC treatable include those caused or characterised by deposits of TTR (eg.  
 CC familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies,

CC including scrapie in sheep, bovine spongiform encephalopathy in cows  
 CC and Creutzfeldt-Jacob disease (CJ) and Gerstmann-Straussler-Scheinker  
 CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),  
 CC ANP (eg. isolated atrial amyloid), kappa or lambda light chain (eg. A-I  
 CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I  
 CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.  
 CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal  
 CC amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other  
 CC examples of amyloidogenic disorders include Huntington's disease and  
 CC inclusion body myocytis. The present sequence is a peptide capable of  
 CC binding an amyloidogenic protein.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FFFL 5  
 DB 2 FFFL 5  
 RESULT 50  
 AAE26296  
 ID AAE26296 standard; peptide; 5 AA.  
 XX  
 AC AAE26296;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE Peptide #18 capable of binding an amyloidogenic protein.  
 XX  
 KW Amyloidogenic protein; Alzheimer's disease; Huntington's disease;  
 KW spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis;  
 KW Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS;  
 KW Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma;  
 KW CJ.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..5 /note= "D-form residues"  
 FT  
 XX WO200242462-A2.  
 PN  
 XX 30-MAY-2002.  
 XX  
 XX 27-NOV-2001; 2001WO-US44581.  
 XX  
 XX 27-NOV-2000; 2000US-253302P.  
 PR  
 XX 29-NOV-2000; 2000US-250198P.  
 PR  
 XX 20-DEC-2000; 2000US-257186P.  
 XX  
 XX (PRAE-) PRAECTIS PHARM INC.  
 PA  
 XX Geffer ML, Israel DI, Joyal JL, Gosselin M;  
 PI WPI; 2002-636427/68.  
 XX  
 DR Novel therapeutic agent useful for treating an amyloidogenic disorder,  
 XX e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain  
 PT constant region linked to a peptide capable of binding amyloidogenic  
 PT protein -  
 XX  
 XX Claim 18; Page 54; 79pp; English.  
 PS  
 CC The invention relates to a compound comprising an immunoglobulin (Ig)  
 CC heavy chain constant region or its fragment that retains the ability  
 CC to bind an FC receptor linked by a linker group or a direct bond to a  
 CC peptide capable of binding an amyloidogenic protein. The invention is  
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,  
 CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide  
 CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda  
 CC light chain, amyloid A, procainitonin, cystatin C, beta2-microglobulin,  
 CC ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein  
 CC and lysozyme from a subject and for treating an amyloidogenic disorder  
 CC such as Alzheimer's disease and spongiform encephalopathy. Disorders  
 CC treatable include those caused or characterised by deposits of TTR (eg.  
 CC familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies,

CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I, gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein and lysozyme from a subject and for treating an amyloidogenic disorder such as Alzheimer's disease and spongiform encephalopathy. Disorders treatable include those caused or characterised by deposits of TTR (eg. familial amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including scrapie in sheep, bovine spongiform encephalopathy in cows and Creutzfeldt-Jacob disease (CU) and Gerstmann-Strausler-Scheinker syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes), ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg. A-I idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg. familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal amyloidosis), lysozyme (eg. hereditary systemic amyloidosis). Other examples of amyloidogenic disorders include Huntington's disease and inclusion body myocytis. The present sequence is a peptide capable of binding an amyloidogenic protein.

XX  
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 2 FFPL 5  
|||||

RESULT 51  
AAE15197  
ID AAE15197 standard; peptide; 5 AA.  
AC AAE15197;  
XX  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Human HGF receptor chain analogue peptide #1.  
XX  
KW Human; N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;  
KW downstream signal transduction pathway; HGF receptor chain analogue;  
XX tumour; Sem-5/Grb2 SH2 binding protein.  
XX  
OS Homo sapiens.  
XX  
PN US6307090-B1.  
XX  
PD 23-OCT-2001.  
XX  
PF 22-JAN-1999; 99US-0236160.  
XX  
PR 22-JAN-1999; 99US-0236160.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Burke TR, Yao Z, King CR;  
XX  
DR WPI; 2002-033269/04.  
XX  
PT New acylated oligopeptides having cell signal inhibiting activity are  
XX useful in the treatment of e.g. psoriasis -  
XX  
PS Disclosure; Column 10; 42pp; English.  
XX  
CC The present invention relates to pharmaceutically active compounds comprising N-oxalyl peptide structure. The compounds of the invention are used in the therapeutic or prophylactic treatment of warm-blooded animal or human body e.g. tumour and psoriasis. They are useful in the diagnostic treatment of diseases depending on the downstream signal transduction pathway. The present peptide sequence is human HGF receptor chain analogue of Sem-5/Grb2 SH2 binding proteins. This

CC peptide is present in the compound of the invention.  
XX  
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11  
Db 1 VNVL 4  
|||||

RESULT 52  
AAE15232  
ID AAE15232 standard; peptide; 5 AA.  
XX  
AC AAE15232;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Human HGF receptor chain analogue peptide #3.  
XX  
KW Human; N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;  
KW downstream signal transduction pathway; HGF receptor chain analogue;  
XX tumour; SHPTP2 N-terminal SH2 binding protein.  
XX  
OS Homo sapiens.  
XX  
PN US6307090-B1.  
XX  
PD 23-OCT-2001.  
XX  
PF 22-JAN-1999; 99US-0236160.  
XX  
PR 22-JAN-1999; 99US-0236160.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Burke TR, Yao Z, King CR;  
XX  
DR WPI; 2002-033269/04.  
XX  
PT New acylated oligopeptides having cell signal inhibiting activity are  
XX useful in the treatment of e.g. psoriasis -  
XX  
PS Disclosure; Column 11; 42pp; English.  
XX  
CC The present invention relates to pharmaceutically active compounds comprising N-oxalyl peptide structure. The compounds of the invention are used in the therapeutic or prophylactic treatment of warm-blooded animal or human body e.g. tumour and psoriasis. They are useful in the diagnostic treatment of diseases depending on the downstream signal transduction pathway. The present peptide sequence is an analogue of human HGF receptor chain of SHPTP2 N-terminal SH2 binding proteins. This peptide is present in the compound of the invention.

XX  
SQ Sequence 5 AA;

Query Match 33.3%; Score 4; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11  
Db 1 VNVL 4  
|||||

RESULT 53  
AAE15324  
ID AAE15324 standard; peptide; 5 AA.  
XX  
AC AAE15324;



XX 07-MAR-2002 (first entry)  
 XX Peptide #5 related to pharmaceutical compounds of the invention.  
 DE N-oxalyl peptide; therapeutic; prophylactic; treatment; psoriasis;  
 XX downstream signal transduction pathway; tumour.  
 KW Unidentified.  
 XX OS US6307090-B1.  
 PN 23-OCT-2001.  
 XX 22-JAN-1999; 99US-0236160.  
 XX 22-JAN-1999; 99US-0236160.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Burke TR, Yao Z, King CR;  
 XX WPI; 2002-033269/04.  
 XX New acylated oligopeptides having cell signal inhibiting activity are  
 PT useful in the treatment of e.g. psoriasis -  
 XX Disclosure; Column 63; 42pp; English.  
 XX The present invention relates to pharmaceutically active compounds  
 CC comprising N-oxalyl peptide structure. The compounds of the invention  
 CC are used in the therapeutic or prophylactic treatment of warm-blooded  
 CC animal or human body e.g. tumour and psoriasis. They are useful in the  
 CC diagnostic treatment of diseases depending on the downstream signal  
 CC transduction pathway. The present sequence is a peptide related to  
 CC pharmaceutical compounds of the invention.  
 XX SQ Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 VNVL 11  
 Db 1 VNVL 4  
 RESULT 54  
 ABG73479  
 ID ABG73479 standard; Peptide; 5 AA.  
 XX AC ABG73479;  
 XX DT 10-MAY-2003 (first entry)  
 XX Natural beta-amyloid peptide modulator compound #22.  
 DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;  
 XX Alzheimer's disease; beta-amyloid deposition; Down's syndrome;  
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;  
 KW neurological impairment; neuroprotective; nootropic.  
 XX Synthetic.  
 XX OS US2002103134-A1.  
 XX PN 01-AUG-2002.  
 XX 29-JUN-2001; 2001US-0895443.  
 XX 27-AUG-1997; 97US-0920162.  
 PR 19-JUL-1999; 99US-0356931.

PR 27-OCT-1995; 95US-0548998.  
 PR 14-MAR-1996; 96US-0616081.  
 PR 27-AUG-1996; 96US-0703675.  
 PR 21-JUL-1997; 97US-0897342.  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;  
 PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;  
 PI Arico-Muendel CC, Phillips K, Hayward NJ;  
 XX WPI; 2003-298609/29.  
 XX Novel compound that modulate natural beta-amyloid peptide aggregation,  
 PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease  
 XX Claim 1; Page 35; 42pp; English.  
 XX The invention relates to a compound that modulates natural beta-amyloid  
 CC peptide aggregation. The peptide is useful for inhibiting aggregation of  
 CC natural beta-amyloid peptides and for treating a disorder associated with  
 CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful  
 CC for detecting the presence or absence of natural beta-amyloid peptides in  
 CC a biological sample, by contacting the biological sample with the  
 CC compound in vitro, where the compound is labelled with a detectable  
 CC substance and detecting the presence or absence of natural beta-amyloid  
 CC peptides. The compound is preferably labelled with radioactive technetium  
 CC or radioactive iodine and is administered to the subject. The compound is  
 CC also useful for prophylactically or therapeutically treating other  
 CC clinical occurrences of beta-amyloid deposition such as in Down's  
 CC syndrome individuals and in patients with hereditary cerebral haemorrhage  
 CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing  
 CC for the sequestration of beta-amyloid proteins at sites that do not lead  
 CC to neurological impairment. This sequence represents a natural  
 CC beta-amyloid peptide modulator compound of the invention.  
 XX SQ Sequence 5 AA;  
 Query Match 33.3%; Score 4; DB 24; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 FFPL 5  
 Db 1 FFPL 4  
 RESULT 55  
 ABG73480  
 ID ABG73480 standard; Peptide; 5 AA.  
 XX AC ABG73480;  
 XX DT 10-MAY-2003 (first entry)  
 XX Natural beta-amyloid peptide modulator compound #23.  
 DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;  
 XX Alzheimer's disease; beta-amyloid deposition; Down's syndrome;  
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;  
 KW neurological impairment; neuroprotective; nootropic.  
 XX Synthetic.  
 XX OS US2002103134-A1.  
 XX PN 01-AUG-2002.  
 XX 29-JUN-2001; 2001US-0895443.  
 XX 27-AUG-1997; 97US-0920162.  
 PR 19-JUL-1999; 97US-0920162.

```

PR 19-JUL-1999; 99US-0356931.
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
PI Arico-Muendel CC, Phillips K, Hayward NJ;
XX
DR WPI; 2003-298609/29.
XX
XX Novel compound that modulate natural beta-amyloid peptide aggregation,
PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
PT
XX
XX Claim 1; Page 35; 42pp; English.
XX
XX The invention relates to a compound that modulates natural beta-amyloid
CC peptide aggregation. The peptide is useful for inhibiting aggregation of
CC natural beta-amyloid peptides and for treating a disorder associated with
CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
CC for detecting the presence or absence of natural beta-amyloid peptides in
CC a biological sample, by contacting the biological sample with the
CC compound in vitro, where the compound is labelled with a detectable
CC substance and detecting the presence or absence of natural beta-amyloid
CC peptides to thus detect the presence or absence of natural beta-amyloid
CC peptides. The compound is preferably labelled with radioactive technetium
CC or radioactive iodine and is administered to the subject. The compound is
CC also useful for prophylactically or therapeutically treating other
CC clinical occurrences of beta-amyloid deposition such as in Down's
CC syndrome individuals and in patients with hereditary cerebral haemorrhage
CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
CC for the sequestration of beta-amyloid proteins at sites that do not lead
CC to neurological impairment. This sequence represents a natural
CC beta-amyloid peptide modulator compound of the invention.
XX
XX SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 FFFL 5
Db 2 FFFL 5
|||
|||
RESULT 56
ABG73481
ID ABG73481 standard; Peptide; 5 AA.
XX
XX AC ABG73481;
XX
XX DT 10-MAY-2003 (first entry)
XX
XX DE Natural beta-amyloid peptide modulator compound #24.
XX
XX DE Natural beta-amyloid peptide; aggregation inhibition; beta-amyloidosis;
KW Alzheimer's disease; beta-amyloid deposition; Down's syndrome;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch-type; HCHWA-D;
KW neurological impairment; neuroprotective; nootropic.
XX
XX OS Synthetic.
XX
XX PN US2002103134-A1.
XX
XX PD 01-AUG-2002.
XX
XX PF 29-JUN-2001; 2001US-0895443.
XX

```

```

PR 27-AUG-1997; 97US-0920162.
PR 19-JUL-1999; 99US-0356931.
PR 27-OCT-1995; 95US-0548998.
PR 14-MAR-1996; 96US-0616081.
PR 27-AUG-1996; 96US-0703675.
PR 21-JUL-1997; 97US-0897342.
XX (PRAE-) PRACIS PHARM INC.
XX
XX Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
PI Arico-Muendel CC, Phillips K, Hayward NJ;
XX
DR WPI; 2003-298609/29.
XX
XX Novel compound that modulate natural beta-amyloid peptide aggregation,
PT is useful for treating amyloidogenic diseases e.g. Alzheimer's disease
PT
XX
XX Claim 1; Page 35; 42pp; English.
XX
XX The invention relates to a compound that modulates natural beta-amyloid
CC peptide aggregation. The peptide is useful for inhibiting aggregation of
CC natural beta-amyloid peptides and for treating a disorder associated with
CC beta-amyloidosis, e.g. Alzheimer's disease. The compound is also useful
CC for detecting the presence or absence of natural beta-amyloid peptides in
CC a biological sample, by contacting the biological sample with the
CC compound in vitro, where the compound is labelled with a detectable
CC substance and detecting the presence or absence of natural beta-amyloid
CC peptides to thus detect the presence or absence of natural beta-amyloid
CC peptides. The compound is preferably labelled with radioactive technetium
CC or radioactive iodine and is administered to the subject. The compound is
CC also useful for prophylactically or therapeutically treating other
CC clinical occurrences of beta-amyloid deposition such as in Down's
CC syndrome individuals and in patients with hereditary cerebral haemorrhage
CC with amyloidosis-Dutch-type (HCHWA-D), and for therapeutically allowing
CC for the sequestration of beta-amyloid proteins at sites that do not lead
CC to neurological impairment. This sequence represents a natural
CC beta-amyloid peptide modulator compound of the invention.
XX
XX SQ Sequence 5 AA;
Query Match 33.3%; Score 4; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 FFFL 5
Db 2 FFFL 5
|||
|||
RESULT 57
AAP40523
ID AAP40523 standard; peptide; 6 AA.
XX
XX AC AAP40523;
XX
XX DT 16-AUG-2002 (updated)
DT 25-JAN-1992 (first entry)
XX
XX DE Sequence of substance P (a putative CNS neurotransmitter peptide)
DE agonist/antagonist.
XX
XX KW Analgesic; antihypertensive; neurotransmitter substance P.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
FT Modified-site 1 /label= H-Pro
FT Modified-site 2 /label= D-Phe
FT Modified-site 4

```

FT Modified-site /label= D-Phe  
 FT 6  
 FT /label= Met-NH2  
 XX  
 PN US4472305-A.  
 XX  
 PD 18-SEP-1984.  
 XX  
 XX 17-MAY-1983; 83US-0495383.  
 XX  
 XX 17-MAY-1983; 83US-0495383.  
 PR  
 XX (STER ) STERLING DRUG INC.  
 XX  
 PI Hansen PE, Morgan BA;  
 XX  
 XX WPI; 1984-249867/40.  
 XX  
 XX N-terminal prolyl hexa:peptide amide(s) - useful as analgesics  
 PT and/or hypotensives  
 XX  
 PS Claim 2; column 25; 14pp; English.  
 XX  
 CC The peptides of the invention are useful as analgesics and/or  
 CC antihypertensives. They may be prepd. by standard methods from the  
 CC corresp. amino acids or peptide subunits.  
 CC (Updated on 16-AUG-2002 to add missing OS field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 33.3%; Score 4; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 FFFL 5  
 Db ||||  
 2 FFFL 5  
 RESULT 58  
 AAP40527  
 ID AAP40527 standard; peptide; 6 AA.  
 AC AAP40527;  
 XX  
 XX 16-AUG-2002 (updated)  
 DT 25-JAN-1992 (first entry)  
 XX  
 DE Sequence of substance P (a putative CNS neurotransmitter peptide)  
 DE agonist/antagonist.  
 XX  
 KW Analgesic; antihypertensive; neurotransmitter substance P.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= H-Pro  
 FT Modified-site 2  
 FT /label= D-Phe  
 FT Modified-site 4  
 FT /label= D-Phe  
 FT Misc-difference 6  
 FT /label= Nle-NH2  
 XX  
 PN US4472305-A.  
 XX  
 PD 18-SEP-1984.  
 XX  
 XX 17-MAY-1983; 83US-0495383.  
 PF  
 XX 17-MAY-1983; 83US-0495383.  
 PR  
 XX

PA (STER ) STERLING DRUG INC.  
 XX  
 PI Hansen PE, Morgan BA;  
 XX  
 XX WPI; 1984-249867/40.  
 XX  
 XX N-terminal prolyl hexa:peptide amide(s) - useful as analgesics  
 PT and/or hypotensives  
 XX  
 PS Claim 2; column 25; 14pp; English.  
 XX  
 XX The peptides of the invention are useful as analgesics and/or  
 CC antihypertensives. They may be prepd. by standard methods from the  
 CC corresp. amino acids or peptide subunits.  
 CC (Updated on 16-AUG-2002 to add missing OS field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 33.3%; Score 4; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 FFFL 5  
 Db ||||  
 2 FFFL 5  
 RESULT 59  
 AAW31486  
 ID AAW31486 standard; Protein; 6 AA.  
 AC AAW31486;  
 XX  
 XX 04-AUG-1998 (first entry)  
 DT  
 XX  
 DE Transcriptional activator peptide fragment LS161.  
 XX  
 KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;  
 KW Protein-protein interaction; Gene therapy; therapeutic; holoenzyme;  
 KW Gal1; DNA binding domain.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9744447-A2.  
 PN  
 XX 27-NOV-1997.  
 PD  
 XX 02-MAY-1997; 97WO-US07338.  
 PF  
 XX 01-MAY-1997; 97US-0017016.  
 PR  
 XX 03-MAY-1996; 96US-0017016.  
 PR  
 XX (HARD ) HARVARD COLLEGE.  
 PA  
 XX  
 XX Lu X, Ptashne M, Wu Y;  
 PI  
 XX WPI; 1998-018502/02.  
 DR  
 DR N-PSDB; AAV02584.  
 XX  
 XX New transcriptional activator containing DNA binding domain bound to  
 PT peptide - useful for controlling gene expression, especially in gene  
 PT therapy, and in protein-protein interaction assays, does not inhibit  
 PT other transcription activators  
 XX  
 PS Example 1; Page 27; 55pp; English.  
 XX  
 XX AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076  
 CC are fragments used in an assay to determine novel transcriptional  
 CC activators. The method involves the production of transcriptional  
 CC activators comprising of a DNA-binding group and a 6-25 amino acid  
 CC peptide that is covalently bonded to the DNA binding group and does not  
 CC represent a fragment of a natural transcription activator.  
 CC Protein-protein interactions are identified in the assay by fusing a

CC DNA-binding domain to a library of DNA fragments and introducing this and  
 CC a fusion of target protein and a polypeptide containing a region of Gal4  
 CC which interacts with Gal4P into a cell containing Gal4P and identifying  
 CC members of the library that interact with the target from activation of  
 CC transcription. Such constructs are used to activate transcription in a  
 CC cell, e.g. for controlling gene activity, particularly in gene therapy  
 CC (e.g. recognizing a site close to a selected therapeutic gene).  
 CC Transcription can be activated without blocking other transcriptional  
 CC activators. They probably act by interacting with a component of the RNA  
 CC polymerase II holoenzyme, Gal4, the strongest known yeast activator.  
 CC which provides a more sensitive assay allowing detection of even weak  
 CC protein-protein interactions. Such activators do not create toxicity  
 CC problems even when overexpressed.

XX Sequence 6 AA;

Query Match 33.3%; Score 4; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
 Db 3 NVLP 6

# RESULT 60

AAB27043  
 ID AAB27043 standard; Peptide; 6 AA.

XX AAB27043;

DT 02-FEB-2001 (first entry)

DE Beta-amyloid peptide modulator #21.

XX Beta-amyloid peptide; neurotropic; neuroprotective; Alzheimer's disease;  
 KW aggregation core domain.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1.6 /note= "D-form residues"

FT Modified-site 3 /note= "[pF]Phe"

FT Modified-site 6 /note= "C-terminal amide"

XX WO200052048-A1.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05574.

XX 04-MAR-1999; 99US-0122736.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Phillips K, Olson GL, Self C;

XX WPI; 2000-594168/56.

XX Novel compounds that are useful as modulators of beta-amyloid peptide  
 aggregation in treating amyloidosis, comprises D-amino acids -  
 Claim 4; Page 76; 87pp; English.

XX The present invention relates to peptides (see AAB27023-B27046) that  
 CC modulate beta-amyloid peptide aggregation, and hence inhibit the  
 CC neurotoxicity of beta-amyloid peptide. The present sequence is one such  
 CC peptide. The beta-amyloid peptide modulators would be useful for  
 CC treating disorders associated with beta-amyloidosis for e.g. Alzheimer's  
 CC disease. The present sequence was designed on the aggregation core domain

CC from beta-amyloid peptide (see AAB27021-B27022).

XX Sequence 6 AA;

Query Match 33.3%; Score 4; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFP 4  
 Db 1 LFFP 4

# RESULT 61

AAB27045

ID AAB27045 standard; Peptide; 6 AA.

XX AAB27045;

DT 02-FEB-2001 (first entry)

DE Beta-amyloid peptide modulator #23.

XX Beta-amyloid peptide; neurotropic; neuroprotective; Alzheimer's disease;  
 KW aggregation core domain.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 1.6 /note= "D-form residues"

FT Modified-site 1 /note= "N-methyl-Leu"

FT Modified-site 4 /note= "[FS]Phe"

FT Modified-site 6 /note= "C-terminal amide"

XX WO200052048-A1.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05574.

XX 04-MAR-1999; 99US-0122736.

XX (PRAE-) PRAECIS PHARM INC.

XX Findeis MA, Phillips K, Olson GL, Self C;

XX WPI; 2000-594168/56.

XX Novel compounds that are useful as modulators of beta-amyloid peptide  
 aggregation in treating amyloidosis, comprises D-amino acids -  
 Claim 4; Page 76; 87pp; English.

XX The present invention relates to peptides (see AAB27023-B27046) that  
 CC modulate beta-amyloid peptide aggregation, and hence inhibit the  
 CC neurotoxicity of beta-amyloid peptide. The present sequence is one such  
 CC peptide. The beta-amyloid peptide modulators would be useful for  
 CC treating disorders associated with beta-amyloidosis for e.g. Alzheimer's  
 CC disease. The present sequence was designed on the aggregation core domain  
 CC from beta-amyloid peptide (see AAB27021-B27022).

XX Sequence 6 AA;

Query Match 33.3%; Score 4; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
 Db 2 FFPL 5

```

Db 3 FFFL 6
RESULT 62
AAB28963
ID AAB28963 standard; Peptide; 6 AA.
XX
XX
AC AAB28963;
XX
XX 29-JAN-2001 (first entry)
XX
XX Peptide encoded by oligonucleotide C.
DE
DE Cat; allergy; human T cell reactive feline protein; hTRFP;
XX immunotherapy.
KW
KW
XX Felis sp.
OS
OS Synthetic.
XX
XX US6120769-A.
PN
PD 19-SEP-2000.
XX
XX 28-APR-1995; 95US-0431184.
XX
XX 02-SEP-1994; 94US-0300928.
PR
PR 03-NOV-1989; 89US-0431565.
PR
PR 28-FEB-1991; 91US-0662276.
PR
PR 13-DEC-1991; 91US-0807529.
PR
PR 25-MAR-1992; 92US-0857311.
PR
PR 15-MAY-1992; 92US-0884718.
XX
XX 15-JAN-1993; 93US-0006116.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
PA
XX
XX Gefter ML, Garman RD., Greenstein JL, Bond JF;
PI
XX
XX WPI; 2000-601477/57.
DR
XX
XX N-PSDB; AAC60128.
XX
XX Detecting, preventing and treating sensitivity to cat protein allergen
PT comprises combining a biological sample with a human T cell reactive
PT feline protein and determining the extent of binding that occurs -
XX
XX
XX Example 25; Column 105-106; 106pp; English.
XX
XX The present invention relates to the detection of sensitivity to a cat
CC protein allergen by combining a blood sample from a subject with a
CC peptide of human T cell reactive feline protein (hTRFP). This method
CC and the hTRFP peptides are useful for diagnosing, preventing and
CC treating cat allergies by reducing or abolishing an individual's
CC allergic response to a cat allergen. DNA encoding the TRFP may be
CC used as probes to locate equivalent sequences present in other species.
CC These may further be used to study the mechanism of immunotherapy of
CC cat allergy, and to design modified derivatives, analogues or
CC functional equivalents useful in immunotherapy. The present
CC sequence was used in the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 33.3%; Score 4; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 LPVV 8
Db 3 LPVV 6
RESULT 63
AAY87707
ID AAY87707 standard; Protein; 6 AA.
XX
XX
AC AAY87707;
XX
XX 22-AUG-2000 (first entry)
XX
XX Feline human TRFP oligonucleotide C derived peptide.
DE
DE T-cell reactive feline protein; TRFP; Fel d I; cat allergen; primer;
XX antiallergic; T cell stimulator; diagnostic; immunotherapy.
KW
KW
XX Felis sp.
OS
XX
XX US6048962-A.
PN
PD 11-APR-2000.
XX
XX 27-APR-1995; 95US-0430014.
XX
XX 02-SEP-1994; 94US-0300928.
PR
PR 03-NOV-1989; 89US-0431565.
PR
PR 28-FEB-1991; 91US-0662276.
PR
PR 13-DEC-1991; 91US-0807529.
PR
PR 25-MAR-1992; 92US-0857311.
PR
PR 15-MAY-1992; 92US-0884718.
XX
XX 15-JAN-1993; 93US-0006116.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
PA
XX
XX Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW;
PI Greenstein JL, Griffith IJ, Garman RD;
XX
XX WPI; 2000-316905/27.
DR
XX
XX N-PSDB; AAA12266.
XX
XX New human T cell reactive feline protein useful for reducing or
PT abolishing individual's allergic response to cat allergen comprising
PT two different covalently linked peptide chains -
XX
XX Example 25; Column 105-106; 106pp; English.
XX
XX This invention describes a novel naturally occurring cat protein allergen
CC (I), human T cell reactive feline protein (TRFP), comprising two
CC different covalently linked peptide chains with a molecular weight of 20
CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
CC under reducing conditions. The products of the invention have
CC antiallergic activity and act as human T cell stimulators. TRFP is useful
CC for reducing or preventing the adverse effects of cat allergens on cat
CC allergic individuals and in ex vivo diagnostic tests to determine which
CC peptides cause sensitivity so as to selectively use them to desensitize
CC a cat sensitive individual. Purified TRFP is also useful for studying
CC the mechanism of immunotherapy of cat allergy and to design modified
CC derivatives, analogs or functional equivalents that are more useful in
CC immunotherapy against cat allergy. DNA sequences encoding TRFP are
CC useful as probes to locate equivalent sequences present in other species
CC (goats, sheep, dogs, rabbits or horses) that may be useful in diagnostics
CC and/or therapeutics. Fully defined and characterized TRFP provides
CC complete and a very simple desensitization therapy. This sequence
CC represents a peptide fragment of TRFP used in the design of a primer
CC which is used in the construction and expression of peptides comprising
CC two or more regions of TRFP in a method described in the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 33.3%; Score 4; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 LPVV 8
Db 3 LPVV 6
RESULT 64
AAY90133

```

ID AAY90133 standard; Peptide; 6 AA.  
 XX  
 AC AAY90133;  
 XX  
 DT 13-JUL-2000 (first entry)  
 XX  
 XX TRFP derived peptide, peptide C.  
 DE  
 XX  
 KW Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;  
 KW house dust; Fel d I; cat allergy; Felis domesticus sensitivity; therapy;  
 KW diagnosis; goat; sheep; horse; rabbit; dog.  
 XX  
 XX Felis domesticus.  
 OS  
 XX  
 FN US6025162-A.  
 XX  
 XX  
 PD 15-FEB-2000.  
 XX  
 XX  
 PF 28-APR-1995; 95US-0430944.  
 XX  
 XX  
 PR 02-SEP-1994; 94US-0300928.  
 PR 03-NOV-1989; 89US-0431565.  
 PR 28-FEB-1991; 91US-0662276.  
 PR 13-DEC-1991; 91US-0807529.  
 PR 25-MAR-1992; 92US-0857311.  
 PR 15-MAY-1992; 92US-0884718.  
 PR 15-JAN-1993; 93US-0006116.  
 XX  
 XX (IMMU-) IMMULOGIC PHARM CORP.  
 PA  
 XX  
 PI Morgenstern JP, Griffith IJ, Rogers BL;  
 XX  
 XX WPI; 2000-181812/16.  
 DR  
 XX  
 XX New human T cell reactive feline protein, useful for desensitizing cat  
 PT allergic individuals to cat allergens -  
 PT  
 XX  
 PS Example 25; Fig 28; 108pp; English.  
 XX  
 CC This sequence is a peptide derived from the human T cell reactive feline  
 CC protein (TRFP) of the invention, and was used to design a PCR  
 CC primer. The protein is a cat protein allergen,  
 CC and was isolated from a vacuum bag extract obtained by affinity  
 CC purification of house dust collected from several homes with cats. TRFP  
 CC is composed of two covalently linked peptide chains, and is also referred  
 CC to as Fel d I. TRFP and its peptides are useful for reducing or  
 CC preventing the adverse effects that exposure to cat allergens normally  
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat  
 CC allergens or block the effect of the allergens). TRFP is also used in  
 CC methods of diagnosing sensitivity to Felis domesticus in an individual.  
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent  
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and  
 CC dog, that may be useful in diagnostic and/or therapeutic applications.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 33.3%; Score 4; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LPVV 8  
 DB 3 LPVV 6  
 RESULT 65  
 AAY51504  
 ID AAY51504 standard; Protein; 6 AA.  
 XX  
 XX AAY51504;  
 AC  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX

DE Human TRFP derived peptide encoding oligonucleotide C.  
 XX  
 XX T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;  
 KW down regulation; immune response; allergen; immunoglobulin E;  
 KW sensitivity; cat protein allergen; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 FN US6019972-A.  
 XX  
 PD 01-FEB-2000.  
 XX  
 XX  
 PF 02-SEP-1994; 94US-0300928.  
 XX  
 XX  
 PR 03-NOV-1989; 89US-0431565.  
 PR 28-FEB-1991; 91US-0662276.  
 PR 13-DEC-1991; 91US-0807529.  
 PR 25-MAR-1992; 92US-0857311.  
 PR 15-MAY-1992; 92US-0884718.  
 PR 15-JAN-1993; 93US-0006116.  
 XX  
 XX (IMMU-) IMMULOGIC PHARM CORP.  
 PA  
 XX  
 PI Garman RD, Greenstein JL, Kuo M, Briner TJ, Morville M, Geffer ML;  
 XX  
 XX WPI; 2000-146862/13.  
 DR  
 DR N-FSDB; AAZ88639.  
 XX  
 XX Peptides of human T cell reactive feline protein for treating  
 PT sensitivity to cat protein allergens comprise at least one T cell  
 PT epitope recognized by a T cell receptor specific for the human T cell  
 PT reactive feline protein -  
 XX  
 PS Example 25; Column 105-106; 105pp; English.  
 XX  
 CC This invention describes a novel peptide (I) of human T cell reactive  
 CC feline protein (hTRFP) having at least one T cell epitope recognized  
 CC by a T cell receptor specific for the human T cell reactive feline  
 CC protein, the peptide consisting of at least 7-30 amino acids, and having  
 CC an amino acid sequence derived from an amino acid sequence comprising  
 CC 94, 96, 97, 109, or 111 residues, given in the specification. The  
 CC peptides down regulate the immune response to the allergen. The peptides  
 CC have reduced immunoglobulin E binding and reduce T cell responsiveness.  
 CC The peptide (I) is useful in compositions for treating sensitivity to a  
 CC cat protein allergen in a subject. AAY51504-Y51516 represent peptides  
 CC used in the design of the oligonucleotides represented in AAZ88639-288650  
 CC which are used to construct peptides comprising of two or more regions of  
 CC human TRFP.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 33.3%; Score 4; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LPVV 8  
 DB 3 LPVV 6  
 RESULT 66  
 AAR64963  
 ID AAR64963 standard; peptide; 7 AA.  
 XX  
 XX AAR64963;  
 AC  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 12-SEP-1995 (first entry)  
 XX  
 XX Peralkylated oligopeptide.  
 XX  
 XX Peralkylated oligopeptides; binding assays; hydrolysis resistance;  
 KW antimicrobial drug design; S. aureus; S. sanguis.



FT the backbone and appropriately methylated.  
 FT side chains."  
 PN WO9500539-A1.  
 XX  
 XX 05-JAN-1995.  
 PD  
 XX 10-JUN-1994; 94WO-US06554.  
 PF  
 XX 17-JUN-1993; 93US-0079144.  
 XX  
 PR 09-JUN-1994; 94US-0257782.  
 XX  
 XX (HOUG-) HOUGHTEN PHARM INC.  
 PA  
 XX Blondelle S, Houghten R, Ostresh JM, Houghten RA;  
 XX WPI; 1995-052001/07.  
 XX  
 XX Sets and libraries of per-alkylated oligopeptide derivs. -  
 PT including new cpds., with selected amino acids at partic.  
 PT positions, used in binding assays to identify sequence with  
 PT optimum binding to e.g. cellular receptors.  
 XX  
 PS Claim 33; Page 117; 162pp; English.  
 XX  
 CC AAR78161-R78169 are peralkylated oligopeptides (POs), which  
 CC together comprise a PO library. This PO library can be used to  
 CC assay peptides for preferential binding to a S. aureus or a  
 CC S. sanguis acceptor, esp. for drug (specifically antimicrobial)  
 CC design. The POs are resistant to enzymatic hydrolysis, also POs  
 CC that are toxic to gram positive bacteria do not cause haemolysis  
 CC of human blood.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 33.3%; Score 4; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LFFF 4  
 Db 2 LFFF 5  
 RESULT 69  
 AAB23226  
 ID AAB23226 standard; peptide; 7 AA.  
 XX  
 AC AAB23226;  
 XX  
 XX 29-JAN-2001 (first entry)  
 XX  
 DE Hsp47-binding phage display heptapeptide, SEQ ID NO:48.  
 XX  
 KW Hsp47-binding heptapeptide; phage display library;  
 KW Hsp47 external domain; carcinoma; cancer; targeting molecule;  
 KW therapy; diagnosis; detection; imaging; drug delivery; invasion;  
 KW migration; metastasis; modulation; tumour; skin; basal cells; colon;  
 KW large intestine; lung; breast; bladder; oral cancer;  
 KW head and neck cancer; larynx; nasopharynx; adrenal cortex;  
 KW apocrine gland; kidney; liver; pancreas; prostate.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200054805-A1.  
 PN  
 XX 21-SEP-2000.  
 PD  
 XX 15-MAR-2000; 2000WO-US06588.  
 PF  
 XX 15-MAR-1999; 99US-0124481.  
 PR  
 XX

(UTMA-) UNIV MARYLAND BALTIMORE.  
 PA  
 XX Sauk JJ;  
 PI  
 XX WPI; 2000-655997/63.  
 DR  
 XX  
 XX Treating, diagnosing or modulating a carcinoma cell, which expresses  
 PT Heat shock protein 47 on its surface, involves administering an agent  
 PT comprising targeting moiety which binds to Hsp47 external domain -  
 XX  
 XX Example 5; Page 9; 87pp; English.  
 PS  
 XX  
 CC The invention relates to methods of treating and diagnosing carcinomas  
 CC in which heat shock protein 47 (Hsp47) is expressed on the surface  
 CC of the carcinoma cells, involving administering an agent comprising a  
 CC targeting moiety which specifically binds to the external domain of  
 CC Hsp47. The invention also relates to peptides (AAB23181-B23203) which  
 CC specifically bind to external domains of such surface-localised Hsp47  
 CC molecules and have sequences encompassed by the generic sequences  
 CC XHYHYXXHYXXHXXHy or HYXXHXXHYXXHXX where X, independently, can be  
 CC any amino acid and Hy, independently, can be any hydrophobic amino acid.  
 CC The invention also encompasses methods of screening for agents which  
 CC bind Hsp47 external domains. Hsp47-binding agents can be used to  
 CC treat Hsp47-expressing carcinomas, and for modulating the activity of a  
 CC tumour cell with respect to invasion, migration, motility or metastasis,  
 CC or to its interaction with the extracellular matrix. The targeting  
 CC moiety (such as an Hsp47-binding peptide, a toxin or an antibody) may be  
 CC coupled with a therapeutic moiety (such as a cytotoxic agent or a  
 CC therapeutic gene) for cancer treatment, or with a detectable moiety for  
 CC imaging. Carcinomas which may be treated or diagnosed according to  
 CC methods of the invention include those of the skin, basal cells, large  
 CC intestine, lung, colon, breast, bladder, oral, head and neck, larynx,  
 CC nasopharynx, adrenal cortex, apocrine glands, kidney, liver, pancreas, or  
 CC prostate. Targeting carcinoma cells with Hsp47-binding agents results in  
 CC efficient delivery of therapeutic agents, reduced doses, reduced side  
 CC effects and sensitive detection or imaging of carcinoma cells. Sequences  
 CC AAB23204-B23240 represent phage display library heptapeptides identified  
 CC as being able to bind Hsp47 in an exmplication of the invention.  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 33.3%; Score 4; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FLPV 7  
 Db 2 FLPV 5  
 RESULT 70  
 AAR61722  
 ID AAR61722 standard; peptide; 8 AA.  
 XX  
 AC AAR61722;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 11-MAY-1995 (first entry)  
 XX  
 DE PLP peptide 74, potential binder of HLA-A2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9420127-A1.  
 PN



```

XX PD 15-SEP-1994.
XX PF 04-MAR-1994; 94WO-US02353.
XX PR 05-MAR-1993; 93US-0027146.
XX PR 04-JUN-1993; 93US-0073205.
XX PR 29-NOV-1993; 93US-0159184.
XX PA (CYTE-) CYTEL CORP.
XX PI Grey HM, Kast WM, Sette A, Sidney J;
XX WI WPI; 1994-302678/37.
XX PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
XX PT for treatment or prophylaxis of cancer, virus infection or
XX PT autoimmune diseases.
XX PS Disclosure; Page 115; 138pp; English.
XX CC AAR61714-837 are potential peptide binders of HLA-A2.1 motif. These
XX CC peptides are thus potentially immunogenic. They were predicted by
XX CC using an algorithm, which assigns a score for each amino acid, at
XX CC each position along a peptide. A peptide is scored in the 'Grouped
XX CC Ratio' algorithm as a product of the scores of each of its residues.
XX CC This value can then be used to predict a population of peptides with
XX CC the highest occurrence of good binders. The peptides of the invention
XX CC can induce cytotoxic T lymphocytes which can react with target cells.
XX CC They can be used for the treatment or prophylaxis of cancer, eg.
XX CC prostate cancer or lymphoma, etc.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 8 AA;
XX Query Match 33.3%; Score 4; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FFFL 5
DB 5 FFFL 8
RESULT 71
AAW39537
ID AAW39537 standard; peptide; 8 AA.
XX AC AAW39537;
XX DT 11-JUN-1998 (first entry)
XX DE HIV-1 pol peptide (pos. 306-313) capable of binding to HLA-A*0301.
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX KW disease; anti-tumour; anti-vital.
XX OS Human immunodeficiency virus type 1.
XX PN WO9741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
WPI; 1997-549891/50.
Method of selecting T cell peptide epitope(s) - by measuring the
stability of HLA class I-peptide complexes on intact B cells
Example 2; Page 62; 109pp; English.
Peptides AAW39430-W39734 are used in a novel method for the selection of
immunogenic T-cell peptide epitopes present in polypeptide antigens. The
method involves the identification of peptide sequences capable of
binding to an HLA (human leukocyte antigen) class I molecule and
measuring the binding of this epitope peptide to the HLA class I
peptide. The stability of binding of the peptide and MHC (major
histocompatibility complex) class I molecule is measured on intact human
B cells carrying the MHC molecule at their cell surfaces. The method can
be used to select peptide epitopes for generating vaccines against a
disease associated with the polypeptide, e.g. cancers or AIDS. The
peptide epitopes are especially T-cell peptide epitopes with strong
anti-tumour and anti-viral immune responses. Peptides AAW39528-W39547 are
conserved human immunodeficiency virus type 1 (HIV-1) pol sequences which
are compliant with the HLA-A*0301 binding motif.
Sequence 8 AA;
Query Match 33.3%; Score 4; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 NVLP 12
DB 1 NVLP 4
RESULT 72
AAB37338
ID AAB37338 standard; Peptide; 8 AA.
XX AC AAB37338;
XX DT 19-FEB-2001 (first entry)
XX DE Peptide linker #23.
XX KW Cytostatic; antiproliferative; vascular endothelial growth factor;
XX KW VEGF; antibody; VEGF2 receptor; cancer; vascularised solid tumour;
XX KW peptide linker.
XX OS Rattus sp.
XX PN WO200064946-A2.
XX PD 02-NOV-2000.
XX PF 28-APR-2000; 2000WO-US11367.
XX PR 28-APR-1999; 99US-0131432.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Thorpe PE, Brekken RA;
XX WI WPI; 2000-687317/67.
XX PT Immunogenic composition for the treatment and diagnosis of cancer
XX PT comprises an anti-VEGF (vascular endothelial growth factor) antibody
XX PT binding the same epitope as the monoclonal antibody ArCC PTA 1595 -
XX PS Disclosure; Page 150; 298pp; English.
XX CC The present invention relates to anti-Vascular Endothelial Growth Factor
XX CC (VEGF) antibodies that bind to the same epitope as the monoclonal
XX CC antibody ArCC PTA 1595 and which significantly inhibit VEGF binding to

```

CC the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF  
 CC receptor VEGFR1. The present sequence is a peptide linker which can be  
 CC used to link the antibodies of the present invention to anti-cellular or  
 CC cytotoxic agents. The anti-VEGF antibodies of the present invention are  
 CC useful for the treatment and diagnosis of cancer, especially vascularised  
 CC solid tumours.

XX Sequence 8 AA;  
 SQ Query Match 33.3%; Score 4; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LPVW 8  
 ||||  
 DB 3 LPVW 6

RESULT 73  
 ABP14646  
 ID ABP14646 standard; Peptide; 8 AA.

XX AC ABP14646;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A03 super motif pol peptide #20.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 168; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

XX Query Match 33.3%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 NVLP 12  
 ||||  
 DB 1 NVLP 4

RESULT 74  
 ABP21858  
 ID ABP21858 standard; Peptide; 8 AA.

XX AC ABP21858;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A03 motif pol peptide #853.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 317; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

```

XX SQ Sequence 8 AA;
Query Match 33.3%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 1 NVLP 4

RESULT 75
ABP23685
ID ABP23685 standard; Peptide; 8 AA.
XX AC ABP23685;
XX DT 15-JUL-2002 (first entry)
XX DE HIV A11 motif pol peptide #627.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr;
XX KW vpu; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PS peptide groups, useful for vaccinating against HIV-1 -
XX Claim 32; Page 354; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 8 AA;
Query Match 33.3%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 1 NVLP 4

Search completed: November 25, 2003, 18:15:43
Job time : 41.8723 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 23.8723 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-4

Perfect score: 12

Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match % | Length | ID                | Description       |
|------------|-------|---------------|--------|-------------------|-------------------|
| 1          | 12    | 100.0         | 12     | US-10-281-652-4   | Sequence 4, Appli |
| 2          | 5     | 41.7          | 5      | US-09-895-443-30  | Sequence 30, Appl |
| 3          | 5     | 41.7          | 8      | US-10-137-867-292 | Sequence 292, App |
| 4          | 5     | 41.7          | 11     | US-09-484-704-16  | Sequence 16, Appl |
| 5          | 5     | 41.7          | 11     | US-09-309-196-57  | Sequence 57, Appl |
| 6          | 5     | 41.7          | 11     | US-09-201-396-38  | Sequence 38, Appl |
| 7          | 5     | 41.7          | 11     | US-09-953-354-68  | Sequence 68, Appl |
| 8          | 5     | 41.7          | 11     | US-10-277-607-38  | Sequence 38, Appl |
| 9          | 4     | 33.3          | 4      | US-09-832-161-23  | Sequence 23, Appl |
| 10         | 4     | 33.3          | 5      | US-09-895-443-24  | Sequence 24, Appl |
| 11         | 4     | 33.3          | 5      | US-09-895-443-25  | Sequence 25, Appl |
| 12         | 4     | 33.3          | 5      | US-09-895-443-26  | Sequence 26, Appl |
| 13         | 4     | 33.3          | 5      | US-09-781-133-20  | Sequence 20, Appl |
| 14         | 4     | 33.3          | 5      | US-09-781-133-21  | Sequence 21, Appl |
| 15         | 4     | 33.3          | 5      | US-09-781-133-22  | Sequence 22, Appl |

|    |   |      |    |                     |                   |
|----|---|------|----|---------------------|-------------------|
| 16 | 4 | 33.3 | 6  | US-08-464-363-13    | Sequence 13, Appl |
| 17 | 4 | 33.3 | 6  | US-08-464-363-53    | Sequence 53, Appl |
| 18 | 4 | 33.3 | 7  | US-09-833-067-26    | Sequence 26, Appl |
| 19 | 4 | 33.3 | 8  | US-09-998-831-37    | Sequence 37, Appl |
| 20 | 4 | 33.3 | 8  | US-10-373-561-37    | Sequence 37, Appl |
| 21 | 4 | 33.3 | 9  | US-08-821-739A-43   | Sequence 43, Appl |
| 22 | 4 | 33.3 | 9  | US-08-464-363-45    | Sequence 45, Appl |
| 23 | 4 | 33.3 | 9  | US-09-865-548A-86   | Sequence 86, Appl |
| 24 | 4 | 33.3 | 9  | US-09-932-165-283   | Sequence 283, App |
| 25 | 4 | 33.3 | 9  | US-09-932-165-290   | Sequence 290, App |
| 26 | 4 | 33.3 | 9  | US-09-932-165-452   | Sequence 452, App |
| 27 | 4 | 33.3 | 9  | US-09-932-165-480   | Sequence 480, App |
| 28 | 4 | 33.3 | 9  | US-09-932-165-660   | Sequence 660, App |
| 29 | 4 | 33.3 | 9  | US-09-932-165-695   | Sequence 695, App |
| 30 | 4 | 33.3 | 9  | US-09-932-165-876   | Sequence 876, App |
| 31 | 4 | 33.3 | 9  | US-10-239-313A-655  | Sequence 655, App |
| 32 | 4 | 33.3 | 9  | US-10-119-536A-183  | Sequence 183, App |
| 33 | 4 | 33.3 | 10 | US-09-894-018-305   | Sequence 305, App |
| 34 | 4 | 33.3 | 10 | US-09-572-404B-1033 | Sequence 1033, Ap |
| 35 | 4 | 33.3 | 10 | US-09-572-404B-1035 | Sequence 1035, Ap |
| 36 | 4 | 33.3 | 10 | US-09-572-404B-1109 | Sequence 1109, Ap |
| 37 | 4 | 33.3 | 10 | US-09-895-298-138   | Sequence 138, App |
| 38 | 4 | 33.3 | 10 | US-09-932-165-388   | Sequence 388, App |
| 39 | 4 | 33.3 | 10 | US-09-932-165-553   | Sequence 553, App |
| 40 | 4 | 33.3 | 10 | US-09-932-165-558   | Sequence 558, App |
| 41 | 4 | 33.3 | 10 | US-09-932-165-751   | Sequence 751, App |
| 42 | 4 | 33.3 | 10 | US-09-932-165-1369  | Sequence 1369, Ap |
| 43 | 4 | 33.3 | 10 | US-09-833-039-129   | Sequence 129, App |
| 44 | 4 | 33.3 | 10 | US-10-231-417-614   | Sequence 614, App |
| 45 | 4 | 33.3 | 10 | US-10-200-708-295   | Sequence 295, App |
| 46 | 4 | 33.3 | 10 | US-10-200-708-318   | Sequence 318, App |
| 47 | 4 | 33.3 | 10 | US-10-177-277-129   | Sequence 129, App |
| 48 | 4 | 33.3 | 10 | US-09-573-822C-403  | Sequence 403, App |
| 49 | 4 | 33.3 | 11 | US-10-057-763-1     | Sequence 1, Appli |
| 50 | 4 | 33.3 | 11 | US-09-828-708-79    | Sequence 79, Appl |
| 51 | 4 | 33.3 | 12 | US-10-057-789-218   | Sequence 218, App |
| 52 | 4 | 33.3 | 12 | US-10-212-628-218   | Sequence 218, App |
| 53 | 4 | 33.3 | 13 | US-10-116-252-22    | Sequence 22, Appl |
| 54 | 4 | 33.3 | 14 | US-09-853-080-32    | Sequence 32, Appl |
| 55 | 4 | 33.3 | 15 | US-09-767-460-12    | Sequence 12, Appl |
| 56 | 4 | 33.3 | 15 | US-09-981-876-224   | Sequence 224, App |
| 57 | 4 | 33.3 | 15 | US-09-148-545-224   | Sequence 224, App |
| 58 | 4 | 33.3 | 15 | US-10-336-491-6     | Sequence 6, Appli |
| 59 | 4 | 33.3 | 16 | US-09-986-480-261   | Sequence 261, App |
| 60 | 4 | 33.3 | 17 | US-09-071-838-88    | Sequence 88, Appl |
| 61 | 4 | 33.3 | 17 | US-09-981-876-221   | Sequence 221, App |
| 62 | 4 | 33.3 | 17 | US-09-148-545-221   | Sequence 221, App |
| 63 | 4 | 33.3 | 17 | US-09-996-069-30    | Sequence 30, Appl |
| 64 | 4 | 33.3 | 17 | US-09-996-069-31    | Sequence 31, Appl |
| 65 | 4 | 33.3 | 17 | US-10-213-512-88    | Sequence 88, Appl |
| 66 | 4 | 33.3 | 18 | US-10-084-813-248   | Sequence 248, App |
| 67 | 4 | 33.3 | 18 | US-10-084-813-249   | Sequence 249, App |
| 68 | 4 | 33.3 | 18 | US-10-084-813-250   | Sequence 250, App |
| 69 | 4 | 33.3 | 18 | US-10-157-031-192   | Sequence 192, App |
| 70 | 4 | 33.3 | 19 | US-10-106-698-7294  | Sequence 7294, Ap |
| 71 | 4 | 33.3 | 19 | US-10-225-567A-1666 | Sequence 1666, Ap |
| 72 | 4 | 33.3 | 20 | US-08-464-363-29    | Sequence 29, Appl |
| 73 | 4 | 33.3 | 20 | US-09-864-761-35505 | Sequence 35505, A |
| 74 | 4 | 33.3 | 20 | US-09-735-705-405   | Sequence 405, App |
| 75 | 4 | 33.3 | 20 | US-09-841-132-156   | Sequence 156, App |
| 76 | 4 | 33.3 | 20 | US-09-850-716A-405  | Sequence 405, App |
| 77 | 4 | 33.3 | 20 | US-09-897-778-405   | Sequence 405, App |
| 78 | 4 | 33.3 | 20 | US-09-731-449-27    | Sequence 27, Appl |
| 79 | 4 | 33.3 | 20 | US-09-928-048A-8    | Sequence 8, Appli |
| 80 | 4 | 33.3 | 20 | US-10-117-982-405   | Sequence 405, App |
| 81 | 4 | 33.3 | 20 | US-10-267-730-27    | Sequence 27, Appl |
| 82 | 4 | 33.3 | 20 | US-10-106-698-7129  | Sequence 7129, Ap |
| 83 | 4 | 33.3 | 20 | US-10-106-698-7253  | Sequence 7253, Ap |
| 84 | 4 | 33.3 | 20 | US-10-106-698-7391  | Sequence 7391, Ap |
| 85 | 4 | 33.3 | 20 | US-10-254-426-27    | Sequence 27, Appl |
| 86 | 3 | 25.0 | 4  | US-08-464-363-25    | Sequence 25, Appl |
| 87 | 3 | 25.0 | 4  | US-09-803-126-34    | Sequence 34, Appl |
| 88 | 3 | 25.0 | 4  | US-09-202-077-11    | Sequence 11, Appl |

89 Sequence 10, Appl  
90 Sequence 12, Appl  
91 Sequence 64, Appl  
92 Sequence 3, Appl  
93 Sequence 9, Appl  
94 Sequence 178, Appl  
95 Sequence 64, Appl  
96 Sequence 10, Appl  
97 Sequence 14, Appl  
98 Sequence 2, Appl  
99 Sequence 55, Appl  
100 Sequence 2, Appl

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895,443  
FILING DATE: 29-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/356,931  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/897,342  
FILING DATE: 21-JUL-1997  
APPLICATION NUMBER: USSN 08/703,675  
FILING DATE: 27-AUG-1996  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Jr., Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-895-443-30

ALIGNMENTS

RESULT 1  
US-10-281-652-4  
Sequence 4, Application US/10281652  
Publication No. US20030091606A1  
GENERAL INFORMATION:  
APPLICANT: STANTON, G. John  
APPLICANT: HUGHES, Thomas K.  
APPLICANT: BOLDOGH, Istvan  
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
FILE REFERENCE: 265.00220101  
CURRENT APPLICATION NUMBER: US/10/281,652  
PRIOR FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: US/09/641,803  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: 60/149,310  
PRIOR FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-4

Query Match 100.0%; Score 12; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFLPVNVLP 12  
| | | | | | | | | | | | | |  
DB 1 LFFFLPVNVLP 12

RESULT 2  
US-09-895-443-30  
Sequence 30, Application US/09895443  
Patent No. US20020103134A1  
GENERAL INFORMATION:  
APPLICANT: Findeis, M. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising D-Amino Acids  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1784  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

Query Match 41.7%; Score 5; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
| | | | |  
DB 1 LFFFL 5

RESULT 3  
US-10-137-867-292  
Sequence 292, Application US/10137867  
Publication No. US20030207349A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C146  
CURRENT APPLICATION NUMBER: US/10/137,867  
CURRENT FILING DATE: 2002-05-03

; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 292  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-867-292

Query Match 41.7%; Score 5; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFEL 5  
Db 1 LFFEL 5

RESULT 4  
US-09-484-704-16  
; Sequence 16, Application US/09484704  
; Patent No. US20020081567A1  
; GENERAL INFORMATION:  
; APPLICANT: Henrickson, Kelly J.  
; APPLICANT: Fan, Jiang (n.m.i.)  
; TITLE OF INVENTION: VIRUS ASSAY METHOD  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/484.704  
; FILING DATE:

; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 650053.91126  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5000  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-484-704-16

Query Match 41.7%; Score 5; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNVL 11  
Db 7 VVNVL 11

RESULT 5  
US-09-309-196-57  
; Sequence 57, Application US/09309196  
; Publication No. US20030008380A1  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M.

; APPLICANT: BROACH, Jim  
; APPLICANT: MANFREDI, John  
; APPLICANT: KLEIN, Christine  
; APPLICANT: MURPHY, Andrew J.  
; APPLICANT: PAUL, Jeremy  
; APPLICANT: TRUEHEART, Joshua  
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR  
; NUMBER OF SEQUENCES: 119  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/309,196  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/322,137  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,328  
; FILING DATE: 31-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/041,431  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOLWKES=2C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-309-196-57

Query Match 41.7%; Score 5; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFELP 6  
Db 6 FFELP 10

RESULT 6  
US-09-201-396-38  
; Sequence 38, Application US/09201396A  
; Publication No. US20030009022A1  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; APPLICANT: Murphy, Andrew J.  
; APPLICANT: Paul, Jeremy  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
; TITLE OF INVENTION: EFFECTORS  
; FILE REFERENCE: CPI-012CP9  
; CURRENT APPLICATION NUMBER: US/09/201,396A  
; CURRENT FILING DATE: 1998-11-30  
; EARLIER APPLICATION NUMBER: 08/582,333

EARLIER FILING DATE: 1996-01-17  
EARLIER APPLICATION NUMBER: 08/322,137  
EARLIER FILING DATE: 1994-10-13  
EARLIER APPLICATION NUMBER: 08/309,313  
EARLIER FILING DATE: 1994-09-20  
EARLIER APPLICATION NUMBER: 08/190,328  
EARLIER FILING DATE: 1994-01-31  
EARLIER APPLICATION NUMBER: 08/041,431  
EARLIER FILING DATE: 1993-03-31  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
US-09-201-396-38

Query Match 41.7%; Score 5; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
| | | | |  
DB 6 FFFLP 10

RESULT 7  
US-09-953-354-68  
Sequence 68, Application US/09953354  
Publication No. US20030054402A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
MURPHY, Andrew J.  
TITLE OF INVENTION: Methods and Compositions for  
Identifying Receptor Effectors  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/953,354  
FILING DATE: 13-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/689,172  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: CPI-012CP7  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-953-354-68

Query Match 41.7%; Score 5; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
| | | | |  
DB 6 FFFLP 10

RESULT 8  
US-10-277-607-38  
Sequence 38, Application US/10277607  
Publication No. US20030166143A1  
GENERAL INFORMATION:  
APPLICANT: Klein, Christine A.  
MURPHY, Andrew J.  
APPLICANT: Paul, Jeremy I.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
EFFECTORS  
FILE REFERENCE: CPI-012CP9CN  
CURRENT APPLICATION NUMBER: US/10/277,607  
CURRENT FILING DATE: 2003-01-31  
PRIOR APPLICATION NUMBER: 09/201,396  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: 60/109,902  
PRIOR FILING DATE: 1998-11-25  
PRIOR APPLICATION NUMBER: PCT/US98/21168  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 08/946,298  
PRIOR FILING DATE: 1997-10-07  
PRIOR APPLICATION NUMBER: 08/689,172  
PRIOR FILING DATE: 1996-08-06  
PRIOR APPLICATION NUMBER: 08/582,333  
PRIOR FILING DATE: 1996-01-17  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
US-10-277-607-38

Query Match 41.7%; Score 5; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
| | | | |  
DB 6 FFFLP 10

RESULT 9  
US-09-832-161-23  
Sequence 23, Application US/09832161  
Publication No. US20030166587A1  
GENERAL INFORMATION:  
APPLICANT: Manning, Anthony M.  
APPLICANT: Mercurio, Frank  
APPLICANT: Amit, Sharon  
APPLICANT: Ben-Neriah, Yinon  
APPLICANT: Davis, Matti  
APPLICANT: Hatzubai, Ada  
APPLICANT: Lavon, Iris  
APPLICANT: Yaron, Avraham  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF  
NF-KB  
FILE REFERENCE: 860098.427  
CURRENT APPLICATION NUMBER: US/09/832,161  
CURRENT FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/210,060  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-832-161-23

Query Match 33.3%; Score 4; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNV 10  
Db 1 VVNV 4

RESULT 10  
US-09-895-443-24  
; Sequence 24, Application US/09895443  
; Patent No. US20020103134A1  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1784

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895,443  
FILING DATE: 29-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/356,931  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/897,342  
FILING DATE: 21-JUL-1997  
APPLICATION NUMBER: USSN 08/703,675  
FILING DATE: 27-AUG-1996  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Jr., Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-895-443-24

Query Match 33.3%; Score 4; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5  
Db 1 FFFL 4

RESULT 11  
US-09-895-443-25  
; Sequence 25, Application US/09895443  
; Patent No. US20020103134A1  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1784

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895,443  
FILING DATE: 29-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/356,931  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/897,342  
FILING DATE: 21-JUL-1997  
APPLICATION NUMBER: USSN 08/703,675  
FILING DATE: 27-AUG-1996  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Jr., Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-895-443-25  
Query Match 33.3%; Score 4; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5  
Db 1 FFFL 4



Db 2 FFFL 5

## RESULT 12

US-09-895-443-26  
 ; Sequence 26, Application US/09895443  
 ; Patent No. US20020103134A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fideis, M. et al.  
 ; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
 ; Aggregation Comprising D-Amino Acids  
 ;  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1784  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/895,443  
 ; FILING DATE: 29-Jun-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/356,931  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: 08/897,342  
 ; FILING DATE: 21-JUL-1997  
 ; APPLICATION NUMBER: USN 08/703,675  
 ; FILING DATE: 27-AUG-1996  
 ; APPLICATION NUMBER: USN 08/616,081  
 ; FILING DATE: 14-MAR-1996  
 ; APPLICATION NUMBER: USN 08/548,998  
 ; FILING DATE: 27-OCT-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConti, Jr., Giulio A.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)742-4214  
 ; INFORMATION FOR SEQ ID NO: 26:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; NAME/KEY: Modified site  
 ; LOCATION: 1-5  
 ; OTHER INFORMATION: /note= D amino acid  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
 US-09-895-443-26

Query Match 33.3%; Score 4; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5  
 ||||  
 Db 2 FFFL 5

## RESULT 13

US-09-781-133-20  
 ; Sequence 20, Application US/09781133  
 ; Patent No. US20020142950A1  
 ; GENERAL INFORMATION:

; APPLICANT: Hayward, Neil J.  
 ; APPLICANT: Gefter, Malcolm L.  
 ; TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG  
 ; FILE REFERENCE: PPI-064  
 ; CURRENT APPLICATION NUMBER: US/09/781,133  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/181,833  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR APPLICATION NUMBER: 60/181,943  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 5  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Each protein is a D-amino acid  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptides  
 US-09-781-133-20

Query Match 33.3%; Score 4; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5  
 ||||  
 Db 1 FFFL 4

## RESULT 14

US-09-781-133-21  
 ; Sequence 21, Application US/09781133  
 ; Patent No. US20020142950A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hayward, Neil J.  
 ; APPLICANT: Gefter, Malcolm L.  
 ; TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG  
 ; FILE REFERENCE: PPI-064  
 ; CURRENT APPLICATION NUMBER: US/09/781,133  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/181,833  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR APPLICATION NUMBER: 60/181,943  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 21  
 ; LENGTH: 5  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Each protein is a D-amino acid  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptides  
 US-09-781-133-21

Query Match 33.3%; Score 4; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5  
 ||||  
 Db 2 FFFL 5

## RESULT 15

US-09-781-133-22  
 ; Sequence 22, Application US/09781133  
 ; Patent No. US20020142950A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hayward, Neil J.

APPLICANT: Gelter, Malcolm L.  
TITLE OF INVENTION: METHODS FOR ENHANCING THE BIOAVAILABILITY OF A DRUG  
FILE REFERENCE: PPI-064  
CURRENT APPLICATION NUMBER: US/09/781,133  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/181,833  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 60/181,943  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 22  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Each protein is a D-amino acid  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptides  
US-09-781-133-22

Query Match 33.3%; Score 4; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFEL 5  
|||||  
Db 2 PFEL 5

RESULT 16  
US-08-464-363-13  
Sequence 13, Application US/08464363  
Publication No. US2003003581SAI  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce L.  
APPLICANT: Morgenstern, Jay  
APPLICANT: Bond, Julian F.  
APPLICANT: Garman, Richard D.  
APPLICANT: Greenstein, Julia L.  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Morville, Malcolm  
TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cockfield  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,363  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/807,529  
FILING DATE: 13-DEC-1991  
APPLICATION NUMBER: US 07/662,276  
FILING DATE: 28-FEB-1991  
APPLICATION NUMBER: US 07/431,565  
FILING DATE: 03-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-015CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-363-13

Query Match 33.3%; Score 4; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8  
|||||  
Db 3 LPVV 6

RESULT 17  
US-08-464-363-53  
Sequence 53, Application US/08464363  
Publication No. US2003003581SAI  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce L.  
APPLICANT: Morgenstern, Jay  
APPLICANT: Bond, Julian F.  
APPLICANT: Garman, Richard D.  
APPLICANT: Greenstein, Julia L.  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Morville, Malcolm  
TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cockfield  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,363  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/807,529  
FILING DATE: 13-DEC-1991  
APPLICATION NUMBER: US 07/662,276  
FILING DATE: 28-FEB-1991  
APPLICATION NUMBER: US 07/431,565  
FILING DATE: 03-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-015CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-464-363-53

Query Match 33.3%; Score 4; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8  
|||||

Db 3 LPVV 6

## RESULT 18

US-09-833-067-26  
; Sequence 26, Application US/09833067  
; Patent No. US2002005488A1  
; GENERAL INFORMATION:  
; APPLICANT: O'HANLEY, PETER  
; APPLICANT: DENICH, KENNETH  
; TITLE OF INVENTION: DISSOCIATED PILL, THEIR PRODUCTION AND USE  
; FILE REFERENCE: 050939/0102  
; CURRENT APPLICATION NUMBER: US/09/833,067  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/196,493  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Sequence: highly hydrophobic region  
; OTHER INFORMATION: of amino acids  
US-09-833-067-26

Query Match 33.3%; Score 4; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 4 LFFF 7

## RESULT 19

US-09-998-831-37  
; Sequence 37, Application US/09998831  
; Patent No. US20020119153A1  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Brekken  
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY  
; TITLE OF INVENTION: INHIBITING VEGF  
; FILE REFERENCE: 4001.002584  
; CURRENT APPLICATION NUMBER: US/09/998,831  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 09/561,108  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-09-998-831-37

## Query Match

33.3%; Score 4; DB 10; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 3 LPVV 6

## RESULT 20

US-10-373-561-37  
; Sequence 37, Application US/10373561

Publication No. US20030175276A1  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Brekken  
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF  
; FILE REFERENCE: 4001.002582  
; CURRENT APPLICATION NUMBER: US/10/373,561  
; CURRENT FILING DATE: 2003-02-24  
; PRIOR APPLICATION NUMBER: US/09/561,499  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/131,432  
; PRIOR FILING DATE: 1993-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-10-373-561-37

Query Match 33.3%; Score 4; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 3 LPVV 6

## RESULT 21

US-08-821-739A-43  
; Sequence 43, Application US/08821739A  
; Publication No. US20020168374A1  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Cells, Esteban  
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
; FILE REFERENCE: 2060.005000A  
; CURRENT APPLICATION NUMBER: US/08/821,739A  
; CURRENT FILING DATE: 1999-03-20  
; PRIOR APPLICATION NUMBER: 60/013,833  
; PRIOR FILING DATE: 1996-03-21  
; PRIOR APPLICATION NUMBER: 08/589,107  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 08/451,913  
; PRIOR FILING DATE: 1995-05-26  
; PRIOR APPLICATION NUMBER: 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; PRIOR APPLICATION NUMBER: 08/186,266  
; PRIOR FILING DATE: 1994-01-25  
; PRIOR APPLICATION NUMBER: 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: 08/027,746  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: 07/926,666  
; PRIOR FILING DATE: 1992-08-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-821-739A-43

## Query Match

33.3%; Score 4; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5

Db 5 FFFL 8

RESULT 22  
US-08-464-363-45  
; Sequence 45, Application US/08464363  
; Publication No. US2003005815A1  
; GENERAL INFORMATION:  
; APPLICANT: Rogers, Bruce L.  
; APPLICANT: Morgenstern, Jay  
; APPLICANT: Bond, Julian F.  
; APPLICANT: Garman, Richard D. L.  
; APPLICANT: Greenstein, Julia L.  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Morville, Malcolm  
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cockfield  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,363  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/807,529  
; FILING DATE: 13-DEC-1991  
; APPLICATION NUMBER: US 07/662,276  
; FILING DATE: 28-FEB-1991  
; APPLICATION NUMBER: US 07/431,565  
; FILING DATE: 03-NOV-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amy E. Mandragouras  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-015CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-464-363-45

Query Match 33.3%; Score 4; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8

Db 6 LPVV 9

RESULT 23  
US-09-865-548A-86  
; Sequence 86, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon

; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES  
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/290,958  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 86  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-86

Query Match 33.3%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VVNV 10

Db 6 VVNV 9

RESULT 24  
US-09-932-165-283  
; Sequence 283, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: PARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 283  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-283

Query Match 33.3%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

Db 5 LFFF 8

RESULT 25  
US-09-932-165-290  
; Sequence 290, Application US/09932165



```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-660

Query Match 33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 2 LFFF 5

RESULT 29
US-09-932-165-695
; Sequence 695, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 695
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-695

Query Match 33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 3 LFFF 6

RESULT 30
US-09-932-165-876
; Sequence 876, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
```

```
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 876
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-876

Query Match 33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
Db 6 LFFF 9

RESULT 31
US-10-239-313A-655
; Sequence 655, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 -- US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 655
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-655

Query Match 33.3%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12
Db 3 NVLP 6

RESULT 32
US-10-119-536A-183
; Sequence 183, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacte
; FILE REFERENCE: 4305/LJ091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
```

; NUMBER OF SEQ ID NOS: 194  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 183  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia trachomatis  
 ; FEATURE:  
 ; NAME/KEY: BINDING  
 ; LOCATION: (1)-(9)  
 ; OTHER INFORMATION: CT841 immunogenic peptide  
 US-10-119-536A-183

Query Match 33.3%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPL 5  
 Db 5 FFPL 8

## RESULT 33

US-09-894-018-305  
 ; Sequence 305, Application US/09894018  
 ; Patent No. US20020119127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPIMMUNE, Inc.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Chestnut, Robert  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Baker, Denisw  
 ; APPLICANT: Newman, Mark  
 ; APPLICANT: Brown, David  
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
 ; FILE REFERENCE: 39963-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/894,018  
 ; CURRENT FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/35568  
 ; PRIOR FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/173,390  
 ; PRIOR FILING DATE: 1999-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/284,221  
 ; PRIOR FILING DATE: 2001-04-16  
 ; NUMBER OF SEQ ID NOS: 368  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 305  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Transgenic mouse  
 US-09-894-018-305

Query Match 33.3%; Score 4; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
 Db 7 LPVV 10

## RESULT 34

US-09-572-404B-1033  
 ; Sequence 1033, Application US/09572404B  
 ; Publication No. US20030078374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 1033  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in BMP1B at 63-72 and may interact with Sequ  
 ; OTHER INFORMATION: in this patent.  
 US-09-572-404B-1033

Query Match 33.3%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
 Db 2 LPVV 5

## RESULT 35

US-09-572-404B-1035  
 ; Sequence 1035, Application US/09572404B  
 ; Publication No. US20030078374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 1035  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in BMP1B at 62-71 and may interact with Sequ  
 ; OTHER INFORMATION: in this patent.  
 US-09-572-404B-1035

Query Match 33.3%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
 Db 3 LPVV 6

## RESULT 36

US-09-572-404B-1109  
 ; Sequence 1109, Application US/09572404B  
 ; Publication No. US20030078374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProPatent version 1.0  
 ; SEQ ID NO 1109  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in BONZO OR STRL33 OR TYMSTR at 197-206 and m  
 ; OTHER INFORMATION: interact with Sequence 1110 in this patent.  
 US-09-572-404B-1109

Query Match 33.3%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6  
|||||  
Db 4 FFLP 7

## RESULT 37

US-09-895-298-138  
; Sequence 138, Application US/09895298  
; Publication No. US20030078405A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 47 Human Secreted Proteins  
; FILE REFERENCE: P2035P1  
; CURRENT APPLICATION NUMBER: US/09/895,298  
; CURRENT FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: 09/591,16  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: PCT/US99/29950  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: 60/113,006  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/112,809  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 138  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-895-298-138

Query Match 33.3%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
|||||  
Db 3 NVLP 6

## RESULT 38

US-09-932-165-388  
; Sequence 388, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 388  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-388

Query Match 33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LFFF 4  
|||||  
Db 7 LFFF 10

## RESULT 39

US-09-932-165-553  
; Sequence 553, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 553  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-553

## Query Match

Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4  
|||||  
Db 7 LFFF 10

## RESULT 40

US-09-932-165-558  
; Sequence 558, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1



; SEQ ID NO 558

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-558

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 3 LFFF 6

RESULT 41

US-09-932-165-751

; Sequence 751, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AVA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 751

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-751

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 3 LFFF 6

RESULT 42

US-09-932-165-1369

; Sequence 1369, Application US/09932165

; Publication No. US20030134784A1

; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY

; APPLICANT: SAFFRAN, DOUGLAS

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE

; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITS, AVA

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER

; FILE REFERENCE: 51158-20014.00

; CURRENT APPLICATION NUMBER: US/09/932,165

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/226,329

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 1508

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1369

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1369

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4

|||

Db 1 LFFF 4

RESULT 43

US-09-833-039-129

; Sequence 129, Application US/09833039

; Publication No. US20030175960A1

; GENERAL INFORMATION:

; APPLICANT: Tureci, Ozlem

; APPLICANT: Sahin, Ugur

; APPLICANT: Pfrendschuh, Michael

; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

; FILE REFERENCE: LUD 5622.1

; CURRENT APPLICATION NUMBER: US/09/833,039

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: US 09/409,455

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: US 09/344,040

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 09/105,839

; PRIOR FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 08/851,130

; PRIOR FILING DATE: 1997-05-05

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 129

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-833-039-129

Query Match

33.3%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred.No. 7.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7

|||

Db 5 FLPV 8

RESULT 44

US-10-231-417-614

; Sequence 614, Application US/10231417

; Publication No. US20030176681A1

; GENERAL INFORMATION:

; APPLICANT: Feng et al.

; TITLE OF INVENTION: 148 Human Secreted Proteins

; FILE REFERENCE: P2019P1

; CURRENT APPLICATION NUMBER: US/10/231,417

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: US/09/296,622

; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 619  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 614  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-231-417-614

Query Match 33.3%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 5 FFPL 8

RESULT 45  
US-10-200-708-295  
; Sequence 295, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 295  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-295

Query Match 33.3%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
Db 4 NVLP 7

RESULT 46  
US-10-200-708-318  
; Sequence 318, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 318  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-318

Query Match 33.3%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
Db 6 NVLP 9

RESULT 47  
US-10-177-277-129  
; Sequence 129, Application US/10177277  
; Publication No. US20030185844A1  
; GENERAL INFORMATION:  
; APPLICANT: Tureci, Ozlem  
; APPLICANT: Sahin, Ugur  
; APPLICANT: Pfreundschuh, Michael  
; APPLICANT: Ramensee, Hans Georg  
; APPLICANT: Stevanovic, Stefan  
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene  
; TITLE OF INVENTION: Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene  
; FILE REFERENCE: LUD 5556.1  
; CURRENT APPLICATION NUMBER: US/10/177,277  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US/09/344,040  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/105,839  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: US 08/851,130  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 129  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-177-277-129

Query Match 33.3%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7  
Db 5 FLPV 8

RESULT 48  
US-09-573-822C-403  
; Sequence 403, Application US/09573822C  
; Publication No. US20030199011A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome  
; FILE REFERENCE: Microbe patent  
; CURRENT APPLICATION NUMBER: US/09/573,822C  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 804  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 403  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: mycoplasma genitalium  
; FEATURE:  
; OTHER INFORMATION: Sequence located in MG130 at 207-216 and may interact with Seq  
; OTHER INFORMATION: in this patent.  
US-09-573-822C-403

Query Match 33.3%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VVNL 11  
|  
|  
|  
Db 4 VVNL 7

## RESULT 49

US-10-057-763-1  
; Sequence 1, Application US/10057763  
; Publication No. US20020155184A1  
; GENERAL INFORMATION:  
; APPLICANT: IZEVIGIE, ERNEST B.  
; TITLE OF INVENTION: PHYTOCHEMOTHERAPY FOR CANCER  
; FILE REFERENCE: 11428.0003.NFUS01 (JASU003)  
; CURRENT APPLICATION NUMBER: US/10/057,763  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/264,035  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Vernonia amygdalina  
US-10-057-763-1

Query Match 33.3%; Score 4; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNV 10  
|  
|  
|  
Db 5 VVNV 8

## RESULT 50

US-09-828-708-79  
; Sequence 79, Application US/09828708  
; Patent No. US20020146753A1  
; GENERAL INFORMATION:  
; APPLICANT: Ditzel, H.  
; APPLICANT: Burton, D.  
; APPLICANT: Schaller, M.  
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici  
; TITLE OF INVENTION: autoimmune disease  
; FILE REFERENCE: 1361.005US1  
; CURRENT APPLICATION NUMBER: US/09/828,708  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-828-708-79

Query Match 33.3%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNV 10  
|  
|  
|  
Db 6 VVNV 9

## RESULT 51

US-10-057-789-218  
; Sequence 218, Application US/10057789  
; Publication No. US20030082522A1

; GENERAL INFORMATION:  
; APPLICANT: Paul Haynes  
; APPLICANT: Jing Wei  
; APPLICANT: John Yates  
; APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES  
; FILE REFERENCE: NADII.022A  
; CURRENT APPLICATION NUMBER: US/10/057,789  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 218  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 9  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-057-789-218

Query Match 33.3%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLP 6  
|  
|  
|  
Db 5 FFLP 8

## RESULT 52

US-10-212-628-218  
; Sequence 218, Application US/10212628  
; Publication No. US20030087329A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul Haynes  
; APPLICANT: Jing Wei  
; APPLICANT: John Yates  
; APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES  
; FILE REFERENCE: NADII.022CP1  
; CURRENT APPLICATION NUMBER: US/10/212,628  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 10/057,789  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 218  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 9  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-212-628-218

Query Match 33.3%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLP 6  
|  
|  
|

Db 5 FFLP 8

## RESULT 53

US-10-116-252-22  
; Sequence 22, Application US/10116252  
; Publication No. US20030028008A1

; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,  
; Polypeptides, and Antibodies  
; FILE REFERENCE: PCT/JP  
; CURRENT APPLICATION NUMBER: US/10/116,252  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: US/09/711,909  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: PCT/US00/13737  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 60/135,167  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 60/143,616  
; PRIOR FILING DATE: 1999-07-13  
; PRIOR APPLICATION NUMBER: 60/152,934  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: 60/189,029  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-116-252-22

## Query Match

Best Local Similarity 33.3%; Score 4; DB 15; Length 13;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6

Db 4 FFLP 7

## RESULT 54

US-09-853-080-32  
; Sequence 32, Application US/09853080  
; Patent No. US20020068303A1

; GENERAL INFORMATION:  
; APPLICANT: Laub, Ruth  
; TITLE OF INVENTION: ANTIGENIC POLYPEPTIDE SEQUENCES OF FACTOR  
; VIII, FRAGMENTS AND/OR EPITOPES OF THESE SEQUENCES  
; FILE REFERENCE: VANWA48.001CPI  
; CURRENT APPLICATION NUMBER: US/09/853,080  
; CURRENT FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: US 08/765,837  
; PRIOR FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: PCT/BE95/00068  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: BE 9400666  
; PRIOR FILING DATE: 1994-07-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: epitope Pro 2292 to Tyr 2305 of C domain of Factor  
; OTHER INFORMATION: VIII  
US-09-853-080-32

## Query Match

33.3%; Score 4; DB 9; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVTN 9

Db 1 PVTN 4

## RESULT 55

US-09-767-460-12  
; Sequence 12, Application US/09767460  
; Patent No. US20020009756A1  
; GENERAL INFORMATION:  
; APPLICANT: Mandell, Arnold  
; APPLICANT: Seitz, Karen  
; APPLICANT: Shlesinger, Michael  
; TITLE OF INVENTION: Algorithms Design of Peptides for Binding and/or Modulation o  
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
; FILE REFERENCE: 01561-0002-CPUS01  
; CURRENT APPLICATION NUMBER: US/09/767,460  
; CURRENT FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-767-460-12

## Query Match

33.3%; Score 4; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11

Db 10 VNVL 13

## RESULT 56

US-09-981-876-224  
; Sequence 224, Application US/09981876  
; Patent No. US20020164669A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: PZ001P1  
; CURRENT APPLICATION NUMBER: US/09/981,876  
; CURRENT FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 09/148,545  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,161  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597

|     |                                      |     |                                      |
|-----|--------------------------------------|-----|--------------------------------------|
| 1   | PRIOR FILING DATE: 1997-05-23        | 2   | PRIOR APPLICATION NUMBER: 60/056,630 |
| 3   | PRIOR APPLICATION NUMBER: 60/047,502 | 4   | PRIOR FILING DATE: 1997-08-22        |
| 5   | PRIOR FILING DATE: 1997-05-23        | 6   | PRIOR APPLICATION NUMBER: 60/056,878 |
| 7   | PRIOR APPLICATION NUMBER: 60/047,633 | 8   | PRIOR FILING DATE: 1997-08-22        |
| 9   | PRIOR FILING DATE: 1997-05-23        | 10  | PRIOR APPLICATION NUMBER: 60/056,662 |
| 11  | PRIOR APPLICATION NUMBER: 60/047,583 | 12  | PRIOR FILING DATE: 1997-08-22        |
| 13  | PRIOR FILING DATE: 1997-05-23        | 14  | PRIOR APPLICATION NUMBER: 60/047,617 |
| 15  | PRIOR APPLICATION NUMBER: 60/047,618 | 16  | PRIOR FILING DATE: 1997-08-22        |
| 17  | PRIOR FILING DATE: 1997-05-23        | 18  | PRIOR APPLICATION NUMBER: 60/056,882 |
| 19  | PRIOR APPLICATION NUMBER: 60/047,503 | 20  | PRIOR FILING DATE: 1997-08-22        |
| 21  | PRIOR FILING DATE: 1997-05-23        | 22  | PRIOR APPLICATION NUMBER: 60/056,637 |
| 23  | PRIOR APPLICATION NUMBER: 60/047,592 | 24  | PRIOR FILING DATE: 1997-08-22        |
| 25  | PRIOR FILING DATE: 1997-05-23        | 26  | PRIOR APPLICATION NUMBER: 60/056,903 |
| 27  | PRIOR APPLICATION NUMBER: 60/047,581 | 28  | PRIOR FILING DATE: 1997-08-22        |
| 29  | PRIOR FILING DATE: 1997-05-23        | 30  | PRIOR APPLICATION NUMBER: 60/056,888 |
| 31  | PRIOR APPLICATION NUMBER: 60/047,584 | 32  | PRIOR FILING DATE: 1997-08-22        |
| 33  | PRIOR FILING DATE: 1997-05-23        | 34  | PRIOR APPLICATION NUMBER: 60/056,879 |
| 35  | PRIOR APPLICATION NUMBER: 60/047,500 | 36  | PRIOR FILING DATE: 1997-08-22        |
| 37  | PRIOR FILING DATE: 1997-05-23        | 38  | PRIOR APPLICATION NUMBER: 60/056,894 |
| 39  | PRIOR APPLICATION NUMBER: 60/047,587 | 40  | PRIOR FILING DATE: 1997-08-22        |
| 41  | PRIOR FILING DATE: 1997-05-23        | 42  | PRIOR APPLICATION NUMBER: 60/056,911 |
| 43  | PRIOR APPLICATION NUMBER: 60/047,492 | 44  | PRIOR FILING DATE: 1997-08-22        |
| 45  | PRIOR FILING DATE: 1997-05-23        | 46  | PRIOR APPLICATION NUMBER: 60/056,636 |
| 47  | PRIOR APPLICATION NUMBER: 60/047,598 | 48  | PRIOR FILING DATE: 1997-08-22        |
| 49  | PRIOR FILING DATE: 1997-05-23        | 50  | PRIOR APPLICATION NUMBER: 60/056,874 |
| 51  | PRIOR APPLICATION NUMBER: 60/047,613 | 52  | PRIOR FILING DATE: 1997-08-22        |
| 53  | PRIOR FILING DATE: 1997-05-23        | 54  | PRIOR APPLICATION NUMBER: 60/056,880 |
| 55  | PRIOR APPLICATION NUMBER: 60/047,582 | 56  | PRIOR FILING DATE: 1997-08-22        |
| 57  | PRIOR FILING DATE: 1997-05-23        | 58  | PRIOR APPLICATION NUMBER: 60/056,894 |
| 59  | PRIOR APPLICATION NUMBER: 60/047,596 | 60  | PRIOR FILING DATE: 1997-08-22        |
| 61  | PRIOR FILING DATE: 1997-05-23        | 62  | PRIOR APPLICATION NUMBER: 60/056,864 |
| 63  | PRIOR APPLICATION NUMBER: 60/047,612 | 64  | PRIOR FILING DATE: 1997-08-22        |
| 65  | PRIOR FILING DATE: 1997-05-23        | 66  | PRIOR APPLICATION NUMBER: 60/056,631 |
| 67  | PRIOR APPLICATION NUMBER: 60/047,632 | 68  | PRIOR FILING DATE: 1997-08-22        |
| 69  | PRIOR FILING DATE: 1997-05-23        | 70  | PRIOR APPLICATION NUMBER: 60/056,845 |
| 71  | PRIOR APPLICATION NUMBER: 60/047,601 | 72  | PRIOR FILING DATE: 1997-08-22        |
| 73  | PRIOR FILING DATE: 1997-05-23        | 74  | PRIOR APPLICATION NUMBER: 60/056,892 |
| 75  | PRIOR APPLICATION NUMBER: 60/047,612 | 76  | PRIOR FILING DATE: 1997-08-22        |
| 77  | PRIOR FILING DATE: 1997-05-23        | 78  | PRIOR APPLICATION NUMBER: 60/047,595 |
| 79  | PRIOR APPLICATION NUMBER: 60/047,632 | 80  | PRIOR FILING DATE: 1997-05-23        |
| 81  | PRIOR FILING DATE: 1997-05-23        | 82  | PRIOR APPLICATION NUMBER: 60/057,761 |
| 83  | PRIOR APPLICATION NUMBER: 60/047,580 | 84  | PRIOR FILING DATE: 05-Sep-1997       |
| 85  | PRIOR FILING DATE: 1997-04-11        | 86  | PRIOR APPLICATION NUMBER: 60/047,599 |
| 87  | PRIOR APPLICATION NUMBER: 60/043,314 | 88  | PRIOR FILING DATE: 1997-05-23        |
| 89  | PRIOR FILING DATE: 1997-04-11        | 90  | PRIOR APPLICATION NUMBER: 60/047,588 |
| 91  | PRIOR APPLICATION NUMBER: 60/043,569 | 92  | PRIOR FILING DATE: 1997-05-23        |
| 93  | PRIOR FILING DATE: 1997-04-11        | 94  | PRIOR APPLICATION NUMBER: 60/047,585 |
| 95  | PRIOR APPLICATION NUMBER: 60/043,311 | 96  | PRIOR FILING DATE: 1997-05-23        |
| 97  | PRIOR FILING DATE: 1997-04-11        | 98  | PRIOR APPLICATION NUMBER: 60/047,586 |
| 99  | PRIOR APPLICATION NUMBER: 60/043,671 | 100 | PRIOR FILING DATE: 1997-05-23        |
| 101 | PRIOR FILING DATE: 1997-04-11        | 102 | PRIOR APPLICATION NUMBER: 60/047,590 |
| 103 | PRIOR APPLICATION NUMBER: 60/043,674 | 104 | PRIOR FILING DATE: 1997-05-23        |
| 105 | PRIOR FILING DATE: 1997-04-11        | 106 | PRIOR APPLICATION NUMBER: 60/047,594 |
| 107 | PRIOR APPLICATION NUMBER: 60/043,669 | 108 | PRIOR FILING DATE: 1997-05-23        |
| 109 | PRIOR FILING DATE: 1997-04-11        | 110 | PRIOR APPLICATION NUMBER: 60/047,589 |
| 111 | PRIOR APPLICATION NUMBER: 60/043,312 | 112 | PRIOR FILING DATE: 1997-05-23        |
| 113 | PRIOR FILING DATE: 1997-04-11        | 114 | PRIOR APPLICATION NUMBER: 60/047,593 |
| 115 | PRIOR APPLICATION NUMBER: 60/043,313 | 116 | PRIOR FILING DATE: 1997-05-23        |
| 117 | PRIOR FILING DATE: 1997-04-11        | 118 | PRIOR APPLICATION NUMBER: 60/047,614 |
| 119 | PRIOR APPLICATION NUMBER: 60/043,672 | 120 | PRIOR FILING DATE: 1997-05-23        |
| 121 | PRIOR FILING DATE: 1997-04-11        | 122 | PRIOR APPLICATION NUMBER: 60/043,578 |
| 123 | PRIOR APPLICATION NUMBER: 60/043,315 | 124 | PRIOR FILING DATE: 1997-04-11        |
| 125 | PRIOR FILING DATE: 1997-04-11        | 126 | PRIOR APPLICATION NUMBER: 60/043,576 |
| 127 | PRIOR APPLICATION NUMBER: 60/048,974 | 128 | PRIOR FILING DATE: 1997-04-11        |
| 129 | PRIOR FILING DATE: 1997-06-06        | 130 | PRIOR APPLICATION NUMBER: 60/047,501 |
| 131 | PRIOR APPLICATION NUMBER: 60/056,886 | 132 | PRIOR FILING DATE: 1997-05-23        |
| 133 | PRIOR FILING DATE: 1997-08-22        | 134 | PRIOR APPLICATION NUMBER             |

```
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 15

Query Match 33.3%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03; 0; Indels
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 FFFL 5
 |||||
Db 8 FFFL 11

RESULT 57
US-09-148-545-224
; Sequence 224, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
```

; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 05-Sep-1997  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 280  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 224  
; LENGTH: 15

Query Match 33.3%; Score 4; DB 11; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 2 FPFL 5  
|||  
Db 8 FPFL 11

## RESULT 58

US-10-336-491-6  
; Sequence 6, Application US/10336491  
; Publication No. US20030148464A1  
; GENERAL INFORMATION:  
; APPLICANT: Hjort, Carsten M.  
; APPLICANT: Pedersen, Henrik  
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells  
; FILE REFERENCE: 5789.200-US  
; CURRENT APPLICATION NUMBER: US/10/336,491  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US/09/501,612  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Aspergillus niger  
US-10-336-491-6

Query Match 33.3%; Score 4; DB 12; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVVN 9  
|||  
Db 6 PVVN 9

## RESULT 59

US-09-986-480-261  
; Sequence 261, Application US/09986480  
; Publication No. US20030027999A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 143 Human Secreted Proteins  
; FILE REFERENCE: PS500P1  
; CURRENT APPLICATION NUMBER: US/09/986,480  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: PCT/US00/12788  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/134,068  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 456  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 261

```
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-480-261

Query Match 33.3%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFP 4
Db 10 LFFP 13

RESULT 60
US-09-071-838-88
; Sequence 88, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yagagari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-88

Query Match 33.3%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLL 6
Db 10 FFLL 13

RESULT 61
US-09-981-876-221
; Sequence 221, Application US/09981876
; Patent No. US20020164669A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
```



; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,669  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,312  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,313  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 05-Sep-1997  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 280  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 221  
; LENGTH: 17

Query Match 33.3%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 LFFF 4  
Db 6 LFFF 9

## RESULT 62

US-09-148-545-221  
; Sequence 221, Application US/09148545  
; Publication No. US20030027132A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 70 Human Secreted Proteins  
; FILE REFERENCE: P2001P1  
; CURRENT APPLICATION NUMBER: US/09/148,545  
; CURRENT FILING DATE: 1998-09-04  
; EARLIER APPLICATION NUMBER: PCT/US98/04482

[illegible]

; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,594  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,589  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,593  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,614  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/043,578  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/043,576  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/047,501  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/043,670  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/056,632  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,664  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,876  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,881  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,909  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,875  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,862  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,887  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/056,908  
 ; EARLIER FILING DATE: 1997-08-22  
 ; EARLIER APPLICATION NUMBER: 60/048,964  
 ; EARLIER FILING DATE: 1997-06-06  
 ; EARLIER APPLICATION NUMBER: 60/057,650  
 ; EARLIER FILING DATE: 1997-09-05  
 ; EARLIER APPLICATION NUMBER: 60/056,884  
 ; EARLIER FILING DATE: 1997-08-22  
 ; NUMBER OF SEQ ID NOS: 280  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 221  
 ; LENGTH: 17

Query Match 33.3%; Score 4; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4  
 Db 6 LFFF 9

## RESULT 63

US-09-996-069-30  
 ; Sequence 30, Application US/09996069  
 ; Publication No. US20030036199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bamdad, Cynthia  
 ; APPLICANT: Bamdad, R. Shoshana  
 ; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI  
 ; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER  
 ; FILE REFERENCE: M01015/70071  
 ; CURRENT APPLICATION NUMBER: US/09/996,069  
 ; CURRENT FILING DATE: 2001-11-27  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 30  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

## US-09-996-069-30

Query Match 33.3%; Score 4; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12  
 Db 5 NVLP 8

## RESULT 64

US-09-996-069-31  
 ; Sequence 31, Application US/09996069  
 ; Publication No. US20030036199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bamdad, Cynthia  
 ; APPLICANT: Bamdad, R. Shoshana  
 ; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INH  
 ; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER  
 ; FILE REFERENCE: M01015/70071  
 ; CURRENT APPLICATION NUMBER: US/09/996,069  
 ; CURRENT FILING DATE: 2001-11-27  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 31  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-069-31

Query Match 33.3%; Score 4; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12  
 Db 5 NVLP 8

## RESULT 65

US-10-213-512-88  
 ; Sequence 88, Application US/10213512  
 ; Publication No. US20030110536A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer, Robert L.  
 ; APPLICANT: Ohad, Nir  
 ; APPLICANT: Kiyosue, Tomohiro  
 ; APPLICANT: Yadegari, Ramin  
 ; APPLICANT: Margossian, Linda  
 ; APPLICANT: Harada, John  
 ; APPLICANT: Goldberg, Robert B.  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
 ; TITLE OF INVENTION: Fruit Development in Plants  
 ; FILE REFERENCE: 023070-086110US  
 ; CURRENT APPLICATION NUMBER: US/10/213,512  
 ; CURRENT FILING DATE: 2002-08-06  
 ; PRIOR APPLICATION NUMBER: US/09/177,206  
 ; PRIOR FILING DATE: 1998-10-22  
 ; PRIOR APPLICATION NUMBER: US 09/071,838  
 ; PRIOR FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 324  
 ; SOFTWARE: PatentIn ver. 2.0  
 ; SEQ ID NO 88  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis sp.  
 US-10-213-512-88

Query Match 33.3%; Score 4; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6  
|||  
Db 10 FFLP 13

## RESULT 66

US-10-084-813-248  
; Sequence 248, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 248  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-248

Query Match 33.3%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6  
|||  
Db 12 FFLP 15

## RESULT 67

US-10-084-813-249  
; Sequence 249, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 249  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-249

Query Match 33.3%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6  
|||  
Db 8 FFLP 11

## RESULT 68

US-10-084-813-250  
; Sequence 250, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 250  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-250

Query Match 33.3%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6  
|||  
Db 4 FFLP 7

## RESULT 69

US-10-157-031-192  
; Sequence 192, Application US/10157031  
; Publication No. US20030108890A1  
; GENERAL INFORMATION:  
; APPLICANT: Baranova, A. V.  
; APPLICANT: Yankovsky, N. K.  
; APPLICANT: Kozlov, A. P.  
; APPLICANT: Lobashev, A. V.  
; APPLICANT: Krukovskaya, L. L.  
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequenc  
; FILE REFERENCE: 2760-103  
; CURRENT APPLICATION NUMBER: US/10/157,031  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 415  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 192  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-031-192

Query Match 33.3%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VNVL 11  
|||  
Db 3 VNVL 6

## RESULT 70

US-10-106-698-7294  
; Sequence 7294, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept

```

; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7294
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-10-106-698-7294

```

```

Query Match 33.3%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 FFFL 5
 ||||
Db 6 FFFL 9

```

```

RESULT 71
US-10-225-567A-1666
; Sequence 1666, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 2000-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1666
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1666

```

```

Query Match 33.3%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 VVNV 10
 ||||
Db 6 VVNV 9

```

```

RESULT 72
US-08-464-363-29

```

```

; Sequence 29, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-464-363-29

```

```

Query Match 33.3%; Score 4; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 LPVV 8
 ||||
Db 15 LPVV 18

```

```

RESULT 73
US-09-864-761-35505
; Sequence 35505, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

```

; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 35505  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AFI46367.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.9  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.8  
; OTHER INFORMATION: EST\_HUMAN HIT: A1820784.1, EVALUE 9.00e-06  
US-09-864-761-35505

Query Match 33.3%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 FLPV 7  
Db 8 FLPV 11

RESULT 74  
US-09-735-705-405  
; Sequence 405; Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Ligu  
; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Panger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Panger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 405  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-405  
Query Match 33.3%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 VVNV 10  
Db 2 VVNV 5  
RESULT 75  
US-09-841-132-156  
; Sequence 156; Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 156  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-156

Query Match 33.3%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 FFLP 6  
Db 10 FFLP 13

Search completed: November 25, 2003, 20:25:29  
Job time : 24.8723 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 13.0851 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-4  
Perfect score: 12  
Sequence: 1 LFFFLPVNVLP 12

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 12    | 100.0       | 12     | 4     | US-09-641-803-4   |
| 2          | 5     | 41.7        | 5      | 2     | US-08-920-162A-30 |
| 3          | 5     | 41.7        | 5      | 3     | US-09-356-931-30  |
| 4          | 5     | 41.7        | 11     | 1     | US-08-552-907-16  |
| 5          | 5     | 41.7        | 11     | 1     | US-08-464-531-57  |
| 6          | 5     | 41.7        | 11     | 2     | US-08-461-598-57  |
| 7          | 5     | 41.7        | 11     | 3     | US-08-691-045-16  |
| 8          | 5     | 41.7        | 11     | 3     | US-08-322-137-57  |
| 9          | 5     | 41.7        | 11     | 3     | US-08-582-333A-68 |
| 10         | 5     | 41.7        | 20     | 1     | US-08-468-543-23  |
| 11         | 5     | 41.7        | 20     | 2     | US-08-469-692-23  |
| 12         | 5     | 41.7        | 20     | 2     | US-08-398-046-23  |
| 13         | 4     | 33.3        | 5      | 2     | US-08-920-162A-24 |
| 14         | 4     | 33.3        | 5      | 2     | US-08-920-162A-25 |
| 15         | 4     | 33.3        | 5      | 2     | US-08-920-162A-26 |
| 16         | 4     | 33.3        | 5      | 3     | US-09-356-931-24  |
| 17         | 4     | 33.3        | 5      | 3     | US-09-356-931-25  |
| 18         | 4     | 33.3        | 5      | 3     | US-09-356-931-26  |
| 19         | 4     | 33.3        | 5      | 4     | US-08-703-675C-24 |
| 20         | 4     | 33.3        | 5      | 4     | US-08-703-675C-25 |
| 21         | 4     | 33.3        | 5      | 4     | US-08-703-675C-26 |
| 22         | 4     | 33.3        | 5      | 4     | US-08-236-160-17  |
| 23         | 4     | 33.3        | 5      | 4     | US-09-236-160-52  |
| 24         | 4     | 33.3        | 6      | 1     | US-08-257-782-28  |
| 25         | 4     | 33.3        | 6      | 1     | US-08-257-782-31  |
| 26         | 4     | 33.3        | 6      | 1     | US-08-257-782-33  |
| 27         | 4     | 33.3        | 6      | 1     | US-07-807-529A-13 |

ALIGNMENTS

RESULT 1  
US-09-641-803-4  
; Sequence 4, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-4

Query Match 100.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LFFFLPVNVLP 12  
Db 1 LFFFLPVNVLP 12

RESULT 2  
US-08-920-162A-30  
; Sequence 30, Application US/08920162A  
; Patent No. 5985242  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide  
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/920,162A  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/703,675

; FILING DATE: 27-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 21-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KARA, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified site  
; LOCATION: 1-5  
; OTHER INFORMATION: /note= D amino acid  
US-08-920-162A-30  
  
Query Match 41.7%; Score 5; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LFFFL 5  
Db 1 LFFFL 5  
  
RESULT 3  
US-09-356-931-30  
; Sequence 30, Application US/09356931  
; Patent No. 6277826  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1784  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/356,931  
; FILING DATE: 19-JUL-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/920,162  
; FILING DATE: 27-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/897,342  
; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/703,675  
; FILING DATE: 27-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:



; NAME: DeConti, Jr., Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PFI-016CP4CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified site  
; LOCATION: 1-5  
; OTHER INFORMATION: /note= D amino acid  
US-09-356-931-30

Query Match 41.7%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFFL 5  
Db 1 LFFFL 5

## RESULT 4

US-08-552-907-16  
; Sequence 16, Application US/08552907  
; Patent No. 5744299  
; GENERAL INFORMATION:  
; APPLICANT: Henrickson, Kelly J.  
; APPLICANT: Fan, Jiang (n.m.i.)  
; TITLE OF INVENTION: HUMAN PARAINFLUENZA VIRUS-1 ASSAY  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/552,907  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 650053.91037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5000  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-552-907-16

Query Match 41.7%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VNVVL 11

Db 7 VNVVL 11

## RESULT 5

US-08-464-531-57  
; Sequence 57, Application US/08464531  
; Patent No. 5789184  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: BROACH, Jim  
; APPLICANT: MANFREDI, John  
; APPLICANT: KLEIN, Christine  
; APPLICANT: MURPHY, Andrew J.  
; APPLICANT: PAUL, Jeremy  
; APPLICANT: TRUEHEART, Joshua  
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE  
; NUMBER OF SEQUENCES: 119  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,531  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/322,137  
; FILING DATE: 13-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/309,313  
; FILING DATE: 20-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,328  
; FILING DATE: 31-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/041,431  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOLWKS=2G  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-464-531-57

Query Match 41.7%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6  
Db 6 FFFLP 10

## RESULT 6

```

US-08-461-598-57
; Sequence 57, Application US/08461598
; Patent No. 5876951
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,598
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-598-57
Query Match 41.7%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFFLP 6
Db 6 PFFLP 10

RESULT 7
US-08-691-045-16
; Sequence 16, Application US/08691045
; Patent No. 6015664
; GENERAL INFORMATION:
; APPLICANT: Henrickson, Kelly J.

```

```

; APPLICANT: Fan, Jiang (n.m.i.)
; TITLE OF INVENTION: VIRUS ASSAY METHOD
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,045
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.91037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-045-16
Query Match 41.7%; Score 5; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VNVNL 11
Db 7 VNVNL 11

RESULT 8
US-08-322-137-57
; Sequence 57, Application US/08322137
; Patent No. 6100042
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,137

```

; FILING DATE: 13-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/309,313  
; FILING DATE: 20-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,328  
; FILING DATE: 31-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/041,431  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOLWKES=2C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-322-137-57

Query Match 41.7%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPLP 6  
Db 6 FFPLP 10

RESULT 9  
US-08-582-333A-68  
; Sequence 68, Application US/08582333A  
; Patent No. 625059  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; TITLE OF INVENTION: Methods and Compositions for  
; IDENTIFYING RECEPTOR EFFECTORS  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/582,333A  
; FILING DATE: 17-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Catherine J. Kara  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: CPI-012CP5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-4214  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-582-333A-68

Query Match 41.7%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFPLP 6  
Db 6 FFPLP 10

RESULT 10  
US-08-468-543-23  
; Sequence 23, Application US/08468543  
; Patent No. 5726153  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Robert S. et al.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,543  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/398,046  
; FILING DATE: 02-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,057  
; FILING DATE: 24-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/048,569  
; FILING DATE: 16-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/694,929  
; FILING DATE: 02-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,215  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,142  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/189,130  
; FILING DATE: 02-MAY-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 04547/002003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-468-543-23

Query Match 41.7%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10  
Db 11 PVNV 15

RESULT 11  
US-08-469-692-23  
; Sequence 23, Application US/08469692  
; Patent No. 5955055  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Robert S. et al.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,692  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/398,046  
; FILING DATE: 02-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,057  
; FILING DATE: 24-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/048,569  
; FILING DATE: 16-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/694,929  
; FILING DATE: 02-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,215  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,142  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/189,130  
; FILING DATE: 02-MAY-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 04547/002002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-469-692-23

Query Match 41.7%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 38;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PVNV 10  
Db 11 PVNV 15

RESULT 12  
US-08-398-046-23  
; Sequence 23, Application US/08398046  
; Patent No. 5972890  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Robert S. et al.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR  
; TITLE OF INVENTION: ARTERIAL IMAGING  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,046  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/201,057  
; FILING DATE:  
; APPLICATION NUMBER: US/08/048,569  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/694,929  
; FILING DATE: May 3, 1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/517,215  
; FILING DATE: May 3, 1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/518,142  
; FILING DATE: May 3, 1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/189,130  
; FILING DATE: May 2, 1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 04547/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-398-046-23

Query Match 41.7%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVNV 10  
Db 11 PVNV 15

RESULT 13



```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-7401
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-08-920-162A-26

Query Match 33.3%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
DB 2 FFFL 5

RESULT 16
US-09-356-931-24
; Sequence 24, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342
; FILING DATE: 21-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Jr., Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1-5
; OTHER INFORMATION: /note= D amino acid
; US-09-356-931-24

Query Match 33.3%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
DB 1 FFFL 4

RESULT 17
US-09-356-931-25
; Sequence 25, Application US/09356931
; Patent No. 6277826
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1784
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/356,931
; FILING DATE: 19-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/920,162
; FILING DATE: 27-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,342

```

; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA: USN 08/703,675  
; FILING DATE: 27-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/616,081  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Jr., Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified site  
; LOCATION: 1-5  
; OTHER INFORMATION: /note= D amino acid  
; US-09-356-931-25

Query Match 33.3%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 2 FFPL 5

RESULT 18  
US-09-356-931-26  
; Sequence 26, Application US/09356931  
; Patent No. 6277826  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1784  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/356,931  
; FILING DATE: 19-JUL-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/920,162  
; FILING DATE: 27-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/897,342  
; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/703,675  
; FILING DATE: 27-AUG-1996  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USN 08/616,081  
; FILING DATE: 14-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Jr., Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-016CP4CN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified site  
; LOCATION: 1-5  
; OTHER INFORMATION: /note= D amino acid  
; US-09-356-931-26

Query Match 33.3%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 2 FFPL 5

RESULT 19  
US-08-703-675C-24  
; Sequence 24, Application US/08703675C  
; Patent No. 6303567  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, Mark A. et al.  
; TITLE OF INVENTION: Modulators of -Amyloid Peptide  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/703,675C  
; FILING DATE: 27-AUG-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/616,081  
; FILING DATE: 14-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
US-08-703-675C-24

Query Match 33.3%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFFL 5  
Db 1 PFFL 4

## RESULT 20

US-08-703-675C-25  
Sequence 25, Application US/08703675C  
Patent No. 6303567

## GENERAL INFORMATION:

APPLICANT: Findexis, Mark A. et al.  
TITLE OF INVENTION: Modulators of -Amyloid Peptide  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/703.675C

FILING DATE: 27-AUG-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/616,081

FILING DATE: 14-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kara, Catherine J.

REGISTRATION NUMBER: 41,106

REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

Aggregation Comprising D-

FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-5  
OTHER INFORMATION: /note= D amino acid  
US-08-703-675C-25

Query Match 33.3%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFFL 5  
Db 2 PFFL 5

## RESULT 21

US-08-703-675C-26

Sequence 26, Application US/08703675C

Patent No. 6303567

## GENERAL INFORMATION:

APPLICANT: Findexis, Mark A. et al.

TITLE OF INVENTION: Modulators of -Amyloid Peptide

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/703.675C

FILING DATE: 27-AUG-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/616,081

FILING DATE: 14-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kara, Catherine J.

REGISTRATION NUMBER: 41,106

REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified site

LOCATION: 1-5

OTHER INFORMATION: /note= D amino acid

US-08-703-675C-26

Query Match 33.3%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 2 FFPL 5  
Db 2 FFPL 5

## RESULT 22

US-09-236-160-17  
; Sequence 17, Application US/09236160A  
; Patent No. 6307090  
; GENERAL INFORMATION:  
; APPLICANT: BURKE Jr., Terrence R.  
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL  
; TITLE OF INVENTION: INHIBITING ACTIVITY  
; FILE REFERENCE: 175895  
; CURRENT APPLICATION NUMBER: US/09/236,160A  
; CURRENT FILING DATE: 1999-01-22  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: mammalian  
US-09-236-160-17

Query Match 33.3%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11  
Db 1 VNVL 4

## RESULT 23

US-09-236-160-52  
; Sequence 52, Application US/09236160A  
; Patent No. 6307090  
; GENERAL INFORMATION:  
; APPLICANT: BURKE Jr., Terrence R.  
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL  
; TITLE OF INVENTION: INHIBITING ACTIVITY  
; FILE REFERENCE: 175895  
; CURRENT APPLICATION NUMBER: US/09/236,160A  
; CURRENT FILING DATE: 1999-01-22  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: mammalian  
US-09-236-160-52

Query Match 33.3%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11  
Db 1 VNVL 4

## RESULT 24

US-08-257-782-28  
; Sequence 28, Application US/08257782  
; Patent No. 5480971  
; GENERAL INFORMATION:  
; APPLICANT: Houghten, Richard A.  
; APPLICANT: Ostrech, John M.  
; APPLICANT: Blondelle, Sylvie  
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Welsh & Katz, Ltd.  
; STREET: 135 South LaSalle Street, Suite 1625  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/257,782  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/079,144  
; FILING DATE: 13-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gamson, Edward P.  
; REGISTRATION NUMBER: 29,381  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-781-9470  
; TELEFAX: 312-781-9548  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..6  
; OTHER INFORMATION: /note= "This is a permethylated  
; OTHER INFORMATION: peptide."  
US-08-257-782-28

Query Match 33.3%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4  
Db 1 LFFF 4

## RESULT 25

US-08-257-782-31  
; Sequence 31, Application US/08257782  
; Patent No. 5480971  
; GENERAL INFORMATION:  
; APPLICANT: Houghten, Richard A.  
; APPLICANT: Ostrech, John M.  
; APPLICANT: Blondelle, Sylvie  
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Welsh & Katz, Ltd.  
; STREET: 135 South LaSalle Street, Suite 1625  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/257,782  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:

RESULT 28

US-07-807-529A-53  
; Sequence 53, Application US/07807529A  
; Patent No. 5547669  
; GENERAL INFORMATION:  
; APPLICANT: Rogers, Bruce L.  
; APPLICANT: Morgenstern, Jay  
; APPLICANT: Bond, Julian F.  
; APPLICANT: Garman, Richard D.  
; APPLICANT: Greenstein, Julia L.  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Morville, Malcolm  
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: One Kendall Square, Building 600  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/807,529A  
; FILING DATE: 19911213  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/662,276  
; FILING DATE: 28-FEB-1991  
; APPLICATION NUMBER: US 07/431,565  
; FILING DATE: 03-NOV-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Channing, Stacey L.  
; REGISTRATION NUMBER: 31,095  
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 494-0060  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-07-807-529A-53

Query Match 33.3%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8  
|||  
Db 3 LPVV 6

RESULT 29  
US-08-577-846-28  
; Sequence 28, Application US/08577846  
; Patent No. 5763193  
; GENERAL INFORMATION:  
; APPLICANT: Houghten, Richard A.  
; APPLICANT: Ostrech, John M.  
; APPLICANT: Blondelle, Sylvie  
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Welsh & Katz, Ltd.  
; STREET: 135 South LaSalle Street, Suite 1625  
; CITY: Chicago  
; STATE: Illinois

; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/577,846  
; FILING DATE: 22-DEC-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/257,782  
; FILING DATE: 09-JUN-1994  
; APPLICATION NUMBER: US 08/079,144  
; FILING DATE: 13-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gamson, Edward P.  
; REGISTRATION NUMBER: 29,381  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-781-9470  
; TELEFAX: 312-781-9548  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..6  
; OTHER INFORMATION: /note="This is a permethylated  
; OTHER INFORMATION: peptide."  
US-08-577-846-28

Query Match 33.3%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4  
|||  
Db 1 LFFF 4

RESULT 30  
US-08-577-846-31  
; Sequence 31, Application US/08577846  
; Patent No. 5763193  
; GENERAL INFORMATION:  
; APPLICANT: Houghten, Richard A.  
; APPLICANT: Ostrech, John M.  
; APPLICANT: Blondelle, Sylvie  
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Welsh & Katz, Ltd.  
; STREET: 135 South LaSalle Street, Suite 1625  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/577,846  
; FILING DATE: 22-DEC-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/257,782  
; FILING DATE: 09-JUN-1994

```
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-781-9470
; TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "This is a permethylated
; OTHER INFORMATION: peptide."
US-08-577-846-31

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 31
US-08-577-846-33
; Sequence 33, Application US/08577846
; Patent No. 5763193
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Ostreich, John M.
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: PERALKYLATED OLIGOPEPTIDE MIXTURES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,846
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,782
; FILING DATE: 09-JUN-1994
; APPLICATION NUMBER: US 08/079,144
; FILING DATE: 13-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-781-9470
; TELEFAX: 312-781-9548
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "This is a permethylated
; OTHER INFORMATION: peptide."
US-08-577-846-33

Query Match 33.3%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
Db 1 LFFF 4

RESULT 32
US-08-300-928C-62
; Sequence 62, Application US/08300928C
; Patent No. 6019972
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; TITLE OF INVENTION: PROTEIN (TRPP)
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-300-928C-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 33
US-08-430-944D-62
; Sequence 62, Application US/08430944D
; Patent No. 6025162
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)742-4214
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-430-944D-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 34
US-08-430-014-62
; Sequence 62, Application US/08430014
; Patent No. 6048962
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,014
```

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-430-014-62

Query Match 33.3%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 3 LPVV 6

RESULT 35
US-08-431-184-62
; Sequence 62, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

US-08-431-184-62

Query Match 33.3%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
Db 3 LPVV 6

RESULT 36

US-08-559-492-10  
; Sequence 10, Application US/08559492  
; Patent No. 5843884  
; GENERAL INFORMATION:  
; APPLICANT: Sims, Peter J.  
; TITLE OF INVENTION: C9 Complement Inhibitor  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1201 West Peachtree  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/559,492  
; FILING DATE: 15-NOV-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMR#154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-873-8794  
; TELEFAX: 404-873-8795  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-559-492-10

Query Match 33.3%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFFL 5  
Db 1 PFFL 4

RESULT 37

US-09-561-500-37  
; Sequence 37, Application US/09561500  
; Patent No. 6342219  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Brekken  
; TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF  
; FILE REFERENCE: 4001.002500  
; CURRENT APPLICATION NUMBER: US/09/561,500  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/131,432

; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-09-561-500-37

Query Match 33.3%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
Db 3 LPVV 6

RESULT 38

US-09-561-108-37  
; Sequence 37, Application US/09561108  
; Patent No. 6342221  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Brekken  
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VE  
; FILE REFERENCE: 4001.002584  
; CURRENT APPLICATION NUMBER: US/09/561,108  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/131,432  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-09-561-108-37

Query Match 33.3%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8  
Db 3 LPVV 6

RESULT 39

US-09-561-526-37  
; Sequence 37, Application US/09561526  
; Patent No. 6416758  
; GENERAL INFORMATION:  
; APPLICANT: Philip E. Thorpe  
; APPLICANT: Rolf A. Brekken  
; TITLE OF INVENTION: ANTIBODY  
; FILE REFERENCE: 4001.002586  
; CURRENT APPLICATION NUMBER: US/09/561,526  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/131,432  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-526-37

Query Match 33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 3 LPVV 6

RESULT 40
US-09-561-499-37
; Sequence 37, Application US/09561499
; Patent No. 6524583
; GENERAL INFORMATION:
; APPLICANT: Philip B. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002582
; CURRENT APPLICATION NUMBER: US/09/561,499
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-561-499-37

Query Match 33.3%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 3 LPVV 6

RESULT 41
US-07-807-529A-45
; Sequence 45, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 19911213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-07-807-529A-45

Query Match 33.3%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 6 LPVV 9

RESULT 42
US-08-934-222-106
; Sequence 106, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-106
Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
Db 5 NVLP 8

RESULT 43
US-08-933-402-106
; Sequence 106, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-106
Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
Db 5 NVLP 8

RESULT 44
US-08-933-402-106
; Sequence 106, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-106
Query Match 33.3%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
Db 5 NVLP 8

RESULT 45
US-08-532-818-106
; Sequence 106, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-106

Query Match 33.3%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 NVLP 12  
DB 5 NVLP 8

RESULT 46  
US-08-942-819-9  
Sequence 9, Application US/08942819  
Patent No. 5965707  
GENERAL INFORMATION:  
APPLICANT: Tam, See-Ying  
APPLICANT: Tsai, Mindy  
APPLICANT: Galli, Stephen J.  
TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF  
TITLE OF INVENTION: RAS-MEDIATED SIGNALING  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/942,819  
FILING DATE: 02-OCT-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/058,520  
FILING DATE: 11-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BIH96-13pA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-9540  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-942-819-9

Query Match 33.3%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 FLPV 7  
DB 5 FLPV 8

RESULT 47  
US-08-159-339A-652  
Sequence 652, Application US/08159339A  
Patent No. 6037135  
GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 652:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-652

Query Match 33.3%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PFPL 5  
 ||||  
 Db 5 PFPL 8

## RESULT 48

US-08-159-339A-694  
 ; Sequence 694, Application US/08159339A  
 ; Patent No. 6037135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kubo, Ralph T.  
 ; APPLICANT: Grey, Howard M.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Cellis, Esteban  
 ; TITLE OF INVENTION: HLA Binding peptides and Their  
 ; NUMBER OF SEQUENCES: 1254  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/159,339A  
 ; FILING DATE: 29-NOV-1993  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/926,666  
 ; FILING DATE: 07-AUG-1992  
 ; APPLICATION NUMBER: US 08/027,746  
 ; FILING DATE: 05-MAR-1993  
 ; APPLICATION NUMBER: US 08/103,396  
 ; FILING DATE: 06-AUG-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Ellen Lauver  
 ; REGISTRATION NUMBER: 32,762  
 ; REFERENCE/DOCKET NUMBER: 018623-005030US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 694:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-159-339A-694

Query Match 33.3%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5  
 ||||  
 Db 2 PFPL 5

RESULT 49  
 US-08-159-339A-695  
 ; Sequence 695, Application US/08159339A  
 ; Patent No. 6037135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Cellis, Esteban  
 ; TITLE OF INVENTION: HLA Binding peptides and Their  
 ; NUMBER OF SEQUENCES: 1254  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/159,339A  
 ; FILING DATE: 29-NOV-1993  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/926,666  
 ; FILING DATE: 07-AUG-1992  
 ; APPLICATION NUMBER: US 08/027,746  
 ; FILING DATE: 05-MAR-1993  
 ; APPLICATION NUMBER: US 08/103,396  
 ; FILING DATE: 06-AUG-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Ellen Lauver  
 ; REGISTRATION NUMBER: 32,762  
 ; REFERENCE/DOCKET NUMBER: 018623-005030US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 695:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-159-339A-695

Query Match 33.3%; Score 4; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFPL 5  
 ||||  
 Db 1 PFPL 4

RESULT 50  
 US-09-231-797-106  
 ; Sequence 106, Application US/09231797  
 ; Patent No. 6084066  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EVANS, Herbert J.  
 ; APPLICANT: KINI, R. Manjunatha  
 ; TITLE OF INVENTION: Polypeptides That Include Conformation-  
 ; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interactio  
 ; NUMBER OF SEQUENCES: 153  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: Suite 500, 3000 K Street NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/231,797  
;/ FILING DATE:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/532,818  
;/ FILING DATE: 03-MAY-1996  
;/ APPLICATION NUMBER: PCT/US94/04294  
;/ FILING DATE: 21-APR-1994  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/143,364  
;/ FILING DATE: 29-OCT-1993  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/051,741  
;/ FILING DATE: 23-APR-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Isaacson, John P.  
;/ REGISTRATION NUMBER: 33,751  
;/ REFERENCE/DOCKET NUMBER: 040433/0148  
;/ INFORMATION FOR SEQ ID NO: 106:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 9 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ US-09-231-797-106

Query Match 33.3%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
Db 5 NVLP 8

RESULT 51  
US-08-934-224-106  
;/ Sequence 106, Application US/08934224  
;/ Patent No. 6100044  
;/ GENERAL INFORMATION:  
;/ APPLICANT: EVANS, Herbert J.  
;/ TITLE OF INVENTION: Polypeptides That Include Conformation-  
;/ TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
;/ TITLE OF INVENTION: Site  
;/ NUMBER OF SEQUENCES: 153  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Foley & Lardner  
;/ STREET: Suite 500, 3000 K Street NW  
;/ CITY: Washington  
;/ STATE: DC  
;/ COUNTRY: USA  
;/ ZIP: 20007  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/934,224  
;/ FILING DATE:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/532,818  
;/ FILING DATE: 03-MAY-1996  
;/ APPLICATION NUMBER: PCT/US94/04294  
;/ FILING DATE: 21-APR-1994  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/143,364  
;/ FILING DATE: 29-OCT-1993  
;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: U.S. 08/051,741  
;/ FILING DATE: 23-APR-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Isaacson, John P.  
;/ REGISTRATION NUMBER: 33,751  
;/ REFERENCE/DOCKET NUMBER: 040433/0148  
;/ INFORMATION FOR SEQ ID NO: 106:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 9 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ US-08-934-224-106

Query Match 33.3%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12  
Db 5 NVLP 8

RESULT 52  
US-08-933-843-106  
;/ Sequence 106, Application US/08933843  
;/ Patent No. 6111069  
;/ GENERAL INFORMATION:  
;/ APPLICANT: EVANS, Herbert J.  
;/ APPLICANT: KINI, R. Manjunatha  
;/ TITLE OF INVENTION: Polypeptides That Include Conformation-  
;/ TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interact  
;/ TITLE OF INVENTION: Site  
;/ NUMBER OF SEQUENCES: 153  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Foley & Lardner  
;/ STREET: Suite 500, 3000 K Street NW  
;/ CITY: Washington  
;/ STATE: DC  
;/ COUNTRY: USA  
;/ ZIP: 20007  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/933,843  
;/ FILING DATE: 19-SEPT-1997  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/532,818  
;/ FILING DATE: 03-MAY-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/143,364  
;/ FILING DATE: 29-OCT-1993  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: U.S. 08/051,741  
;/ FILING DATE: 23-APR-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Isaacson, John P.  
;/ REGISTRATION NUMBER: 33,751  
;/ REFERENCE/DOCKET NUMBER: 040433/0148  
;/ INFORMATION FOR SEQ ID NO: 106:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 9 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ US-08-933-843-106

Query Match 33.3%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NVLP 12

```
Db 5 NVLP 8
|||||
RESULT 53
US-08-934-223-106
; Sequence 106, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-223-106

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|||||
Db 5 NVLP 8

RESULT 54
US-09-413-492-106
; Sequence 106, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-106

Query Match 33.3%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|||||
Db 5 NVLP 8

RESULT 55
US-09-522-955A-9
; Sequence 9, Application US/09522955A
; Patent No. 650942
; GENERAL INFORMATION:
; APPLICANT: Tam, See-Ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF RAS-MEDICATED
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 1440.1089-004
; CURRENT APPLICATION NUMBER: US/09/522,955A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19056
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/942,819
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: US 60/058,520
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(9)
```

; OTHER INFORMATION: Xaa = Any Amino Acid  
; OTHER INFORMATION: GTPase binding homology motif II  
US-09-522-955A-9

Query Match 33.3%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLPV 7  
Db 5 FLPV 8

RESULT 56  
US-08-159-339A-717  
; Sequence 717, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Eteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 717:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-717

Query Match 33.3%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 7 FFPL 10

RESULT 57  
US-08-159-339A-718  
; Sequence 718, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Eteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 718:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-718

Query Match 33.3%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFPL 5  
Db 2 FFPL 5

RESULT 58  
US-08-159-339A-719  
; Sequence 719, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Eteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254

;  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 719:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-719  
  
Query Match 33.3%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 2 PFFL 5  
Db 1 PFFL 4  
  
RESULT 59  
US-09-101-886B-56  
; Sequence 56, Application US/09101886B  
; Patent No. 6197507  
; GENERAL INFORMATION:  
; APPLICANT: BERG, THOMAS  
; APPLICANT: TOLLERSRUD, OLE K  
; APPLICANT: NILSEN, OLIVIND  
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BARBARA G. ERNST  
; STREET: 555 13TH STREET, NW SUITE 701E  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

;  
; APPLICATION NUMBER: US/09/101,886B  
; FILING DATE: 29-JANUARY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB97/00109  
; FILING DATE: 12-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-240  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: not relevant  
; ANTI-SENSE: not relevant  
; FRAGMENT TYPE: internal  
US-09-101-886B-56  
  
Query Match 33.3%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 5 LPVV 8  
Db 3 LPVV 6  
  
RESULT 60  
US-09-344-040C-129  
; Sequence 129, Application US/09344040C  
; Patent No. 6548064  
; GENERAL INFORMATION:  
; APPLICANT: Tureci, Ozlem  
; APPLICANT: Sahin, Ugur  
; APPLICANT: Pfreundschuh, Michael  
; APPLICANT: Ramensee, Hans Georg  
; APPLICANT: Stevanovic, Stefan  
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Dete  
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Ge  
; FILE REFERENCE: LUD 5556.1  
; CURRENT APPLICATION NUMBER: US/09/344,040C  
; CURRENT FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/105,839  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: US 08/851,130  
; PRIOR FILING DATE: 1997-05-05  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 129  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-344-040C-129  
  
Query Match 33.3%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 4 FLPV 7  
Db 5 FLPV 8  
  
RESULT 61  
US-09-347-926-16  
; Sequence 16, Application US/09347926

; Patent No. 6440386  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, SHUI-ON  
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELED PROTEINS  
; FILE REFERENCE: 018733/0936  
; CURRENT APPLICATION NUMBER: US/09/347,926  
; CURRENT FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-347-926-16

Query Match 33.3%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPV 7  
Db 1 FLPV 4

RESULT 62  
US-08-194-981E-16  
; Sequence 16, Application US/08194981E  
; Patent No. 5886157  
; GENERAL INFORMATION:  
; APPLICANT: GUENGERICH, F. Peter  
; APPLICANT: GUO, Zuyu  
; APPLICANT: SANDHU, Punam  
; APPLICANT: GILLAM, Elizabeth M. J.  
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF  
; TITLE OF INVENTION: HUMAN  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: Suite 1200, 127 Peachtree Street, NE  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/194,981E  
; FILING DATE: February 10, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth Selby  
; REGISTRATION NUMBER: 38,298  
; REFERENCE/DOCKET NUMBER: 22000.0022  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; FRAGMENT TYPE: N-terminal  
US-08-194-981E-16

Query Match 33.3%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 FLPV 7  
Db 8 FLPV 11

RESULT 63  
US-09-501-612A-6  
; Sequence 6, Application US/09501612A  
; Patent No. 6544765  
; GENERAL INFORMATION:  
; APPLICANT: Pedersen, Henrik  
; APPLICANT: Hjord, Carsten M.  
; TITLE OF INVENTION: Oxaloacetate Hydrolase Deficient Fungal Host Cells  
; FILE REFERENCE: 5789-200-US  
; CURRENT APPLICATION NUMBER: US/09/501.612A  
; CURRENT FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Aspergillus niger  
US-09-501-612A-6

Query Match 33.3%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVVN 9  
Db 6 PVVN 9

RESULT 64  
US-09-490-702B-12  
; Sequence 12, Application US/09490702B  
; Patent No. 6560542  
; GENERAL INFORMATION:  
; APPLICANT: Mandell, Arnold  
; APPLICANT: Selz, Karen  
; APPLICANT: Shlesinger, Michael  
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation o  
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
; FILE REFERENCE: 01561-0002-00US00  
; CURRENT APPLICATION NUMBER: US/09/490,702B  
; CURRENT FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: synthetic  
US-09-490-702B-12

Query Match 33.3%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11  
Db 10 VNVL 13

RESULT 65  
US-09-009-953-15  
; Sequence 15, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:

```

; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-009-953-15

Query Match 33.3%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 5 FFLP 8

RESULT 66
US-09-009-953-25
; Sequence 25, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-009-953-25

Query Match 33.3%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 13 FFLP 16

RESULT 67
US-09-177-249-88
; Sequence 88, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Vadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-88

Query Match 33.3%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FFLP 6
Db 10 FFLP 13

```



```
RESULT 68
US-08-828C-28
; Sequence 28, Application US/08392828C
; Patent No. 5795962
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAOKI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO
; TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,828C
; FILING DATE: 28-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, PAULA A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FUN-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..18
; OTHER INFORMATION: /note= "TABLE 2, PEPTIDE 7"
US-08-392-828C-28
Query Match 33.3%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 8 LPVV 11

RESULT 69
US-09-330-945-28
; Sequence 28, Application US/09330945
; Patent No. 6077946
; GENERAL INFORMATION:
; APPLICANT: IWANAGA, SADAOKI
; APPLICANT: MUTA, TATSUSHI
; APPLICANT: SEKI, NORIAKI
; APPLICANT: ODA, TOSHIO
; TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
; TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT A
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
```

```
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/119,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FUN-032DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "TABLE 2, PEPTIDE 7"
US-09-330-945-28
Query Match 33.3%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 8 LPVV 11

RESULT 70
US-08-918-288-59
; Sequence 59, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 09/282,357  
; FILING DATE: 08/853,524  
; APPLICATION NUMBER: 08/853,524  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 08/199,382  
; FILING DATE: 18-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 29500-20050.25  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-887-0763  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-918-288-59

Query Match 33.3%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFEL 5  
Db 6 FFEL 9

RESULT 71  
US-09-282-357-59  
; Sequence 59, Application US/09282357  
; Patent No. 6242580  
; GENERAL INFORMATION:  
; APPLICANT: BOINE, Irving  
; APPLICANT: MOYLE, William R.  
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE  
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/282,357  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/918,288  
; FILING DATE: 25 AUG-1997  
; APPLICATION NUMBER: 08/853,524  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: 08/199,382  
; FILING DATE: 18-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 29500-20050.25  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-887-0763  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-282-357-59

Query Match 33.3%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFEL 5  
Db 6 FFEL 9

RESULT 72  
US-07-807-529A-29  
; Sequence 29, Application US/07807529A  
; Patent No. 5547669  
; GENERAL INFORMATION:  
; APPLICANT: Rogers, Bruce L.  
; APPLICANT: Morgenstern, Jay  
; APPLICANT: Bond, Julian F.  
; APPLICANT: Garman, Richard D.  
; APPLICANT: Greenstein, Julia L.  
; APPLICANT: Kuo, Wei-chang  
; APPLICANT: Morville, Malcolm  
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: One Kendall Square, Building 600  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02139  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/807,529A  
; FILING DATE: 19911213  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/662,276  
; FILING DATE: 28-FEB-1991  
; APPLICATION NUMBER: US 07/431,565  
; FILING DATE: 03-NOV-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Channing, Stacey L.  
; REGISTRATION NUMBER: 31,095  
; REFERENCE/DOCKET NUMBER: IPC-027/Imi-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 494-0060  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-07-807-529A-29

Query Match 33.3%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVW 8  
Db 15 LPVW 18

```

RESULT 73
US-08-743-553-1
; Sequence 1, Application US/08743553
; Patent No. 5824636
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, B.B.
; TITLE OF INVENTION: NOVEL ANTIPROLIFERATIVE PROTEIN FROM
; TITLE OF INVENTION: BACILLUS THURINGIENSIS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler, GILBRETH & ADLER, P.C.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,553
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,636
; FILING DATE: 05/31/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Dr. Benjamin A.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5789
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: No
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-743-553-1

Query Match 33.3%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VNVV 10
Db 4 VNVV 7

RESULT 74
US-08-300-928C-78
; Sequence 78, Application US/08300928C
; Patent No. 6019972
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; TITLE OF INVENTION: PROTEIN (TRFP)

```

```

; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMT E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-300-928C-78

Query Match 33.3%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPVV 8
Db 15 LPVV 18

RESULT 75
US-08-430-944D-78
; Sequence 78, Application US/08430944D
; Patent No. 6025162
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-430-944D-78

Query Match 33.3%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
Db 15 LPVV 18
 ||||
 ||||

Search completed: November 25, 2003, 20:16:00
Job time : 14.0851 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-5  
Perfect score: 15  
Sequence: 1 DLBMPVLPEPPFFV 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 4     | 26.7        | 16     | PC4371 | telomeric and tetr |
| 2          | 4     | 26.7        | 17     | JQ2030 | hypothetical 1.9K  |
| 3          | 3     | 20.0        | 6      | A61049 | halo-toxin - Pseud |
| 4          | 3     | 20.0        | 6      | I51317 | bHLH transcription |
| 5          | 3     | 20.0        | 8      | A39308 | glycine reductase  |
| 6          | 3     | 20.0        | 9      | A61620 | locustamyotropin I |
| 7          | 3     | 20.0        | 9      | S66635 | alpha-2-macroglobu |
| 8          | 3     | 20.0        | 9      | FD0443 | 3-oxoacid CoA-tran |
| 9          | 3     | 20.0        | 10     | B33710 | ornithine decarbox |
| 10         | 3     | 20.0        | 10     | A44646 | neurotoxin-associa |
| 11         | 3     | 20.0        | 10     | I44644 | neurotoxin-associa |
| 12         | 3     | 20.0        | 11     | S32575 | ribosomal protein  |
| 13         | 3     | 20.0        | 11     | P58501 | 43.5K bile stone p |
| 14         | 3     | 20.0        | 11     | A55149 | tetracenomycin A2  |
| 15         | 3     | 20.0        | 11     | PA0028 | protein QA300042 - |
| 16         | 3     | 20.0        | 11     | C61497 | seed protein ws-18 |
| 17         | 3     | 20.0        | 11     | P50257 | 31K protein 3208 - |
| 18         | 3     | 20.0        | 11     | A54348 | N-acetylglucosamin |
| 19         | 3     | 20.0        | 12     | PA0037 | plastocyanin 2 - A |
| 20         | 3     | 20.0        | 13     | S09395 | hypothetical prote |
| 21         | 3     | 20.0        | 13     | PL0157 | Ig kappa chain V-I |
| 22         | 3     | 20.0        | 13     | PH1772 | T cell receptor al |
| 23         | 3     | 20.0        | 13     | S01904 | H+-transporting tw |
| 24         | 3     | 20.0        | 14     | A60737 | pollen allergen Lo |
| 25         | 3     | 20.0        | 14     | C33098 | 223K exoantigen -  |
| 26         | 3     | 20.0        | 14     | A23996 | beta-granin - rat  |
| 27         | 3     | 20.0        | 15     | T09463 | ribosomal protein  |
| 28         | 3     | 20.0        | 15     | PA0024 | protein QA300050 - |
| 29         | 3     | 20.0        | 15     | P50452 | 32K protein 3306 - |

|     |   |      |    |   |        |                     |
|-----|---|------|----|---|--------|---------------------|
| 30  | 3 | 20.0 | 15 | 2 | PA0059 | protein QF200021 -  |
| 31  | 3 | 20.0 | 15 | 2 | PA0088 | protein QF200051 -  |
| 32  | 3 | 20.0 | 15 | 2 | B61457 | alpha-glucosidase   |
| 33  | 3 | 20.0 | 15 | 2 | C61511 | milk band B protei  |
| 34  | 3 | 20.0 | 15 | 2 | PT0205 | insulin-like growt  |
| 35  | 3 | 20.0 | 15 | 2 | A46909 | voltage-dependent   |
| 36  | 3 | 20.0 | 15 | 2 | A31902 | bone acidic glycop  |
| 37  | 3 | 20.0 | 15 | 2 | A45096 | thyrotropin-releas  |
| 38  | 3 | 20.0 | 16 | 1 | A49761 | locustapyrokinin -  |
| 39  | 3 | 20.0 | 16 | 2 | S03405 | hydrogenase (EC 1.  |
| 40  | 3 | 20.0 | 16 | 2 | C45133 | casein kinase II (  |
| 41  | 3 | 20.0 | 16 | 2 | T37075 | hypothetical prote  |
| 42  | 3 | 20.0 | 16 | 2 | S09732 | photosystem I prot  |
| 43  | 3 | 20.0 | 16 | 2 | C61414 | chymotrypsin (EC 3  |
| 44  | 3 | 20.0 | 16 | 2 | S68730 | bleomycin-binding   |
| 45  | 3 | 20.0 | 17 | 2 | I65274 | glutathione S-tran  |
| 46  | 3 | 20.0 | 17 | 2 | S05033 | photosystem II pro  |
| 47  | 3 | 20.0 | 17 | 2 | S50742 | proteinase inhibit  |
| 48  | 3 | 20.0 | 17 | 2 | B61414 | chymotrypsin (EC 3  |
| 49  | 3 | 20.0 | 17 | 2 | A60570 | Ig mu heavy chain   |
| 50  | 3 | 20.0 | 17 | 2 | B31769 | T-cell receptor de  |
| 51  | 3 | 20.0 | 17 | 2 | I55612 | thyroid hormone re  |
| 52  | 3 | 20.0 | 17 | 2 | G85956 | hypothetical prote  |
| 53  | 3 | 20.0 | 18 | 2 | B24735 | glutathione transf  |
| 54  | 3 | 20.0 | 18 | 2 | S29264 | ovohemerythrin - d  |
| 55  | 3 | 20.0 | 18 | 2 | S48863 | cyclin C - mouse (  |
| 56  | 3 | 20.0 | 18 | 2 | I40062 | shikimate 5-dehydr  |
| 57  | 3 | 20.0 | 18 | 2 | S46241 | NAD(P)H:flavin oxi  |
| 58  | 3 | 20.0 | 18 | 2 | S71592 | serine proteinase   |
| 59  | 3 | 20.0 | 18 | 2 | I46653 | T-cell receptor de  |
| 60  | 3 | 20.0 | 19 | 2 | C56049 | superoxide dismuta  |
| 61  | 3 | 20.0 | 19 | 2 | S59485 | hydroxyproline-rich |
| 62  | 3 | 20.0 | 19 | 2 | I40063 | shikimate 5-dehydr  |
| 63  | 3 | 20.0 | 19 | 2 | S43641 | carboxylesterase (  |
| 64  | 3 | 20.0 | 19 | 2 | A61144 | probable flagellar  |
| 65  | 3 | 20.0 | 19 | 2 | S69153 | Neb-colloostatin -  |
| 66  | 3 | 20.0 | 19 | 2 | A39504 | octamer-binding pr  |
| 67  | 3 | 20.0 | 19 | 2 | I46654 | T-cell receptor de  |
| 68  | 3 | 20.0 | 19 | 2 | S68394 | H+-transporting tw  |
| 69  | 3 | 20.0 | 20 | 2 | C54052 | phosphoribosyl-AMP  |
| 70  | 3 | 20.0 | 20 | 2 | S50741 | probable trypsin i  |
| 71  | 3 | 20.0 | 20 | 2 | B44581 | bombinin H Met-8 -  |
| 72  | 3 | 20.0 | 20 | 2 | S06466 | T-cell receptor al  |
| 73  | 3 | 20.0 | 20 | 2 | PL0145 | carbon-monoxide de  |
| 74  | 3 | 20.0 | 20 | 2 | B30208 | hypothetical prote  |
| 75  | 3 | 20.0 | 20 | 2 | B60365 | chymotrypsin inhib  |
| 76  | 3 | 20.0 | 20 | 2 | S77989 | cytochrome-c oxida  |
| 77  | 3 | 20.0 | 20 | 2 | A61414 | chymotrypsin (EC 3  |
| 78  | 3 | 20.0 | 20 | 2 | S46479 | retinoid-X-recepto  |
| 79  | 3 | 20.0 | 20 | 2 | S58382 | hypothetical prote  |
| 80  | 3 | 20.0 | 20 | 2 | I46652 | T-cell receptor de  |
| 81  | 3 | 20.0 | 20 | 2 | A48406 | annexin VI homolog  |
| 82  | 3 | 20.0 | 20 | 2 | A61526 | major milk gland p  |
| 83  | 3 | 20.0 | 20 | 2 | A85659 | hypothetical prote  |
| 84  | 3 | 13.3 | 3  | 3 | A33802 | thyrotropin-releas  |
| 85  | 2 | 13.3 | 3  | 3 | I78890 | tyrosine protein k  |
| 86  | 2 | 13.3 | 4  | 2 | S53508 | starvation-induced  |
| 87  | 2 | 13.3 | 4  | 2 | I54357 | schwannomin - mous  |
| 88  | 2 | 13.3 | 4  | 2 | A26209 | protein-glutamine   |
| 89  | 2 | 13.3 | 5  | 1 | HOR0HA | proctolin - Americ  |
| 90  | 2 | 13.3 | 5  | 2 | JN0862 | peptidyl-dipeptida  |
| 91  | 2 | 13.3 | 5  | 2 | JN0860 | peptidyl-dipeptida  |
| 92  | 2 | 13.3 | 5  | 2 | E42364 | flagellar protein   |
| 93  | 2 | 13.3 | 5  | 2 | FQ0009 | angiotensin-conver  |
| 94  | 2 | 13.3 | 5  | 2 | T14908 | hypothetical prote  |
| 95  | 2 | 13.3 | 5  | 2 | S55237 | zinc-binding prote  |
| 96  | 2 | 13.3 | 5  | 2 | B37988 | acid proteinase li  |
| 97  | 2 | 13.3 | 5  | 2 | A44692 | fulcin - giant Af   |
| 98  | 2 | 13.3 | 5  | 2 | A60411 | proctolin - Atlant  |
| 99  | 2 | 13.3 | 5  | 2 | JS0319 | subesophageal gang  |
| 100 | 2 | 13.3 | 5  | 2 | S53595 | hypothetical prote  |

## ALIGNMENTS

```

RESULT 1
PC4371
telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4371
R: Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A:Reference number: PC4371; MUID:97445086; PMID:9299414
A:Accession: PC4371
A:Molecule type: protein
A:Residues: 1-16 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 26.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEP 11
 |||||
Db 5 PVEP 8

RESULT 2
JQ2030
Hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus
N:Alternate names: ORF2 mini gene protein
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNVP
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JQ2030
R: Russell, R.L.Q.; Rohmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A:Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsug
A:Reference number: PQ0633; MUID:93286576; PMID:8389803
A:Accession: JQ2030
A:Molecule type: DNA
A:Residues: 1-17 <RUS>
A:Cross-references: DDBJ:DL3375; NID:g222217; PID:BAA02640.1; PID:d1003144; PID:g2222222

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 |||||
Db 2 VLPV 5

RESULT 3
A61049
halo-toxin - Pseudomonas syringae pv. mori
C:Species: Pseudomonas syringae pv. mori
A:Note: host mulberry tree
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C:Accession: A61049
R: Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A:Reference number: A61049
A:Accession: A61049
A:Molecule type: protein
A:Residues: 1-6 <KAJ>
A:Note: sequence confirmed by synthesis
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C:Keywords: toxin

Query Match 20.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEP 11
 |||||
Db 5 PVEP 8

```

```

QY 11 PFP 13
 |||||
Db 1 PFP 3

RESULT 4
I51317
bHLH transcription factor inhibitor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51317
R: Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A:Title: Id gene activity during Xenopus embryogenesis.
A:Reference number: I51316; MUID:95344988; PMID:7619724
A:Accession: I51317
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <ZHA>
A:Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:g4261994
C:Genetics:
A:Gene: Xidib

Query Match 20.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
 |||||
Db 4 EPF 6

RESULT 5
A39308
glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - Clostridium stick
C:Species: Clostridium sticklandii
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
C:Accession: A39308
R: Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A:Title: Glycine reductase protein C. Properties and characterization of its role in
A:Reference number: A39308; MUID:92042141; PMID:1939235
A:Accession: A39308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STA>
C:Function:
A:Description: glycine reductase complex catalyzes the reductive deamination of glycyl
C:Keywords: ATP; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 |||||
Db 3 PVL 5

RESULT 6
A61620
locustamytropin III - migratory locust
C:Species: locusta migratoria (migratory locust)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R: Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamytropin III and IV, two
A:Reference number: A61620
A:Accession: A61620
A>Status: preliminary
A:Molecule type: protein

```

A;Residues: 1-9 <SCH>  
 A;Keywords: amidated carboxyl end; neuropeptide  
 F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15  
 |||  
 Db 4 PFV 6

## RESULT 7

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)  
 C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup-Jensen, L.; Petersen, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

FEBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain of alpha-2-macroglobulin

A;Reference number: S66634; PMID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary

A;Molecule type: Protein

A;Residues: 1-9 &lt;DOL&gt;

Query Match 20.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPF 14  
 |||  
 Db 4 FPF 6

## RESULT 8

PD0443

3-Oxoadic CoA-transferase (EC 2.8.3.5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999

C;Accession: PD0443

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0443

A;Molecule type: protein

A;Residues: 1-9 &lt;KAW&gt;

C;Keywords: CoA-transferase

Query Match 20.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10  
 |||  
 Db 7 PVE 9

## RESULT 9

B33710

ornithine decarboxylase leader peptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999

C;Accession: B33710

R;Wen, L.; Huang, J.K.; Blackshear, P.J.

J. Biol. Chem. 264, 9016-9021, 1989

A;Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory elements

A;Reference number: A33710; PMID:89255378; PMID:2722815

A;Accession: B33710

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-10 <WEN>  
 C;Cross-references: GB:J04791; NID:G205807; PIDN:AAA66163.1; PID:G806309  
 C;Superfamily: unassigned leader peptides

Query Match 20.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 |||  
 Db 8 PVL 10

## RESULT 10

A44646

neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C;Accession: A44646

R;Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without

A;Reference number: A44644; PMID:92143938; PMID:1781887

A;Contents: type A

A;Accession: A44646

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 &lt;SOM&gt;

A;Note: sequence extracted from NCBI backbone (NCBIP:83774)

A;Note: 6-Trp was also found

C;Keywords: hemagglutinin

Query Match 20.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 7 VLP 9

## RESULT 11

I44644

neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C;Accession: I44644

R;Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without

A;Reference number: A44644; PMID:92143938; PMID:1781887

A;Contents: type B

A;Accession: I44644

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 &lt;SOM&gt;

A;Note: sequence extracted from NCBI backbone (NCBIP:83783)

C;Keywords: hemagglutinin

Query Match 20.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 7 VLP 9

## RESULT 12

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid *Conopholis americana* (squawroot)  
 C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 13-Aug-1999  
 C;Accession: S32575  
 R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; depamphilis, C.W.; Palmer, J.D.  
 Curr. Genet. 20, 515-518, 1991  
 A;Title: Lack of a functional plastid tRNA (Cys) gene is associated with loss of photosynthesis in *Conopholis americana*  
 A;Reference number: S32575; MUID:92145776; PMID:1723664  
 A;Accession: S32575  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-11 <TAY>  
 A;Cross-references: ENBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276  
 C;Genetics:  
 A;Gene: rps2  
 A;Genome: plastid  
 C;Superfamily: Escherichia coli ribosomal protein S2  
 C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3  
 ||||  
 DB 9 DLE 11

RESULT 13  
 F58501  
 43.5K bile stone protein - unidentified bacterium (fragment)  
 C;Species: unidentified bacterium  
 C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
 C;Accession: F58501  
 R;Binette, J.P.; Binette, M.B.  
 A;Description: The Protein Sequence Database, October 1996  
 A;Reference number: A58501  
 A;Accession: F58501  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <BIN>  
 A;Experimental source: human bile with stones  
 A;Note: 6-Asn and 8-Ala were also found

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10  
 ||||  
 DB 9 PVE 11

RESULT 14  
 A55149  
 tetraenomycin A2 oxygenase (EC 1.-.-.-) - Streptomyces glaucescens (fragment)  
 N;Alternate names: tcmA2 oxygenase; tcmG  
 C;Species: Streptomyces glaucescens  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Mar-1996  
 C;Accession: A55149  
 R;Shen, B.; Hutchinson, C.R.  
 J. Biol. Chem. 269, 30726-30733, 1994  
 A;Title: Triple hydroxylation of tetraenomycin A2 to tetraenomycin C in Streptomyces glaucescens  
 A;Reference number: A55149; MUID:95074090; PMID:7982994  
 A;Accession: A55149  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <SHE>  
 C;Genetics:  
 A;Start codon: TTG  
 C;Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 ||||  
 DB 7 PVL 9

RESULT 15  
 PA0028  
 protein QA300042 - Arabidopsis thaliana (fragment)  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C;Accession: PA0028  
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A;Reference number: PA0001  
 A;Accession: PA0028  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAM>  
 A;Experimental source: seed  
 C;Keywords: seed

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13  
 ||||  
 DB 6 PFP 8

RESULT 16  
 C61497  
 seed protein wa-18 - winged bean (fragment)  
 C;Species: Psophocarpus tetragonolobus (winged bean)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
 C;Accession: C61497  
 R;Hirano, H.  
 J. Protein Chem. 8, 115-130, 1989  
 A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis  
 A;Reference number: A61491; MUID:89351606; PMID:2765119  
 A;Accession: C61497  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <HIR>  
 C;Keywords: glycoprotein; seed

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 ||||  
 DB 7 PVL 9

RESULT 17  
 PS0257  
 31K protein 3208 - rice (strain Nihonbare) (fragment)  
 C;Species: Oryza sativa (rice)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C;Accession: PS0257  
 R;Tsugita, A.; Kamo, M.  
 submitted to JIPID, April 1993  
 A;Reference number: PS0209  
 A;Accession: PS0257  
 A;Molecule type: protein  
 A;Residues: 1-11 <TSU>  
 A;Experimental source: callus, strain Nihonbare  
 C;Comment: molecular weight 31K, pI 5.9.



Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3  
 |||  
 Db 5 DLE 7

## RESULT 18

A54348

N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)  
 C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: A54348

R;Shilatifard, A.; Cummings, R.D.

Biochemistry 33, 4273-4282, 1994

A;Title: Purification and characterization of N-acetylglucosamine-6-sulfate sulfatase fr

A;Reference number: A54348; MUID:94206936; PMID:8155645

A;Accession: A54348

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 &lt;SHI&gt;

C;Keywords: sulfuric ester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12  
 |||  
 Db 2 EPF 4

## RESULT 19

PA0037

plastocyanin 2 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C;Accession: PA0037

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

Submitted to JIPD, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A;Reference number: PA0001

A;Accession: PA0037

A;Molecule type: protein

A;Residues: 1-12 &lt;KAM&gt;

A;Experimental source: stem

Query Match 20.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 5 VLP 7

## RESULT 20

S09395

Hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 24-Jul-1997

C;Accession: S09395

R;Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Holtk

EMBO J. 8, 2359-2364, 1989

A;Title: The interference of truncated with normal potassium channel subunits leads to a

A;Reference number: S09395; MUID:90005442; PMID:2551680

A;Accession: S09395

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 &lt;GIS&gt;

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 |||  
 Db 5 LPV 7

## RESULT 21

PL0157

Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PFC) - human (fragme

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Feb-1997

C;Accession: PL0157; C61458

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-a

A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: PL0157

A;Molecule type: protein

A;Residues: 1-13 &lt;BRO&gt;

A;Accession: C61458

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 &lt;BR2&gt;

C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glyco

C;Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 |||  
 Db 11 LPV 13

## RESULT 22

PH1772

T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: PH1772

R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1772

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 &lt;POR&gt;

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11  
 |||  
 Db 4 VEP 6

## RESULT 23

S01904

H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chl

C;Species: Chloroplast Arabidopsis thaliana (mouse-ear cress)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 03-Jun-2002

C;Accession: S01904

R;Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.

Nucleic Acids Res. 16, 10372, 1988

A;Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon-subunit and elongator

A;Reference number: S01903; MUID:89057486; PMID:2904134  
 A;Accession: S01904  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-13 <CHE>  
 A;Cross-references: EMBL:X12889; NID:g11332; PIDN:CAA31380.1; PID:g829297  
 C;Genetics:  
 A;Gene: atpB  
 A;Genome: chloroplast  
 C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4  
 |||  
 Db 5 LEM 7

RESULT 24  
 A60737  
 pollen allergen Lol p IV - perennial ryegrass (fragments)  
 C;Species: Lolium perenne (perennial ryegrass)  
 C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 17-Mar-1999  
 C;Accession: A60737  
 R;Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kisil, F.T.  
 Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1989  
 A;Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.  
 A;Reference number: A60737; MUID:90007726; PMID:2793222  
 A;Accession: A60737  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <JAG>  
 C;Keywords: pollen

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 |||  
 Db 4 PVL 6

RESULT 25  
 C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C;Species: Plasmodium falciparum  
 C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C;Accession: C33098  
 R;Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A;Reference number: A33098  
 A;Accession: C33098  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <NIC>

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 1 VLP 3

RESULT 26  
 A23996  
 beta-granin - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Jun-1993

C;Accession: A23996  
 R;Hutton, J.C.; Hansen, F.; Peshavaria, M.  
 FEBS Lett. 188, 336-340, 1985  
 A;Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely related to the insulin B-chain  
 A;Reference number: A23996; MUID:85285598; PMID:3896848  
 A;Accession: A23996  
 A;Molecule type: protein  
 A;Residues: 1-14 <HUT>

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 |||  
 Db 1 LPV 3

RESULT 27  
 T09463  
 ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)  
 C;Species: mitochondrion Pylaiella littoralis  
 C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 13-Aug-1999  
 C;Accession: T09463  
 R;Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.  
 J. Mol. Biol. 277, 1047-1057, 1998  
 A;Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial ribosomal protein S14  
 A;Reference number: Z16681; MUID:98239704; PMID:9571021  
 A;Accession: T09463  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-15 <ROU>  
 A;Cross-references: EMBL:AF034976; NID:g3243103; PID:g3243104  
 A;Experimental source: strain Roscoff  
 C;Genetics:  
 A;Gene: rps14  
 A;Genome: mitochondrion  
 C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 20.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 6 VLP 8

RESULT 28  
 PA0024  
 protein QA300050 - Arabidopsis thaliana (fragment)  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C;Accession: PA0024  
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A;Reference number: PA0001  
 A;Accession: PA0024  
 A;Molecule type: protein  
 A;Residues: 1-15 <KAM>  
 A;Experimental source: seed

Query Match 20.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13  
 |||  
 Db 6 PFP 8

RESULT 29  
 A23996  
 beta-granin - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Jun-1993

```

PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0452
R;Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PS0452
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: bran, strain Nihonbare
C;Comment: molecular weight 32K, pI 5.3.

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFP 13
 |||
Db 6 PFP 8

RESULT 30
PA0059
protein OF200021 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0059
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0059
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLE 3
 |||
Db 3 DLE 5

RESULT 31
PA0088
protein OF2000051 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0088
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0088
A;Molecule type: protein
A;Residues: 1-15 <CHO>

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7
 |||
Db 13 PVL 15

RESULT 32
B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C;Accession: B61457
R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification and characterization
A;Reference number: A61457; MUID:90095988; PMID:2689637
A;Accession: B61457
A;Molecule type: protein
A;Residues: 1-15 <BAN>
C;Genetics:
A;Genetic code: SGCS
A;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; moi

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
 |||
Db 1 VLP 3

RESULT 33
C61511
milk band B protein - Australian echidna (fragment)
C;Species: Tachyglossus aculeatus (Australian echidna)
C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C;Accession: C61511
R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
Comp. Biochem. Physiol. B 99, 99-118, 1991
A;Title: Some monotreme milk "whey" and blood proteins.
A;Reference number: A61511; MUID:92070088; PMID:1959333
A;Accession: C61511
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <GRI>
C;Keywords: glycoprotein

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PFP 14
 |||
Db 13 PFP 15

RESULT 34
PT0205
insulin-like growth factor-binding protein, bone - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994
C;Accession: PT0205; A33175
R;Bautista, C.M.; Baylink, D.J.; Mohan, S.
Biochem. Biophys. Res. Commun. 176, 756-763, 1991
A;Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from human
A;Reference number: PT0205; MUID:91222244; PMID:1709017
A;Accession: PT0205
A;Molecule type: protein
A;Residues: 1-15 <BAU>

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11
 |||
Db 7 VEP 9

RESULT 35
I46909
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kda i:

```

C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999  
 C:Accession: I46909  
 R:Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.  
 Neuron 8, 899-906, 1992  
 A:Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.  
 A:Reference number: I46909; MUID:92265303; PMID:1316766  
 A:Accession: I46909  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <MAL>  
 A:Cross-references: GB:S36895; NID:G249481; PIDN:AAB22180.1; PID:G249482

Query Match 20.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4  
 |||  
 Db 13 LEM 15

RESULT 36  
 A31902  
 bone acidic glycoprotein-75 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 31-Dec-1993  
 C:Accession: A31902  
 R:Gorski, J.P.; Shimizu, K.  
 J. Biol. Chem. 263, 15938-15945, 1988

A:Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone  
 A:Reference number: A31902; MUID:89034045; PMID:2846530  
 A:Accession: A31902  
 A:Molecule type: protein  
 A:Residues: 1-15 <GOR>  
 A>Note: 14-Glu and 15-Glu were also found  
 C:Keywords: Glycoprotein

Query Match 20.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 |||  
 Db 1 LPV 3

RESULT 37  
 A45096  
 thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A45096  
 R:de la Pena, F.; Delgado, L.M.; del Camino, D.; Barros, F.  
 J. Biol. Chem. 267, 25703-25708, 1992

A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alternative splicing  
 A:Reference number: A45096; MUID:93100278; PMID:1334485  
 A:Accession: A45096  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <DEL>  
 A:Cross-references: GB:S51512; NID:G261982; PIDN:AAB224549.1; PID:G261983  
 A:Experimental source: GH3 anterior pituitary cells  
 A>Note: sequence extracted from NCBI backbone (NCBIP:120927)

Query Match 20.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 |||  
 Db 7 PVL 9

RESULT 38  
 A49761

locustapyrokinin - migratory locust  
 C:Species: Locusta migratoria (migratory locust)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 08-Dec-1995  
 C:Accession: A49761  
 R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.  
 Gen. Comp. Endocrinol. 81, 97-104, 1991  
 A:Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic  
 A:Reference number: A49761; MUID:91224474; PMID:2026322  
 A:Accession: A49761

A:Molecule type: protein  
 A:Residues: 1-16 <SCH>  
 C:Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut  
 C:Superfamily: pyrokinin  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15  
 |||  
 Db 11 PFV 13

RESULT 39  
 S03405

hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)  
 C:Species: Alcaligenes eutrophus  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998  
 C:Accession: S03405  
 R:Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.  
 Biochim. Biophys. Acta 995, 1-9, 1989  
 A:Title: Immunological comparison of subunits isolated from various hydrogenases of a  
 A:Reference number: S03404; MUID:89166625; PMID:2493816  
 A:Accession: S03405

A:Molecule type: protein  
 A:Residues: 1-16 <LOR>  
 A:Experimental source: strain H16, DMS 541  
 C:Superfamily: hydrogenase (NiFe) small chain  
 C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein;

Query Match 20.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 |||  
 Db 8 PVL 10

RESULT 40  
 C45133

casein kinase II (EC 2.7.1.1-) alpha chain - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Jun-1996  
 C:Accession: C45133  
 R:Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.  
 J. Biol. Chem. 267, 23789-23796, 1992  
 A:Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the a:  
 A:Reference number: A45133; MUID:93054738; PMID:1331100  
 A:Accession: C45133

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-16 <OU1>  
 A:Experimental source: endoplasmic reticulum, pancreas  
 A>Note: sequence extracted from NCBI backbone (NCBIP:118799)  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein;

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPF 12  
|||  
Db 6 EPF 8

## RESULT 41

T37075  
hypothetical protein SCJ30.08 - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: T37075  
R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1999  
A;Accession: T37075  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-16 <SAN>  
A;Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070; SCOEDB:SCJ30.08  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SCJ30.08

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPV 6  
|||  
Db 1 MPV 3

## RESULT 42

S09732  
Photosystem I protein psaJ - spinach chloroplast (fragment)  
C;Species: Chloroplast Spinacia oleracea (spinach)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Feb-1997  
C;Accession: S09732  
R;Keuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.  
FEBS Lett. 263, 274-278, 1990  
A;Title: Polypeptide composition of higher plant photosystem I complex. Identification of  
A;Reference number: S09730; MUID:90242987; PMID:2185953  
A;Accession: S09732  
A;Molecule type: protein  
A;Residues: 1-16 <IKE>  
C;Genetics:  
A;Gene: psaJ  
A;Genome: chloroplast  
C;Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7  
|||  
Db 12 PVL 14

## RESULT 43

C61414  
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)  
C;Species: Pseudemys scripta (slider)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 07-May-1999  
C;Accession: C61414  
R;Bhargava, A.K.; Barnard, E.A.  
J. Mol. Evol. 2, 187-198, 1973  
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determi

A;Reference number: A61414; MUID:76146602; PMID:4807189  
A;Accession: C61414  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BHA>  
C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7  
|||  
Db 8 PVL 10

## RESULT 44

S68730  
bleomycin-binding protein - Streptomyces verticillus (fragment)  
C;Species: Streptomyces verticillus  
C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 17-Mar-1999  
C;Accession: S68730  
R;Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na  
FEBS Lett. 362, 80-84, 1995  
A;Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St.  
ai characterisation.  
A;Reference number: S68730; MUID:95212588; PMID:7535252  
A;Accession: S68730  
A;Molecule type: protein  
A;Residues: 1-16 <SUG>  
A;Experimental source: ATCC 15003  
C;Keywords: antibiotic resistance

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7  
|||  
Db 9 PVL 11

## RESULT 45

I65274  
glutathione S-transferase Ya subunit (put.) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 18-Jun-1999  
C;Accession: I65274  
R;Rothkopf, G.S.; Telakowski-Hopkins, C.A.; Stotish, R.L.; Pickett, C.B.  
Biochemistry 25, 993-1002, 1986  
A;Title: Multiplicity of glutathione S-transferase genes in the rat and association w  
A;Reference number: I52395; MUID:8618772; PMID:2421763  
A;Accession: I65274  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-17 <RES>  
A;Cross-references: GB:M12894; NID:G204504; PIDN:AAA41289.1; PID:G204505  
C;Superfamily: glutathione transferase

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9  
|||  
Db 1 LPV 3

## RESULT 46

S05033  
photosystem II protein psbL - Synecococcus sp. (strain Copeland) (fragment)  
N;Alternate names: photosystem II 5K protein  
C;Species: Synecococcus sp.

C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993

C;Accession: S05033

R;Ikeuchi, M.; Koike, H.; Inoue, Y.

PBS Lett. 251, 155-160, 1989

A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II

A;Reference number: S05030

A;Accession: S05033

A;Molecule type: protein

A;Residues: 1-17 <IKS>

A;Note: the source is designated as Synechococcus vulcanus

C;Genetics:

A;Gene: psbL

C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10

Db 9 PVE 11

RESULT 47

S50742

proteinase inhibitor (Kunitz-type) 1-related protein - potato (fragment)

N;Alternate names: PKPI minor protein

C;Species: Solanum tuberosum (potato)

C;Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996

C;Accession: S50742

R;Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.

Plant Mol. Biol. 26, 961-969, 1994

A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitors

A;Reference number: S50741; MUID:95093035; PMID:8000008

A;Accession: S50742

A;Molecule type: protein

A;Residues: 1-17 <MIT>

Query Match

Best Local Similarity 20.0%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7

Db 7 PVL 9

RESULT 48

B61414

chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)

C;Species: Chrysemys picta (painted turtle)

C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 07-May-1999

C;Accession: B61414

R;Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2, 187-198, 1973

A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined

A;Reference number: A61414; MUID:76146602; PMID:4807189

A;Accession: B61414

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <BHA>

C;Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 20.0%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7

Db 8 PVL 10

RESULT 49

A60570

Ig mu heavy chain disease extra sequence - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 16-Aug-1996

C;Accession: A60570

R;Mihaesco, C.; Ferrara, P.; Guillemot, J.C.; Congy, N.; Gendron, M.C.; Roy, J.P.; Si

Mol. Immunol. 27, 771-776, 1990

A;Title: A new extra sequence at the amino terminal of a mu heavy chain disease prote

A;Reference number: A60570; MUID:90384486; PMID:2119480

A;Accession: A60570

A;Molecule type: protein

A;Residues: 1-17 <MIH>

C;Comment: This sequence is derived from the amino terminus of an abnormal immunoglob

C;Keywords: immunoglobulin

Query Match

Best Local Similarity 20.0%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7

Db 6 PVL 8

RESULT 50

B31769

T-cell receptor delta-2 chain J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 05-Nov-1999

C;Accession: B31769

R;Loeh, E.V.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.

Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988

A;Title: Human T-cell-receptor delta chain: genomic organization, diversity, and exp

A;Reference number: A94221; MUID:89071766; PMID:2974163

A;Accession: B31769

A;Molecule type: DNA

A;Residues: 1-17 <LOH>

A;Cross-references: GB:L36386; NID:g540455; PIDN:AAA61108.1; PID:g540456

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 20.0%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11

Db 15 VEP 17

RESULT 51

I55612

thyroid hormone receptor beta - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I55612

R;Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee,

J. Clin. Invest. 94, 506-515, 1994

A;Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to

A;Reference number: I55612; MUID:94314950; PMID:8040303

A;Accession: I55612

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-17 <RES>

A;Cross-references: GB:S72623; NID:g633779; PIDN:AAB31420.1; PID:g633780

C;Genetics:

A;Gene: TRbeta

Query Match

Best Local Similarity 20.0%; Score 3; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PVL 15

Db 15 PVL 15

Db 7 PFV 9

## RESULT 52

G85956  
hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL956)  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: G85956  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: G85956  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <STO>  
A:Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP:Z4331  
A:Experimental source: strain O157:H7, substrain EDL956  
C:Genetics:  
A:Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFF 13  
|||  
Db 6 PFF 8

## RESULT 53

B24735  
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 18-Jun-1993  
C:Accession: B24735  
R:Mannervik, B.; Alin, P.; Guthenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jornvall  
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985  
A:Title: Identification of three classes of cytosolic glutathione transferase common to  
A:Reference number: A24735; MUID:86042634; PMID:3864155  
A:Accession: B24735  
A:Molecule type: protein  
A:Residues: 1-18 <MAN>  
C:Superfamily: glutathione transferase  
C:Keywords: transferase

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
|||  
Db 4 PVL 6

## RESULT 54

S29264  
ovoheemerythrin - duck leech (fragment)  
N:Alternate names: 14K yolk protein  
C:Species: Theromyzon tessulatatum (duck leech)  
C>Date: 19-Mar-1997 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: S29264  
R:Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.  
Eur. J. Biochem. 209, 563-569, 1992  
A:Title: Ovoheemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech  
A:Reference number: S29264; MUID:93049299; PMID:1425663  
A:Accession: S29264  
A:Molecule type: protein  
A:Residues: 1-18 <BAE>  
A:Cross-references: PIDN:AB23969.1; PID:g258980  
C:Superfamily: hemerythrin

C:Keywords: egg yolk; oxygen carrier

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12  
|||  
Db 5 EPF 7

## RESULT 55

S48863  
cyclin C - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: S48863  
R:Wu, L.; Hall, P.L.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: S48863  
A:Accession: S48863  
A:Molecule type: mRNA  
A:Residues: 1-18 <WUL>  
A:Cross-references: EMBL:X82403; NID:g563901; PIDN:CAA57797.1; PID:g563902

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
|||  
Db 10 PVL 12

## RESULT 56

I40062  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C:Species: Buchnera aphidicola  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C:Accession: I40062  
R:Roubbakhsh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A:Title: Characterization of a putative 238-5S rRNA operon of Buchnera aphidicola (enc  
A:Reference number: I40061; MUID:95212914; PMID:7535281  
A:Accession: I40062  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-18 <RES>  
A:Cross-references: EMBL:U10496; NID:g854711; PIDN:AAA79125.1; PID:g854712  
C:Genetics:  
A:Gene: aroE  
C:Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
|||  
Db 8 VLP 10

## RESULT 57

S46241  
NAD(P)H-flavin oxidoreductase (EC 1.-.-.-) - Vibrio fischeri  
C:Species: Vibrio fischeri  
C>Date: 10-Dec-1994 #sequence\_revision 12-May-1995 #text\_change 16-Oct-1998  
C:Accession: S46241  
R:inouye, S.  
FEBS Lett. 347, 163-168, 1994  
A:Title: NAD(P)H-flavin oxidoreductase from the bioluminescent bacterium, Vibrio fisch  
A:Reference number: S46241; MUID:94307374; PMID:8033996  
A:Accession: S46241

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <INO>  
C;Keywords: NAD; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLE 3  
|||  
Db 7 DLE 9

## RESULT 58

Serine proteinase inhibitor, 31K - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 13-Sep-1998  
C;Accession: S71592  
R;Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.  
Arch. Biochem. Biophys. 317, 311-314, 1995  
A;Title: Novel extracellular matrix-associated serine proteinase inhibitors from human S71592  
A;Reference number: S71592; MUID:95177668; PMID:7872799

A;Accession: S71592  
A;Molecule type: protein  
A;Residues: 1-18 <RAO>

C;Function:

A;Description: involved in turnover of connective tissues

C;Keywords: serine proteinase inhibitor

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPF 12  
|||  
Db 5 EPF 7

## RESULT 59

T-cell receptor delta-chain J-delta-2 - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 30-May-1997  
C;Accession: I46653  
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.  
J. Immunol. 155, 1981-1993, 1995

A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old

A;Reference number: I46623; MUID:95363165; PMID:7636249

A;Accession: I46653

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-18 <YAN>

A;Cross-references: GB:D49561; NID:g1041174; PID:g1041175

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11  
|||  
Db 16 VEP 18

## RESULT 60

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (fragment)  
C;Species: unidentified organism  
C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 20-Apr-2000  
C;Accession: C56049  
R;Binette, J.P.; Binette, M.B.

Scanning Microsc. 8, 233-239, 1994  
A;Title: Sequencing of proteins extracted from stones.  
A;Reference number: A56049; MUID:95215817; PMID:7701298  
A;Accession: C56049

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <BIN>

A;Experimental source: urate-calcium oxalate kidney stones

A;Note: the source is designated as Homo sapiens, however the true source probably or

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8  
|||  
Db 4 VLP 6

## RESULT 61

hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Dec-1998  
C;Accession: S59485; S59484; S59483  
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to diffe

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59485

A;Molecule type: protein

A;Residues: 1-19 <WOJ>

A;Note: hydroxyproline-rich cell wall glycoprotein, 42K

A;Accession: S59484

A;Molecule type: protein

A;Residues: 1-15 <WOW>

A;Note: hydroxyproline-rich cell wall glycoprotein, 84K

A;Accession: S59483

A;Molecule type: protein

A;Residues: 1-14 <WOP>

A;Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component

C;Superfamily: proline-rich protein 3

C;Keywords: Glycoprotein; hydroxyproline

F;6.11.16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVE 10  
|||  
Db 6 PVE 8

## RESULT 62

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C;Species: Buchnera aphidicola  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999

C;Accession: I40063

R;Roubbakhsh, D.; Baumann, P.

Gene 155, 107-112, 1995

A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (en

A;Reference number: I40061; MUID:95212914; PMID:7535281

A;Accession: I40063

A;Status: preliminary; translated from GB/EMBL/DDJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: EMBL:U10497; NID:g854713; PIDN:AAA79126.1; PID:g854714

C;Genetics:

A;Gene: aroE



S69153  
Neb-colloostatatin - flesh fly (*Sarcophaga bullata*)  
C/Species: *Sarcophaga bullata*  
C/Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 19-May-2000  
C/Accession: S69153  
R:/ByElemsn, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van  
Eur J. Biochem. 228, 45-49, 1995  
A/Title: Neb-colloostatatin, a second folliculastatin of the grey fleshfly, *Neobellieria bullata*  
A/Reference number: S69153; MUID:95188911; PMID:7893009  
A/Accession: S69153  
A/Molecule type: protein  
A/Residues: 1-19 <BYL>

H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii (S68394)  
 N;Alternate names: ATP synthase chain G  
 C;Species: Chlamydomonas reinhardtii  
 C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
 C;Accession: S68394  
 R;Riedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H. FEBS Lett. 377, 163-166, 1995  
 A;Title: Isolation of Cf(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminus of the CF(0)CF(1) complex  
 A;Reference number: S68388; MUID:96128220; PMID:8543042  
 A;Accession: S68394  
 A;Molecule type: protein

A;Residues: 1-19 <PIE>  
 A;Experimental source: strain CW15  
 C;Genetics:  
 A;Genome: nuclear  
 C;Keywords: Chloroplast; hydrolase

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 ||||  
 DB 11 LPV 13

## RESULT 69

C54052  
 Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3.5.4.19)  
 C;Species: Klebsiella pneumoniae  
 C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2002  
 C;Accession: C54052  
 R;Rieder, G.; Merrick, M.J.; Castorff, H.; Kleiner, D.  
 J. Biol. Chem. 269, 14386-14390, 1994  
 A;Title: Function of hisP and hisH gene products in histidine biosynthesis.  
 A;Reference number: A54052; MUID:94237842; PMID:8182043  
 A;Accession: C54052  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-20 <RIE>  
 A;Experimental source: MSal  
 A;Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIPI:148610)  
 C;Genetics:  
 A;Gene: hisIE  
 C;Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein  
 C;Keywords: histidine biosynthesis; hydrolase; multifunctional enzyme

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6  
 ||||  
 DB 15 MPV 17

## RESULT 70

S50741  
 probable trypsin inhibitor - potato (fragment)  
 N;Alternate names: KPI major protein  
 C;Species: Solanum tuberosum (potato)  
 C;Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 11-Jan-2000  
 C;Accession: S50741  
 R;Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
 Plant Mol. Biol. 26, 961-969, 1994  
 A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitors  
 A;Reference number: S50741; MUID:95093035; PMID:8000008  
 A;Accession: S50741  
 A;Molecule type: protein  
 A;Residues: 1-20 <MIT>  
 C;Superfamily: cathepsin D inhibitor

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 ||||  
 DB 2 VLP 4

## RESULT 71

B44581  
 bombinin H Met-8 - yellow-bellied toad

C;Species: Bombina variegata (yellow-bellied toad)  
 C;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 11-Jan-2000  
 C;Accession: B44581  
 R;Mignogna, G.; Simmaco, M.; Kreil, G.; Barra, D.  
 EMBO J. 12, 4829-4832, 1993  
 A;Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the  
 A;Reference number: S39612; MUID:94039967; PMID:8223431  
 A;Accession: B44581  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <MIT>  
 C;Superfamily: bombinin H precursor  
 C;Keywords: amidated carboxyl end; D-amino acid  
 F;2/Modified site: D-allo-isoleucine (Ile) #status experimental  
 F;2/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7  
 ||||  
 DB 4 PVL 6

## RESULT 72

S06466  
 T-cell receptor alpha chain J segment (DO) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 06-Jun-1997  
 C;Accession: S06466  
 R;Yague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.  
 Nucleic Acids Res. 16, 11355-11364, 1988  
 A;Title: The structure of V-alpha and J-alpha segments in the mouse.  
 A;Reference number: S06466; MUID:89083566; PMID:2849763  
 A;Accession: S06466  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-20 <YAG>  
 A;Experimental source: strain Balb/c  
 C;Genetics:  
 A;Map position: 14  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: glycoprotein; heterodimer; T-cell receptor  
 F;1-18/Domain: J segment <USE>  
 F;19-20/Domain: C region (fragment) <CRE>

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11  
 ||||  
 DB 16 VEP 18

## RESULT 73

PL0145  
 carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava  
 C;Species: Pseudomonas carboxydoflava  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
 C;Accession: PL0145  
 R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
 Arch. Microbiol. 152, 335-341, 1989  
 A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot  
 A;Reference number: PL0138; MUID:90055678; PMID:2818128  
 A;Accession: PL0145  
 A;Molecule type: protein  
 A;Residues: 1-20 <KRA>  
 C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,  
 C;Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11  
|||  
DB 18 VEP 20

## RESULT 74

B30208  
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa  
C:Species: Neurospora crassa  
C>Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993  
C:Accession: B30208  
R:Patel, J.L.; Obach, M.J.; Legerton, T.L.; Yanofsky, C.  
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988  
A:Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein s  
A:Reference number: A30208; MUID:88234499; PMID:2967496  
A:Accession: B30208  
A:Molecule type: DNA  
A:Residues: 1-20 <PAL>  
A:Cross-references: GB:J03262

Query Match 20.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFP 13  
|||  
DB 6 PFP 8

## RESULT 75

B60365  
chymotrypsin inhibitor 2 - tobacco hornworm (fragment)  
C:Species: Manduca sexta (tobacco hornworm)  
C>Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 03-Feb-1994  
C:Accession: B60365  
R:Kanost, M.R.  
Insect Biochem. 20, 141-147, 1990  
A:Title: Isolation and characterization of four serine proteinase inhibitors (serpins) f  
A:Reference number: A60365  
A:Accession: B60365  
A:Molecule type: protein  
A:Residues: 1-20 <KAN>  
C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 20.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15  
|||  
DB 6 PFV 8

Search completed: November 25, 2003, 18:28:17

Job time : 14.8032 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15

Sequence: 1 DLEMPVLVBPFFV 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: SwissProt\_41.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 4     | 26.7        | 12     | 1  | TM2A_METMA  |
| 2          | 3     | 20.0        | 9      | 1  | LMT3_LOCM1  |
| 3          | 3     | 20.0        | 9      | 1  | ULAH_HUMAN  |
| 4          | 3     | 20.0        | 10     | 1  | FAR6_PANRE  |
| 5          | 3     | 20.0        | 10     | 1  | UHA3_HUMAN  |
| 6          | 3     | 20.0        | 11     | 1  | RR2_CONAM   |
| 7          | 3     | 20.0        | 13     | 1  | FIBB_RABIT  |
| 8          | 3     | 20.0        | 13     | 1  | PEDI_HYDAT  |
| 9          | 3     | 20.0        | 13     | 1  | TENE_RANTE  |
| 10         | 3     | 20.0        | 13     | 1  | UHA3_CANFA  |
| 11         | 3     | 20.0        | 13     | 1  | YPE2_LACLC  |
| 12         | 3     | 20.0        | 14     | 1  | UC15_MAIZE  |
| 13         | 3     | 20.0        | 15     | 1  | UC16_MAIZE  |
| 14         | 3     | 20.0        | 15     | 1  | UC25_MAIZE  |
| 15         | 3     | 20.0        | 16     | 1  | LPK1_LOCM1  |
| 16         | 3     | 20.0        | 17     | 1  | PSBL_SYNVU  |
| 17         | 3     | 20.0        | 18     | 1  | AL12_CYDPO  |
| 18         | 3     | 20.0        | 18     | 1  | HEMH_THETS  |
| 19         | 3     | 20.0        | 19     | 1  | COOT_SABSU  |
| 20         | 3     | 20.0        | 20     | 1  | COXN_THUOB  |
| 21         | 3     | 20.0        | 20     | 1  | MAX7_BOMMX  |
| 22         | 3     | 20.0        | 20     | 1  | MAX8_BOMMX  |
| 23         | 3     | 20.0        | 20     | 1  | PSAL_SYNVU  |
| 24         | 3     | 20.0        | 20     | 1  | SB60_MAIZE  |
| 25         | 3     | 20.0        | 20     | 1  | TRYL_STREX  |
| 26         | 2     | 13.3        | 5      | 1  | E103_LITRU  |
| 27         | 2     | 13.3        | 5      | 1  | PAP2_PARMA  |
| 28         | 2     | 13.3        | 5      | 1  | PRCT_PERAM  |
| 29         | 2     | 13.3        | 5      | 1  | SUGA_ACHDO  |
| 30         | 2     | 13.3        | 5      | 1  | TPIS_CANFA  |
| 31         | 2     | 13.3        | 6      | 1  | ACPH_RABIT  |
| 32         | 2     | 13.3        | 6      | 1  | CIP1_MYTED  |
| 33         | 2     | 13.3        | 6      | 1  | CIP2_MYTED  |

|     |   |      |    |   |            |
|-----|---|------|----|---|------------|
| 34  | 2 | 13.3 | 6  | 1 | E101_LITRU |
| 35  | 2 | 13.3 | 6  | 1 | TRP1_PSEPU |
| 36  | 2 | 13.3 | 7  | 1 | ALL3_CARMA |
| 37  | 2 | 13.3 | 7  | 1 | CARP_MYTED |
| 38  | 2 | 13.3 | 7  | 1 | CCF1_ENTFA |
| 39  | 2 | 13.3 | 7  | 1 | E105_LITRU |
| 40  | 2 | 13.3 | 7  | 1 | FAR1_HELTI |
| 41  | 2 | 13.3 | 7  | 1 | PH2_LYCES  |
| 42  | 2 | 13.3 | 7  | 1 | UNO6_PINPS |
| 43  | 2 | 13.3 | 7  | 1 | WWA1_ACHFU |
| 44  | 2 | 13.3 | 7  | 1 | WWA3_ACHFU |
| 45  | 2 | 13.3 | 8  | 1 | ALL6_CYDPO |
| 46  | 2 | 13.3 | 8  | 1 | ANG2_BORJA |
| 47  | 2 | 13.3 | 8  | 1 | CAD1_ENTFA |
| 48  | 2 | 13.3 | 8  | 1 | CUP_THICU  |
| 49  | 2 | 13.3 | 8  | 1 | COM2_CONPU |
| 50  | 2 | 13.3 | 8  | 1 | PRK2_PERAM |
| 51  | 2 | 13.3 | 8  | 1 | PRK3_PERAM |
| 52  | 2 | 13.3 | 8  | 1 | UC26_MAIZE |
| 53  | 2 | 13.3 | 8  | 1 | UF06_MOUSE |
| 54  | 2 | 13.3 | 9  | 1 | B843_SERPL |
| 55  | 2 | 13.3 | 9  | 1 | CCAP_CARMA |
| 56  | 2 | 13.3 | 9  | 1 | COXE_THUOB |
| 57  | 2 | 13.3 | 9  | 1 | FAR5_PENMO |
| 58  | 2 | 13.3 | 9  | 1 | FIBB_ERYPA |
| 59  | 2 | 13.3 | 9  | 1 | KNL3_BOMVA |
| 60  | 2 | 13.3 | 9  | 1 | LMP1_LOCM1 |
| 61  | 2 | 13.3 | 9  | 1 | OXYA_SCYCA |
| 62  | 2 | 13.3 | 9  | 1 | OXIF_SCYCA |
| 63  | 2 | 13.3 | 9  | 1 | OXIT_EISFO |
| 64  | 2 | 13.3 | 9  | 1 | OXIV_SQAC  |
| 65  | 2 | 13.3 | 9  | 1 | TRSP_BOMMO |
| 66  | 2 | 13.3 | 9  | 1 | SAMP_MUSCA |
| 67  | 2 | 13.3 | 9  | 1 | ULAE_HUMAN |
| 68  | 2 | 13.3 | 9  | 1 | UN19_CLOPA |
| 69  | 2 | 13.3 | 9  | 1 | UPA3_HUMAN |
| 70  | 2 | 13.3 | 10 | 1 | ANG1_BOTJA |
| 71  | 2 | 13.3 | 10 | 1 | ANGT_BOVIN |
| 72  | 2 | 13.3 | 10 | 1 | ANGT_CHICK |
| 73  | 2 | 13.3 | 10 | 1 | CATB_SHEEP |
| 74  | 2 | 13.3 | 10 | 1 | COXA_ONCMY |
| 75  | 2 | 13.3 | 10 | 1 | ESL_LACCA  |
| 76  | 2 | 13.3 | 10 | 1 | GAJU_HUMAN |
| 77  | 2 | 13.3 | 10 | 1 | GON1_PETMA |
| 78  | 2 | 13.3 | 10 | 1 | GON3_ONCKE |
| 79  | 2 | 13.3 | 10 | 1 | GONL_SQAC  |
| 80  | 2 | 13.3 | 10 | 1 | ODP2_BOVIN |
| 81  | 2 | 13.3 | 10 | 1 | PNEU_HUMAN |
| 82  | 2 | 13.3 | 10 | 1 | PNEU_RAT   |
| 83  | 2 | 13.3 | 10 | 1 | PKV_LOCM1  |
| 84  | 2 | 13.3 | 10 | 1 | Q20B_COMTE |
| 85  | 2 | 13.3 | 10 | 1 | RL16_ACHLA |
| 86  | 2 | 13.3 | 10 | 1 | RT02_BOVIN |
| 87  | 2 | 13.3 | 10 | 1 | SLAP_BACTG |
| 88  | 2 | 13.3 | 10 | 1 | TEMK_RANTE |
| 89  | 2 | 13.3 | 10 | 1 | TKNB_CHICK |
| 90  | 2 | 13.3 | 10 | 1 | TKNB_ONCMY |
| 91  | 2 | 13.3 | 10 | 1 | TKNK_PIG   |
| 92  | 2 | 13.3 | 10 | 1 | TKUL_URRIN |
| 93  | 2 | 13.3 | 10 | 1 | TPIS_NICPL |
| 94  | 2 | 13.3 | 10 | 1 | UPAS_HUMAN |
| 95  | 2 | 13.3 | 10 | 1 | URE3_MORMO |
| 96  | 2 | 13.3 | 10 | 1 | UXB1_YEAST |
| 97  | 2 | 13.3 | 10 | 1 | XNBN_DICB4 |
| 98  | 2 | 13.3 | 11 | 1 | ANGT_CRIGE |
| 99  | 2 | 13.3 | 11 | 1 | BPBP_AKSHA |
| 100 | 2 | 13.3 | 11 | 1 | BRK_MEGFL  |

#### ALIGNMENTS

RESULT 1

TM2A METWA  
ID TM2A METWA STANDARD; PRT; 12 AA.  
AC P80652;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M  
DE methyltransferase 28 kDa subunit) [Fragment].  
OS Methanosarcina mazei (Methanosarcina frisia).  
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
OX NCBI\_TaxID=2209;  
RN [1]  
RP SEQUENCE.  
RX STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
RX MEDLINE=96370840; PubMed=8774736;  
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
RA "Sodium ion translocation by N5-methyltetrahydromethanopterin;  
RT coenzyme M methyltransferase from Methanosarcina mazei Goe1  
RT reconstituted in ether lipid liposomes.";  
RL Eur. J. Biochem. 239:857-864(1996).  
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
CC METHANOGENESIS. THE FORMATION OF METHYL-COENZYME M AND  
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
CC TETRAHYDROMETHANOPTERIN.  
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
CC (methylthio)ethanesulfonate.  
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
KW Transferase; Methyltransferase; Transmembrane protein.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; 6DB4A5766232D76B CRC64;  
Query Match 26.7%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PVLP 8  
Db 6 PVLP 9

RESULT 2  
LMT3 LOCMI  
ID LMT3 LOCMI STANDARD; PRT; 9 AA.  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamycotropin 3 (LOM-MT-3).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
RA de Loof A.;  
RT "Isolation, identification and synthesis of locustamycotropin III and  
RT IV, two additional neuropeptides of Locusta migratoria: members of the  
RT locustamycotropin peptide family.";  
RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A61620; A61620.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYOKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.

FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 PFV 15  
Db 4 PFV 6

RESULT 3  
ULAH HUMAN  
ID ULAH HUMAN STANDARD; PRT; 9 AA.  
AC P31934;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of liver tissue (Spot 94) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Liver;  
RX MEDLINE=94147969; PubMed=8313870;  
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
RA "Human liver protein map: update 1993.";  
RL Electrophoresis 14:1216-1222(1993).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.5, ITS MW IS: 12 kDa.  
CC SWISS-2DPAGE; P31934; HUMAN.  
DR NON\_TER 1 1  
FT VARIANT 3 3 A -> L.  
FT NON\_TER 1 1 /FTID=VAR\_000001.  
FT NON\_TER 3 3  
SQ SEQUENCE 9 AA; 990 MW; FICCTB172AB6DDCA CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLE 3  
Db 5 DLE 7

RESULT 4  
FAR6 PANRE  
ID FAR6 PANRE STANDARD; PRT; 10 AA.  
AC P82560;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RX Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of FMRFamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.

FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15  
DB 6 PFV 8

RESULT 5  
CH33 HUMAN  
ID \_H33 HUMAN STANDARD; PRT; 10 AA.  
AC P40930; 1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=95203287; PubMed=7895732;  
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
RT "The human myocardial two-dimensional gel protein database: update  
1994.";  
RL Electrophoresis 15:1459-1465(1994).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 6.8. ITS MW IS: 47.3 Kda.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11  
DB 2 VEP 4

RESULT 6  
R22 CONAM  
ID \_R22 CONAM STANDARD; PRT; 11 AA.  
AC P42341;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chloroplast 30S ribosomal protein S2 (Fragment).  
GN RPS2.  
OS Conopholis americana (Squawroot).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Lamiales; Orobanchaceae; Orobanchaceae; Conopholis.  
OX NCBI\_TaxID=4179;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92145776; PubMed=1723664;  
RA Taylor G., Wolfe K.H., Morden K.W., Depamphilis C.W., Palmer J.D.;  
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss  
of photosynthesis in a lineage of parasitic plants.";  
RL Curr. Genet. 20:515-518(1991).  
CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X64567; CAA45868.1; -.  
DR PIR; S32575; S32575.  
DR HAMAP; MF\_00291; -.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
DR PROSITE; PS00963; RIBOSOMAL\_S2\_2; PARTIAL.  
KW Ribosomal protein; Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3  
DB 9 DLE 11

RESULT 7  
FIBB RABIT  
ID \_FIBB RABIT STANDARD; PRT; 13 AA.  
AC P14478;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals.";  
RL Acta Chem. Scand. 19:1789-1791(1965).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.  
FT MOD\_RES 4 4 SULFATION.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;  
Query Match 20.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
DB 8 VLP 10

RESULT 8  
PEDI HYDAT  
ID \_PEDI HYDAT STANDARD; PRT; 13 AA.  
AC P80578;  
DT 01-OCT-1996 (Rel. 34, Created)

```

DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
OS Pedin.
OC Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and Characterization of two new morphogenetically active
 peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
 DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
7 VLP 9

RESULT 9
TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tempurin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX TISSUE=Skin secretion;
RC MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 Barra D.,
RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the breviniin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
1 VLP 3

RESULT 10
UHA3 CANFA STANDARD; PRT; 13 AA.
ID UHA3 CANFA
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

```

```

DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_SEQUENCE.
RP SEQUENCE.
RX TISSUE=Heart;
RC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
Db |||
7 PVE 9

RESULT 11
YPEZ_LACLC STANDARD; PRT; 13 AA.
ID YPEZ_LACLC
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8188586;
RA Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
 Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning
 and nucleotide sequencing of pept and construction of a chromosomal
 deletion mutant.";
RL J. Bacteriol. 176:2854-2861(1994).
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
CC -!-
DR EMBL; L27596; AAA20625.1; -
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
Db |||
5 EPF 7

RESULT 12

```

```

UC15_MAIZE
ID UC15_MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON TER 1 1
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 5 LPV 7

RESULT 13
UC16_MAIZE
ID UC16_MAIZE STANDARD; PRT; 15 AA.
AC P80622;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 308)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.
DR Maize-2DPAGE; P80622; COLEOPTILE.
DR MaizeDB; 123948; -.
FT NON TER 1 1
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11

```

```

DB 12 VEP 14

RESULT 14
UC25_MAIZE
ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.
DR Maize-2DPAGE; P80631; COLEOPTILE.
DR MaizeDB; 123957; -.
FT NON TER 1 1
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1580 MW; 83C54CFC0CE1614D0 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
DB 10 PVE 12

RESULT 15
LPK1_LOOMI
ID LPK1_LOOMI STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=91224474; PubMed=2026322;
RA Schoofs L., Holman G.N., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RT myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.

```



SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 PFV 15  
 Db 11 PFV 13  
 RESULT 16  
 PSBL\_SYNNU  
 ID PSBL\_SYNNU STANDARD; PRT; 17 AA.  
 AC P12241;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)  
 DE (fragment).  
 GN PSBL.  
 OS Synchococcus vulcanus (Thermosynechococcus vulcanus).  
 OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.  
 OX NCBI\_TaxID=32053;  
 RN [1]  
 RP SEQUENCE.  
 RA Ikeuchi M., Koike H., Inoue Y.;  
 RT "Identification of psbI and psbL gene products in cyanobacterial  
 photosystem II reaction center preparation.";  
 RL FEBS Lett 351:155-160(1989).  
 CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME  
 CC -!- B559.  
 CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.  
 CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.  
 DR FIR; S05033; S05033.  
 DR InterPro; IPR003372; PSII\_PsBL.  
 DR Pfam; PF02419; PSBL; 1.  
 KW Photosynthesis; Photosystem II.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PVE 10  
 Db 9 PVE 11  
 RESULT 17  
 ALL2\_CYDPO  
 ID ALL2\_CYDPO STANDARD; PRT; 18 AA.  
 AC P82153;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 2.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=96034539; PubMed=9392829;  
 RA Duve H., Janssen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RA "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 18 18  
 AMIDATION.

SQ SEQUENCE 18 AA; 2169 MW; 8B66679C0CDF175C CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPV 9  
 Db 11 LPV 13  
 RESULT 18  
 HEMH\_THERS  
 ID HEMH\_THERS STANDARD; PRT; 18 AA.  
 AC P80155;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ovohemerythrin (Yp14) (fragment).  
 OS Thermomyza tessulatum (Leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
 OX NCBI\_TaxID=13286;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Oocyte;  
 RX MEDLINE=93049299; PubMed=1425663;  
 RA Baert J.-L., Britel M., Sauviere P., Malecha J.;  
 RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from  
 vitellogenin in leech.";  
 RL Eur. J. Biochem. 209:563-569(1992).  
 CC -!- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE  
 CC -!- IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the hemerythrin family.  
 DR FIR; S29264; S29264.  
 DR HSP; P02247; 2MHR.  
 DR InterPro; IPR002063; Hemerythrin.  
 DR Pfam; PF01814; Hemerythrin; 1.  
 DR PROSITE; PS00550; HEMERYTHRIN; PARTIAL.  
 KW Oxygen transport; Metal-binding; Iron; Yolk.  
 FT NON TER 18  
 SQ SEQUENCE 18 AA; 2368 MW; 33397EE587C81F1 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 EPF 12  
 Db 5 EPF 7  
 RESULT 19  
 COOT\_SARBU  
 ID COOT\_SARBU STANDARD; PRT; 19 AA.  
 AC Q09148;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE NEB-collostatin (Folliculostatin).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95188911; PubMed=7883009;  
 RA Byllemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,  
 RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;  
 RT "Neb-collostatin, a second folliculostatin of the grey fleshfly,  
 RT Neobellieria bullata.";

```

RL Eur. J. Biochem. 228:45-49(1995).
CC -!- FUNCTION: HAS AN OSTIATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR; S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 7 LPV 9

RESULT 20
CORN_THUOB STANDARD; PRT; 20 AA.
AC P80980;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCB1_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
DR PIR; S77989; S77989.
KW Oxidoreductase; Mitochondrion.
FT NON PER 20
SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
DB 17 MPV 19

RESULT 21
MAX7_BOMMX STANDARD; PRT; 20 AA.
AC P83086;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 41, Last annotation update)
DE Maximin 7.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;

RL Eur. J. Biochem. 228:45-49(1995).
CC -!- FUNCTION: HAS AN OSTIATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -!- CAUTION: NEB-COLLOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR; S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
DB 7 LPV 9

RESULT 20
CORN_THUOB STANDARD; PRT; 20 AA.
AC P80980;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCB1_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
DR PIR; S77989; S77989.
KW Oxidoreductase; Mitochondrion.
FT NON PER 20
SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6
DB 17 MPV 19

RESULT 21
MAX7_BOMMX STANDARD; PRT; 20 AA.
AC P83086;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 41, Last annotation update)
DE Maximin 7.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;

```

```

[1]
RN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin secretion;
RC Chen T.B., McClean S., Orr D.F., Bjorson A.J., Rao P.F., Shaw C.;
RA "Isolation and structural characterisation of antimicrobial peptides
RT from the venom of the Chinese large-webbed bell toad (Bombina
RT maxima).";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antimicrobial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1947 MW; EC7541AALBF3BD49 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 4 PVL 6

RESULT 22
MAX8_BOMMX STANDARD; PRT; 20 AA.
AC P83087;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Maximin 8.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCB1_TaxID=161274;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.F., Bjorson A.J., Rao P.F., Shaw C.;
RT "Isolation and structural characterisation of antimicrobial peptides
RT from the venom of the Chinese large-webbed bell toad (Bombina
RT maxima).";
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antimicrobial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6BE2F949 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 4 PVL 6

RESULT 23
PSAL_SYNVU STANDARD; PRT; 20 AA.
AC P25937;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit XI (PSI-L) (PSI subunit V)
DE (Fragment).
KW PSAL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCB1_TaxID=32053;

```

```

RN SEQUENCE
RX MEDLINE=89338747; PubMed=2503399;
RA koike H., Ikeuchi M., Hiyama T., Inoue Y.;
RT Identification of photosystem I components from the cyanobacterium,
RL Synechococcus vulcanus by N-terminal sequencing.";
FEBS Lett. 253:257-263(1989).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CELLULAR
CC -1- THYLAKOID MEMBRANE (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
DR HAMAP; MF 00447; -; 1.
DR InterPro; IPR003757; PSI_Psal.
DR Pfam; PF02605; Psal; 1.
DR Photosystem I; Photosynthesis, Thylakoid, Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2170 MW; 730FECDD2EA02A2C CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFV 15
Db 12 PFV 14

RESULT 24
SB60_MAIZE
ID SB60_MAIZE STANDARD; PRT; 20 AA.
AC P82868;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=sv. Cecilia; TISSUE=Coleoptile;
RX MEDLINE=21948208; PubMed=11950979;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins. Purification and expression analysis in
RT maize.";
RL Plant Physiol. 128:1303-1312(2002)
CC -1- FUNCTION: May have spermidine-binding activity.
CC -1- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -1- SUBCELLULAR LOCATION: Microsomal membrane.
CC -1- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
DR GO; GO:0005792; C:cytosol; NAS.
KW Membrane; Microsome.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2093 MW; 7FD730C00391579A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11
Db 6 VEP 8

RESULT 25
TRYL-STREX
ID TRYL-STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease (EC 3.4.21.-) (fragment).

```

```

OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX MEDLINE=95291424; PubMed=7773379;
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13.";
EL Microbiology 141:1017-1025(1995).
CC -1- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
DR MEROPS; SOL101; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPF 14
Db 12 FPF 14

RESULT 26
E103_LITRU
ID E103_LITRU STANDARD; PRT; 5 AA.
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FV 15
Db 1 FV 2

RESULT 27
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Pardon II (PXII) (Fragment).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;  
OC Soleiidae; Soleidae; Pardachirus.  
OX NCBI\_TaxID=31087;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=3782138;  
RA Lazarovici P, Primor N, Loew L M;  
RT "Purification and pore-forming activity of two hydrophobic  
RP polypeptides from the secretion of the Red sea moles sole (Pardachirus  
RL marmoratus)."; 261:16704-16713(1986).  
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant  
CC properties. Forms voltage-dependent, ion-permeable channels  
CC in membranes. At high concentration causes cell membrane lysis.  
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PARDACHIN FAMILY.  
KW Toxin.  
FT NON TER  
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 FP 13  
DB 4 FP 5  
RESULT 28  
PRCT PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1993 (Rel. 31, Last annotation update)  
DE Proctolin  
OS Periplaneta americana (American cockroach).  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Skarratt A.N., Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
RT in insects."; Life Sci. 17:1253-1256(1975).  
RN [2]  
RP BIOLOGICAL SOURCE.  
RC SPECIES=P.americana;  
RX MEDLINE=81225865; PubMed=6113690;  
RA O'Shea M., Adams M.E.;  
RT "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.polyphemus;  
RX MEDLINE=90287800; PubMed=2356151;  
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
RA Shabanowitz J.;

RT "Identification of proctolin in the central nervous system of the  
RT horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=C.maenas;  
RX MEDLINE=86232789; PubMed=2872661;  
RA Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
RT pericardial organs of the shore crab, Carcinus maenas."; Peptides 7:67-72(1986).  
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
CC THE CRAB PERICARDIAL ORGANS.  
DR PIR; A01644; HOSHOA.  
DR PIR; A60411; A60411.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 649 MW; 71E7673B46000000 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 LP 8  
DB 3 LP 4  
RESULT 29  
SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P19991;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Suboesophageal ganglion pentapeptide.  
OS Achetia domestica (House cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Achetia.  
OX NCBI\_TaxID=6997;  
RN [1]  
RP SEQUENCE.  
RC "Isolation and structure of a peptide isolated from the  
RT suboesophageal ganglion of Achetia domestica (orthoptera)."; Comp. Biochem. Physiol. 88C:185-187(1987).  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL  
CC GANGLIA.  
DR PIR; JS0319; JS0319.  
DR PIR; JS0319; JS0319.  
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDD8000000 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PF 12  
DB 4 PF 5  
RESULT 30  
TPIS\_CANFA STANDARD; PRT; 5 AA.  
AC P54714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).  
GN TPI1.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone  
 CC phosphate  
 CC -!- PATHWAY: Plays an important role in several metabolic pathways.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 DR HSC-2DPAGE; P54714; DOG.  
 DR InterPro; IPR000652; Triophos\_ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 DR Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 KW Pentose shunt.  
 KW NON TER 1 1  
 FT NON TER 5 5  
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 FV 15  
 DB 1 FV 2

RESULT 31  
 ACPH RABBIT  
 ID ACPH RABBIT STANDARD; PRT; 6 AA.  
 AC P25154;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)  
 DE (APH) (Acylaminoacyl-peptidase) (Fragment).  
 GN APH.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=92222120; PubMed=1807161;  
 RA Krishna R.G., Chin C.C.Q., Wolf F.;  
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
 RT unblocking with N-acylaminoacyl-peptide hydrolase.";  
 RL Anal. Biochem. 199;45-50(1991).  
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
 CC + peptide  
 CC -!- SUBUNIT: Homotetramer.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.  
 DR PROSITE; PS00708; PRO ENDOPEP\_SER; PARTIAL.  
 DR MEROPS; S09.004; -.  
 DR InterPro; IPR002471; Prol endopep\_ser.  
 DR PROSITE; PS00708; PRO ENDOPEP\_SER; PARTIAL.  
 KW Hydrolase; Acetylation.  
 FT MOD RES 1 1 ACETYLATION.  
 FT NON TER 6 6  
 SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VL 7  
 DB 5 VL 6

RESULT 32  
 CIP1 MYTED  
 ID CIP1 MYTED STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 DE Mytilus edulis (Blue mussel).  
 OS Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC -!- SIMILARITY: TO MIP II.  
 DR PIR; A27696; A27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 FV 15  
 DB 5 FV 6

RESULT 33  
 CIP2 MYTED  
 ID CIP2 MYTED STANDARD; PRT; 6 AA.  
 AC P13737;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide II (MIP II).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC -!- SIMILARITY: TO MIP I.  
 DR PIR; B27696; B27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FV 15  
DB 5 FV 6

RESULT 34  
ID\_E101\_LITRU STANDARD; PRT; 6 AA.  
AC P82036;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litori electrica. Comparison with the skin peptides from Litoria  
RT rubella";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 6 AMIDATION.  
SQ SEQUENCE 6 AA; 792 MW; 6693704772C9A000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FV 15  
DB 1 FV 2

RESULT 35  
ID\_TRPI\_PSEPU STANDARD; PRT; 6 AA.  
AC P36414;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE TrpBA operon transcriptional activator (Fragment).  
GN TRPI.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PPG1 C1S;  
RX MEDLINE=89335926; PubMed=2503057;  
RA Eberly L., Crawford I.P.;  
RT "DNA sequence of the cryptophan synthase genes of Pseudomonas  
RT putida";  
RL Biochimie 71:521-531(1989).  
CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING  
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
CC TRPBA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X13299; CAA31660.1; --  
DR InterPro; IPR000847; HTH\_LYSR.  
DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
KW Tryptophan biosynthesis; Transcription regulation; Activator;  
KW DNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DL 2  
DB 4 DL 5

RESULT 36  
ID\_ALL3\_CARMA STANDARD; PRT; 7 AA.  
AC P81806;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 3.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Fortunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 7 AA; 796 MW; 672879CDB476B70 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EP 11  
DB 1 EP 2

RESULT 37  
ID\_CARP\_MYTED STANDARD; PRT; 7 AA.  
AC P10420;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 01-MAR-1989 (Rel. 10, Last annotation update)  
DE Catch-relaxing peptide (CARP).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6650;  
RN [1]  
RP SEQUENCE.

```

RX MEDLINE=89052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC -!- INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 673407267669DB0 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 MP 5
DB 2 MP 3

RESULT 38
CCFL_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adst J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID pCF10.
DR PIR; A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 PV 15
DB 6 PV 7

RESULT 39
EI05_LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Reddyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RT TISSUE=Skin secretion;

```

```

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EP 11
DB 3 EP 4

RESULT 40
FARI_HELTI STANDARD; PRT; 7 AA.
ID FARI_HELTI
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."
RL Peptides 15:31-36(1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76A810 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 PF 12
DB 3 PF 4

RESULT 41
PPH2_LYCPS STANDARD; PRT; 7 AA.
ID PPH2_LYCPS
AC P83379;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme lESAP2 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND

```

RP GLYCOSYLATION.  
 RC STRAIN=CV. MoneyMaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 esculentum) cell cultures.";  
 RL Eur. J. Biochem. 269:6278-6286 (2002).  
 CC -1- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 alcohol + phosphate.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Glycosylated.  
 CC -1- MISCELLANEOUS: In L. esculentum there are at least two isozymes of  
 purple acid phosphatase.  
 KW Hydrolase; Glycoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DL 2  
 ||  
 6 DL 7

RESULT 42  
 UN06 PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OK NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.

RX TISSUE=Needle;  
 RC MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 proteins.";  
 RL Electrophoresis 20:1098-1108 (1999).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LP 8  
 ||  
 5 LP 6

RESULT 43  
 WWA1 ACHFU STANDARD; PRT; 7 AA.  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wwamide-1.

OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OK NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108 (1993).  
 CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS  
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.  
 DR PIR; S33245; S33245.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EM 4  
 ||  
 3 EM 4

RESULT 44  
 WWA3 ACHFU STANDARD; PRT; 7 AA.  
 AC P35921;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wwamide-3.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OK NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108 (1993).  
 DR PIR; S33244; S33244.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7  
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EM 4  
 ||  
 3 EM 4

RESULT 45  
 ALL6 CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiaastatin 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;



OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997)  
 RT "-1- SIMILARITY. BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC "-1- SIMILARITY. BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LP 8  
 DB 1 LP 2  
 RESULT 46  
 ANG2 BOTJA STANDARD; PRT; 8 AA.  
 AC Q10582;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide 11 (fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca".  
 RL Comp Biochem Physiol 113B:467-473(1996)  
 CC "-1- SIMILARITY. BELONGS TO THE SERPIN FAMILY.  
 DR InterPro: IPR002125; Serpinin.  
 KW PROSITE; PS00284; SERPIN; PARTIAL.  
 FT Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 PF 12  
 DB 7 PF 8  
 RESULT 47  
 CADI\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CADI.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, cADI, that  
 RT induces plasmid transfer in Streptococcus faecalis.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC "-1- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PADI.  
 KW Pheromone.  
 FT SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VL 7  
 DB 5 VL 6  
 RESULT 48  
 CLP THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC "-1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;  
 SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PV 6  
 DB 2 PV 3  
 RESULT 49  
 COM2\_CONFU STANDARD; PRT; 8 AA.  
 AC P58785;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=41690;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN=Clipperton Island; TISSUE=Venom;  
 RX MEDLINE=99388839; PubMed=10461743;  
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 RA Oliveira B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 RT dynamics in the contryphan family.";

RL J. Pept. Res. 54:93-99(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -!- SIMILARITY: BELONGS TO THE CRYPTOPHAN FAMILY.  
 KW Toxin; Hydroxylation; D-amino acid.  
 FT DISULFID 2 4  
 FT MOD RES 4 8 D-LEUCINE.  
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7  
 ||  
 DB 3 VL 4

## RESULT 50

PPK2\_PERAM STANDARD; PRT; 8 AA.

AC P82692;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Pyrokinin-2 (Pea-PK-2) (FAPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."  
 RT J. Comp. Neurol. 419:352-363(2000).  
 RL Peptides 18:473-478(1997).  
 RN [2]

RP TISSUE SPECIFICITY.  
 RP MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."  
 RT J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: P800839; PYROKININ; FALSE NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8  
 FT SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12  
 ||  
 DB 3 PF 4

## RESULT 51

PPK3\_PERAM STANDARD; PRT; 8 AA.

AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (FAPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retocerebral complex;  
 RA MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurochemical organs of the American cockroach."  
 RT Insect Biochem. Mol. Biol. 29:139-144(1999).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RP MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach."  
 RT J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8  
 FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12  
 ||  
 DB 3 PF 4

## RESULT 52

UC26\_MAIZE STANDARD; PRT; 8 AA.

AC P80632;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907) (Fragment).  
 OS Zea mays (Maize).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACAD Clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Toulzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernellet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."  
 RT Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 7.0. ITS MW IS: 57.2 kDa.  
 CC Maize-2DFAGE; P80632; COLEOPTILE.  
 FT NON\_TER 1  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 BP 11  
||  
Db 2 BP 3

## RESULT 53

UF06\_MOUSE  
ID \_UF06\_MOUSE STANDARD; PRT; 8 AA.  
AC P38644;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RC MEDLINE=9500907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 817 MW; A35D0878676B05B1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 10 BP 11  
||  
Db 3 BP 4

## RESULT 54

BS43\_SERPL  
ID \_BS43\_SERPL STANDARD; PRT; 9 AA.  
AC P83375;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bacteriocin serracin P 43 kDa subunit (Fragment).  
OS Serratia plymuthica.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=82996;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC STRAIN=J7;  
RC MEDLINE=22293561; PubMed=12406769;  
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,  
RA Van Beeumen J., Thonart P.;  
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and  
its activity against *Erwinia amylovora*, the fire blight pathogen.";  
RL Appl. Environ. Microbiol. 68:5704-5710(2002).  
CC -1- FUNCTION: Major component of a prophage tail sheath (Probable).  
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacterium  
CC *E. amylovora*.  
DR InterPro: IPR006498; Tail tube.  
DR Pfam: PF04985; Phage tube\_1.  
KW Antibiotic; Bacteriocin.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1095 MW; 1B6D412C871E1FB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VL 7  
||  
Db 8 VL 9

## RESULT 55

CCAP\_CARMA  
ID \_CCAP\_CARMA STANDARD; PRT; 9 AA.  
AC P38556;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Cardioactive peptide (CCAP).  
OS Carcinus maenas (Common shore crab) (Green crab),  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
OS Tenebrio molitor (Yellow mealworm), and  
OS Spodoptera eridania (Southern armyworm).  
OC Rukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Rubrachyura; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OX NCBI\_TaxID=6759, 7130, 7067, 37547;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.maenas; TISSUE=pericardial organs;  
RC Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
shore crab *Carcinus maenas*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=M.sexta;  
RC MEDLINE=93050243; PubMed=1426284;  
RA Cheung C.C., Loi F.K., Sylwester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
hawkmoth, *Manduca sexta*.";  
RL FEBS Lett. 313:165-168(1992).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;  
RC MEDLINE=94176032; PubMed=8129851;  
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from *Tenebrio  
molitor* and *Spodoptera eridania*.";  
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).  
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
CC INTO THE HEMOLYMPH.  
DR FIR; A66363; A66363.  
DR FIR; S27233; S27233.  
KW Neuropeptide; Amidation.  
FT DISULFID 3 9  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44BB9 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PF 12  
||  
Db 1 PF 2

## RESULT 56

CXEL\_THUOB  
ID \_CXEL\_THUOB STANDARD; PRT; 9 AA.  
AC P80975;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).  
OS *Thunnus obesus* (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 OX NCBI\_TaxID=8241;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=97454291; PubMed=9310366;  
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
 RA Kadenbach B.;  
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
 RT liver.";  
 RL Eur. J. Biochem. 248:99-103(1997).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.  
 DR PIR; S77984; S77984.  
 DR InterPro; IPR001349; COX6A.  
 DR PROSITE; PS01329; COX6A; PARTIAL.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON TER 1  
 FT NON TER 9  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 FV 15  
 DB 6 FV 7  
 RESULT 57  
 FAR5 PENNO  
 ID FAR5 PENNO STANDARD; PRT; 9 AA.  
 AC P83320;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuroptide FLPS (SWESLELRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupem J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petson A.;  
 RT "Seven novel FMRamide-like neuroptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FAP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 1106 MW; B50B07340735A766 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MP 5

Db 2 MP 3  
 RESULT 58  
 FIBB ERYPA  
 ID FIBB ERYPA STANDARD; PRT; 9 AA.  
 AC P19346;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 DE FGB.  
 GS Erythrocybus patas (Red quonon) (Husar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Erythrocybus.  
 OX NCBI\_TaxID=9538;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85289140; PubMed=3928610;  
 RA Nakamura S., Takenaka O., Takahashi K.;  
 RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and  
 RT patas monkey (Erythrocybus patas): their amino acid sequences,  
 RT restricted mutations, and a molecular phylogeny for macaques,  
 RT guenons, and baboons.";  
 RL J. Biochem. 97:1487-1492(1985).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA) LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 DR PIR; D24180; D24180.  
 DR InterPro; IPR002181; Fibrinogen C.  
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1  
 FT NON TER 9  
 FT NON TER 9  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VL 7  
 DB 4 VL 5  
 RESULT 59  
 KNL3 BOMVA  
 ID KNL3 BOMVA STANDARD; PRT; 9 AA.  
 AC P83058;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE [Thr6]bradykinin.  
 OS Bombina variegata (Yellow-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8348;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Bjournson A.J., McLean S., Rao P.F., Shaw C.;  
 RT "Cloning and post-translational processing of frog skin kininogens.";  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat  
 CC arterial smooth muscle and constriction of intestinal smooth

CC muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
KW Amphibian defense peptide; Vasodilator; Bradykinin.  
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PF 12  
DB 7 PF 8  
RESULT 60  
LMIP LOCM1 STANDARD; PRT; 9 AA.  
AC P31759;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1993 (Rel. 27, Last annotation update)  
DE Locustamyo-inhibiting peptide (LOM-MIP).  
OS Locusta migratoria (migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92179466; PubMed=1796179;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamyo-inhibiting  
RT peptide (LOM-MIP), a novel biologically active neuro-peptide from  
RT Locusta migratoria.";  
RL Regul. Pept. 36:111-119(1991).  
CC -!- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND  
CC -!- OVIDUCT.  
CC -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS  
CC -!- IN THE SUBESOPHAGEAL GANGLION.  
DR PIR; A60065; AKLQIM.  
KW Amidation; Neuropeptide.  
FT MOD RES 9 9  
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DL 2  
DB 4 DL 5  
RESULT 61  
OXVA SCYCA STANDARD; PRT; 9 AA.  
AC P42996;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Asvatocin.  
OS Scyliorhinus canicula (spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95062247; PubMed=7972045;  
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;

RT "Special evolution of neurohypophysial hormones in cartilaginous  
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
RT isolated from the spotted dogfish (Scyliorhinus canicula).";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD RES 9 9  
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PV 6  
DB 7 PV 8  
RESULT 62  
OXYP SCYCA STANDARD; PRT; 9 AA.  
AC P42997;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Phasvatocin.  
OS Scyliorhinus canicula (spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95062247; PubMed=7972045;  
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;  
RT "Special evolution of neurohypophysial hormones in cartilaginous  
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
RT isolated from the spotted dogfish (Scyliorhinus canicula).";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD RES 9 9  
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PV 6  
DB 7 PV 8  
RESULT 63  
OXYT EISFO STANDARD; PRT; 9 AA.  
AC P42998;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Annetocin.  
OS Eلسenia foetida (Common brandling worm) (Common dung-worm).

OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
 OC Lumbricina; Lumbricidae; Eisenia.  
 (1)  
 NCBI\_TaxID=6396;  
 RN SEQUENCE.  
 RP TISSUE=Pituitary;  
 RC MEDLINE=94121660; PubMed=8292046;  
 RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,  
 RA Nomoto K.;  
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,  
 RL Eisenia foetida.";  
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).  
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
 CC NEPHRIDIAL FUNCTION.  
 CC NEPHRIDIAL FUNCTION.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: PC2021; PC2021.  
 DR InterPro: IPR000981; Neurhyp\_horm.  
 DR Pfam: PF00220; hormone4; A.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 996 MW; D4EB76EB45412C9 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 FV 15  
 DB 2 FV 3  
 RESULT 64  
 OXVY\_SQUAC STANDARD; PRT; 9 AA.  
 AC P43000;  
 DT 01-NOV-1995 (Rel. 32; Created)  
 DT 01-NOV-1995 (Rel. 32; Last sequence update)  
 DT 01-NOV-1995 (Rel. 32; Last annotation update)  
 DE Valitocin.  
 OS Squalus acanthias (Spiny dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.  
 OX NCBI\_TaxID=7797;  
 (1)  
 RN SEQUENCE.  
 RP MEDLINE=73031727; PubMed=5083097;  
 RA Acher R., Chauvet J., Chauvet M.-T.;  
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides  
 RT isolated from a cartilaginous fish, Squalus acanthias.";  
 RL Eur. J. Biochem. 29:12-19(1972).  
 (2)  
 RN SEQUENCE.  
 RP MEDLINE=72128038; PubMed=4622083;  
 RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;  
 RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-  
 RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the  
 RT spiny dog-fish (Squalus acanthias).";  
 RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro: IPR000981; Neurhyp\_horm.  
 DR Pfam: PF00220; hormone4; I.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 996 MW; 17ED76EB456D04B CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FV 6  
 DB 7 FV 8  
 RESULT 65  
 PTSP\_BOMMO STANDARD; PRT; 9 AA.  
 AC P82003;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 DE Prothoracicostatic peptide (Bom-PTSP).  
 DE Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 (1)  
 RN SEQUENCE.  
 RP STRAIN=C145 X N140; TISSUE=Brain;  
 RC MEDLINE=20002634; PubMed=10531308;  
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
 RA Katsuka H.;  
 RT "Identification of a prothoracicostatic peptide in the larval brain of  
 RT the silkworm, Bombyx mori.";  
 RL J. Biol. Chem. 274:31169-31173(1999).  
 (2)  
 RN ERRATUM.  
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
 RA Katsuka H.;  
 RL J. Biol. Chem. 275:9892-9892(2000).  
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic  
 CC gland.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.  
 KW Hormone; Amidation.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DL 2  
 DB 4 DL 5  
 RESULT 66  
 SAMP\_MUSCA STANDARD; PRT; 9 AA.  
 AC P19055;  
 DT 01-NOV-1990 (Rel. 16; Created)  
 DT 01-NOV-1990 (Rel. 16; Last sequence update)  
 DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 DE Serum amyloid P-component (SAP) (Fragment).  
 OC Mustelus canis (Smooth dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;  
 OC Mustelus.  
 OX NCBI\_TaxID=7812;  
 (1)  
 RN SEQUENCE.  
 RP MEDLINE=83160932; PubMed=6403520;  
 RA Robey F.A., Tanaka T., Liu T.-Y.;  
 RT "Isolation and characterization of two major serum proteins from the  
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P  
 RT component.";  
 RL J. Biol. Chem. 258:3889-3894(1983).  
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCORD

```

CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
CC PIR; B20569; B20569.
CC DR INTERPRO: IPR001759; Pentaxin.
CC DR PROSITE: PS00289; PENTAXIN; PARTIAL.
CC KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
CC FT DOMAIN 1
CC FT NON_TER 9
CC SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 12 PP 13
Db 2 PP 3

RESULT 67
ULAE HUMAN
ID ULAE HUMAN STANDARD; PRT; 9 AA.
AC P31931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8113870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
CC SWISS-2DPAGE; P31931; HUMAN.
FT NON_TER 9
FT SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 2 LE 3
Db 6 LE 7

RESULT 68
UN19 CLOPA
ID UN19 CLOPA STANDARD; PRT; 9 AA.
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
CC NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=53291870; PubMed=9629918;

```

```

RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
CC VARIANT 8
CC FT NON_TER 9
CC FT SEQUENCE 9 AA; 1128 MW; E33B9B0AF5BB19DA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 3 EM 4
Db 7 EM 8

RESULT 69
UPA3 HUMAN
ID UPA3 HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
CC SWISS-2DPAGE; P30089; HUMAN.
FT NON_TER 1
FT NON_TER 9
FT SEQUENCE 9 AA; 1056 MW; 26F2B1BAP769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 12 PP 13
Db 4 PP 5

RESULT 70
ANG1 BOTJA
ID ANG1 BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lophosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
CC Viperidae; Crotalinae; Bothrops.
CC NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;

```

```

RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON TER 10
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 71
ANGT_BOVIN
ID _ANGT_BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)
DE (Fragment).
GN AGT OR SERPIN A8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliot D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RL Biochem. J. 63:246-254(1957).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC plasma.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10
SQ SEQUENCE 10 AA; 1282 MW; CEF5DD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 72
ANGT_CHICK
ID _ANGT_CHICK STANDARD; PRT; 10 AA.
AC P01018;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III)
DE (Fragment).
GN AGT OR SERPIN A8.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RA MEDLINE=74127845; PubMed=4361802;
RX Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
RT angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C. japonica;
RX MEDLINE=9084684; PubMed=2191893;
RA Takei I., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
RT inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A60824; A60824.
DR PIR; A90917; A90917.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10
SQ SEQUENCE 10 AA; 1232 MW; CEF5DD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PF 12
DB 7 PF 8

RESULT 73
CATB_SHEEP
ID CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B) (Fragment).
GN Ovis aries (Sheep).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.

```



```

OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RA MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows pepidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro: IPR000169; SHPOT acsite.
DR PROSITE: PS00640; THIOL PROTEASE ASN; PARTIAL.
DR PROSITE: PS00139; THIOL PROTEASE CYS; PARTIAL.
DR PROSITE: PS00639; THIOL PROTEASE HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LP 8
DB 1 LP 2

RESULT 74
COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR: S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C53C5B1AB02C33D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

```

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VE 10
DB 5 VE 6

RESULT 75
ESL_LACCA STANDARD; PRT; 10 AA.
ID ESL_LACCA
AC P81758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE.
RC STRAIN=IFPL731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KW Hydrolase; Serine esterase.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VL 7
DB 6 VL 7

Search completed: November 25, 2003, 18:17:25
Job time : 7.26064 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15

Sequence: 1 DLEMPVLPEPPFV 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description         |
|------------|-------|-------------|--------|--------|---------------------|
| 1          | 5     | 33.3        | 20     | Q8KUI9 | Q8kui9 neisseria m  |
| 2          | 4     | 26.7        | 8      | P82598 | P82598 rattus norv  |
| 3          | 4     | 26.7        | 16     | Q9WMG6 | Q9wmg6 sigma virus  |
| 4          | 4     | 26.7        | 17     | Q65373 | Q65373 argyria pseu |
| 5          | 4     | 26.7        | 18     | Q8CJD4 | Q8cjd4 rattus norv  |
| 6          | 4     | 26.7        | 19     | Q11338 | Q11338 molluscum c  |
| 7          | 4     | 26.7        | 20     | Q9R3R7 | Q9r3r7 mycobacteri  |
| 8          | 3     | 20.0        | 7      | O50556 | O50556 actinobacil  |
| 9          | 3     | 20.0        | 8      | Q9TRX8 | Q9trx8 bos taurus   |
| 10         | 3     | 20.0        | 8      | Q89498 | Q89498 murine hepa  |
| 11         | 3     | 20.0        | 9      | P82568 | P82568 streptococc  |
| 12         | 3     | 20.0        | 9      | Q9P8E5 | Q9p8e5 kluyveromyc  |
| 13         | 3     | 20.0        | 9      | Q9UCN5 | Q9ucn5 homo sapien  |
| 14         | 3     | 20.0        | 9      | Q9FXL0 | Q9fxl0 lilium long  |
| 15         | 3     | 20.0        | 9      | O64972 | O64972 avian rous-  |
| 16         | 3     | 20.0        | 10     | Q9R5N2 | Q9r5n2 clostridium  |

Q9r5n1 clostridium  
Q9r5n3 clostridium  
Q9n1xi equus cabal  
Q8wbr7 chaitophoru  
Q9qvj5 rattus sp.  
Q63389 rattus norv  
Q9qvj6 rattus sp.  
Q9esv5 mus musculu  
Q8ife7 ficedula al  
Q8ij33 ficedula hy  
P82700 leucophaea  
Q9s6z9 psophocarpa  
Q9hba4 homo sapien  
Q9ugsl homo sapien  
Q9gi96 sargassum p  
Q988f0 sea mays (m  
P82441 nicotiana t  
Q96d66 homo sapien  
Q9twt4 titius serr  
Q33417 digitalis p  
Q88176 mus musculu  
Q9qv66 rattus sp.  
Q9pbb5 duck hepati  
Q9wmg5 sigma virus  
P82830 rana luteiv  
P83159 anabaena sp  
Q9tww0 trypanosoma  
Q70599 rattus norv  
Q9e0n0 human herpe  
Q9e0n1 human herpe  
Q99bw2 human herpe  
Q9r5z5 streptococc  
Q9jp39 pseudomonas  
Q8rkn0 escherichia  
Q9bxx4 homo sapien  
Q9hcx8 homo sapien  
Q9bxq0 homo sapien  
Q28822 cryptolagus  
Q8hz79 bos taurus  
Q9trq5 mus sp. maj  
Q9tnq1 mus sp. ber  
Q9t3g9 solanum tub  
Q37016 nicotiana a  
Q78794 pyralia l  
Q98f1 sea mays (m  
Q9qv34 rattus sp.  
Q8xms4 escherichia  
P82597 bacillus sp  
Q9ucd4 homo sapien  
Q9trk9 canis fami  
Q9trn9 homo sapien  
Q36789 solanum nig  
Q9quw8 cavia (guin  
Q9pt90 gallus gall  
Q95794 homo sapien  
Q95795 homo sapien  
Q9v3f6 homo sapien  
Q9uc43 homo sapien  
Q9trh5 bos taurus  
Q98k1 solanum tub  
Q8v9k6 human papill  
Q8x4a4 escherichia  
Q9gr1 bordetella  
Q9uc87 homo sapien  
Q9ucf4 homo sapien  
Q9bqt0 homo sapien  
Q9hbd9 homo sapien  
Q9uc58 homo sapien  
Q9tww9 tetrahymena  
Q98365 myosurus mi  
Q9t2g8 solanum tub  
Q98f99 populus tre  
Q61840 mus musculu

90 Q94q2 pseudomonas  
 91 Q44608 buchnera ap  
 92 P74875 salmonella  
 93 O87732 streptomyces  
 94 Q87732 streptomyces  
 95 Q9UC82 homo sapien  
 96 Q9TUG5 latrodectus  
 97 Q9TRP6 bos taurus  
 98 Q9TU42 mammutus p  
 99 Q9TU41 loxodonta v  
 100 Q36925 nicotiana v  
 Q9S8M8 trititum ae

## ALIGNMENTS

## RESULT 1

Q8KUI9 PRELIMINARY; PRT; 20 AA.  
 AC Q8KUI9  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Nitrogen regulatory protein P-II (Fragment).  
 OS Neisseria meningitidis.  
 OC Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]\_TaxID=487;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Cil.  
 RX MEDLINE=22040572; PubMed=12045242;  
 RA Comanducci M., Bandini S., Brunelli B., Adu-Bobie J., Arico B.,  
 RA Capeccchi B., Giuliani M.M., Maignani V., Santini L., Savino S.,  
 RA Granoff D.M., Gaugant D.A., Fizza M., Rappelli R., Mora M.,  
 RT "Nada, a novel vaccine candidate of Neisseria meningitidis."  
 RL J. Exp. Med. 195;1445-1454 (2002).  
 DR EMBL; AF52480; AAMS3107.1; -.  
 DR InterPro; IPR002187; PII\_glnB.  
 DR Pfam; PF00543; P-II; 1.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2165 MW; 5C8529B59D995B5C CRC64;

Query Match 33.3%; Score 5; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVE 10  
 Db 1 VLPVE 5

## RESULT 2

P82598 PRELIMINARY; PRT; 8 AA.  
 AC P82598  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]\_TaxID=10116;  
 RP SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISUS=Liver;  
 RX MEDLINE=20198203; PubMed=10731662;  
 RA Kim K.-Y., Choi I., Kim S.-S.;  
 RT "Purification and characterization of a novel inhibitor of the  
 RT proliferation of hepatic stellate cells."  
 RL J. Biochem. 127:23-27 (2000).  
 SQ SEQUENCE 17 AA; 1882 MW; BFEC2A959495FE6A CRC64;

Query Match 26.7%; Score 4; DB 12; Length 17;

CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE  
 CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.  
 CC -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG  
 CC PROTEIN.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 26.7%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 83e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11  
 Db 3 PVEP 6

## RESULT 3

Q9WMG6 PRELIMINARY; PRT; 16 AA.  
 AC Q9WMG6  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE 2 protein (fragment).  
 GN 2.  
 OS Sigma virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; unclassified Rhabdoviridae.  
 OX NCBI\_TaxID=11301;  
 RN [1]\_TaxID=11301;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212481; PubMed=8384742;  
 RA Teninges D., Bras F., Dezelee S.;  
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
 RT overlap."  
 RL Virology 193:1018-1023 (1993).  
 DR EMBL; S57847; AAD40699.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 26.7%; Score 4; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVEP 8  
 Db 11 PVEP 14

## RESULT 4

Q65373 PRELIMINARY; PRT; 17 AA.  
 AC Q65373  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE ORF 2 minigene.  
 OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus  
 OS (OPSNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=10450;  
 RN [1]\_TaxID=10450;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93286576; PubMed=8389803;  
 RA Russell R.L., Rohmann G.F.;  
 RT "Nucleotide sequence of the ubiquitin-39k gene region from the Orgyia  
 RT pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."  
 RL J. Gen. Virol. 74:1191-1195 (1993).  
 DR EMBL; D13375; BAA02640.1; -.  
 SQ SEQUENCE 17 AA; 1882 MW; BFEC2A959495FE6A CRC64;

Query Match 26.7%; Score 4; DB 12; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 6 VLPV 9  
Db 2 VLPV 5

RESULT 5  
Q8CJDA PRELIMINARY; PRT; 18 AA.  
ID Q8CJDA  
AC Q8CJDA  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Podocin (Fragment).  
GN NPHS2  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,  
RA Roselli S., Antignac C., Matsuyama M., Ideura T.;  
RT "Rat genome fragment containing a part of exons and all of the 3'UTR  
of Nphs2 as well as microsatellite sites."  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB094124; BAC23094.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2033 MW; D47829DCFF0EF4B CRC64;

Query Match 26.7%; Score 4; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 8 PVEP 11  
Db 4 PVEP 7

RESULT 6  
O11338 PRELIMINARY; PRT; 19 AA.  
ID O11338  
AC O11338  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE H1-7-1 protein (Fragment).  
GN H1-7-1  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OX NCBI\_TaxID=10280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,  
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;  
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation  
of a Gene Map of Molluscum Contagiosum Virus."  
RL Virus Genes 0:0-0(1997).  
DR EMBL; U86916; AAB57971.1; -.  
DR InterPro; IPR004900; Pox\_P35.  
DR Pfam; PF03213; Pox\_P35; 1.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;

Query Match 26.7%; Score 4; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 6 VLPV 9  
Db 1

Db 12 VLPV 15

RESULT 7  
Q9RSR7 PRELIMINARY; PRT; 20 AA.  
ID Q9RSR7  
AC Q9RSR7  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DB 30,000 DALTON NATIVE antigen (Fragment).  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92078747; PubMed=1720803;  
RA Salata R.A., Sanson A.J., Malhotra I.J., Wiker H.G., Harboe M.,  
RA Phillips N.B., Daniel T.M.;  
RT "Purification and characterization of the 30,000 dalton native antigen  
of Mycobacterium tuberculosis and characterization of six monoclonal  
antibodies reactive with a major epitope of this antigen."  
RL J. Lab. Clin. Med. 118:589-598(1991).  
DR HSSP; P31953; 1DQV.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2218 MW; 7950F039639EE959 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 7 LPVE 10  
Db 6 LPVE 9

RESULT 8  
O50556 PRELIMINARY; PRT; 7 AA.  
ID O50556  
AC O50556  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE GlyA (Fragment).  
GN GLYA  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
actinomycetemcomitans).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33384;  
RX MEDLINE=96355846; PubMed=8751884;  
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
RA Kraig B.;  
RT "cis Elements and trans factors are both important in strain-specific  
regulation of the leukotoxin gene in Actinobacillus  
actinomycetemcomitans."  
RL Infect. Immun. 64:3451-3460(1996).  
DR EMBL; U51862; AAB88721.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 7 LPV 9  
Db 3 LPV 5

## RESULT 9

Q9TRX8 PRELIMINARY; PRT; 8 AA.  
 AC Q9TRX8  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Osteopontin (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomii;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91282766; PubMed=1676261;  
 RA Prince C.W., Dickie D., Krumdieck C.L.;  
 RT "Osteopontin, a substrate for transglutaminase and factor XIII  
 activity.";  
 RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).  
 FT NON TER 1 1  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db |||  
 1 LPV 3

## RESULT 10

Q89498 PRELIMINARY; PRT; 8 AA.  
 AC Q89498  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
 DE CORONAVIRUS proviral defective INTERFERING particle (DLSSE) OBTAINED  
 DE AFTER SERIAL PASSAGE 17, with 2 recombination sites and ORFs (DLSSE).  
 OS Murine hepatitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11138;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89020822; PubMed=2845661;  
 RA Makino S., Shieh C.K., Soe L.H., Baker S.C., Lai M.M.;  
 RT "Primary structure and translation of a defective interfering RNA of  
 murine coronavirus.";  
 RL Virology 166:550-560(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88062951; PubMed=2824826;  
 RA Soe L.H., Shieh C.K., Baker S.C., Chang M.F., Lai M.M.C.;  
 RT "Sequence and translation of the murine coronavirus 5' end genomic RNA  
 reveals the N-terminal structure of the putative RNA polymerase.";  
 RL J. Virol. 61:3968-3976(1987).  
 DR EMBL; M23258; AAA91862.1; -.  
 DR EMBL; M18040; AAA46465.1; -.  
 SQ SEQUENCE 8 AA; 815 MW; ECB732C72862D766 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6  
 Db |||  
 1-MPV 3

## RESULT 11

P82568 PRELIMINARY; PRT; 9 AA.  
 AC P82568  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE Unknown protein from 2D-page (fragment).  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=13114;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC STRAIN=JRS4;  
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,  
 RA VanBogelen R.A.;  
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
 proteins.";  
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.  
 CC -!- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.  
 FT NON TER 1 1  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db |||  
 1 LPV 3

## RESULT 12

Q9P8E5 PRELIMINARY; PRT; 9 AA.  
 AC Q9P8E5  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE HIS4 protein (Fragment).  
 GN HIS4.  
 OS Kluyveromyces lactis (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
 OX NCBI\_TaxID=28985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=NRRL-Y1140;  
 RC MEDLINE=99449382; PubMed=10518937;  
 RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;  
 RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities  
 RT and differences to Saccharomyces cerevisiae HIS4 gene.";  
 RL FEBS Lett. 458:72-76(1999).  
 DR EMBL; AJ238494; CAB87125.1; -.  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D72D2D767 CRC64;

Query Match 20.0%; Score 3; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db |||  
 2 LPV 4

## RESULT 13

Q9UCN5 PRELIMINARY; PRT; 9 AA.  
 ID Q9UCN5

AC Q9UCN5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE "Cell-surface heparin/HEPARANSULFATE-binding protein peptide 2 (Fragment)."  
 DE  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92291065; PubMed=1601862;  
 RA Raboudi N., Julian J., Rohde L.H., Carson D.D.;  
 RT "Identification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95).";  
 RL J. Biol. Chem. 267:11930-11939(1992)  
 SQ SEQUENCE 9 AA; 1008 MW; CB56D0544732C732 CRC64;  
 Query Match 20.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PVL 7  
 Db 1 PVL 3  
 RESULT 14  
 Q9FXLO PRELIMINARY; PRT; 9 AA.  
 AC Q9FXLO;  
 DT 01-MAR-2001 (TrEMBLrel. 15, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 15, Last sequence update)  
 DE "Lilium longiflorum (Trumpet lily)."  
 DE LILIA protein (Fragment).  
 GN LILIA  
 OS Lilium longiflorum (Trumpet lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Liliaceae;  
 CX NCBI\_TaxID=4690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Hinomoto;  
 RA Uefuji H., Takase H., Hitatsuka K.;  
 RT "Lilium longiflorum LILIA gene, promoter region and partial sequence.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050987; BAB17856.1;  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;  
 Query Match 20.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MPV 6  
 Db 6 MPV 8  
 RESULT 15  
 Q64972 PRELIMINARY; PRT; 9 AA.  
 AC Q64972;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE "Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env protein (fragment)."  
 DE Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env protein (fragment).  
 OS Avian rous-associated virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.  
 CX NCBI\_TaxID=11950;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=99037349; PubMed=2846875;  
 RA Marx M., Crisanti P., Eychene A., Bechade C., Laugier D., Ghysdael J., Pessac B., Calothy G.;  
 RT "Activation and transduction of c-mil sequences in chicken neuroretina cells induced to proliferate by infection with avian lymphomatosis virus.";  
 RL J. Virol. 62:4627-4633(1988).  
 DR EMBL; M25399; AAA42548.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;  
 Query Match 20.0%; Score 3; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPV 9  
 Db 6 LPV 8  
 RESULT 16  
 Q9RSN2 PRELIMINARY; PRT; 10 AA.  
 AC Q9RSN2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE "Neurotoxin type A HN+ 57 kDa SUBUNIT=SAMPLE 2 (Fragment)."  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92143938; PubMed=1781887;  
 RA Somers E., DasGupta B.R.;  
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";  
 RL J. Protein Chem. 10:415-425(1991).  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1225 MW; EC3DE932D366C1BA CRC64;  
 Query Match 20.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VLP 8  
 Db 7 VLP 9  
 RESULT 17  
 Q9RSN1 PRELIMINARY; PRT; 10 AA.  
 AC Q9RSN1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE "Neurotoxin type A HN+ 57 kDa subunit (Fragment)."  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92143938; PubMed=1781887;  
 RA Somers E., DasGupta B.R.;  
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";

RL J. Protein Chem. 10:415-425(1991).

FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1172 MW; E5DAE932D416C1BA CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
DB 7 VLP 9

RESULT 18

Q9R5N3 PRELIMINARY; PRT; 10 AA.

ID Q9R5N3  
AC Q9R5N3  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
DE Neurotoxin type B Hx+ 57 Aa subunit (Fragment).

OS Clostridium botulinum.  
OC Clostridia; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
CX NCBI\_TaxID=1491;

RN [1]

RP SEQUENCE.

RX MEDLINE=92143938; PubMed=1781887;

RA Somers E.; Dasgupta B.R.;

RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";

RL J. Protein Chem. 10:415-425(1991).

FT NON\_TER 1 1

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
DB 7 VLP 9

RESULT 19

Q9N1X1 PRELIMINARY; PRT; 10 AA.

ID Q9N1X1  
AC Q9N1X1  
DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)  
DE Alcohol dehydrogenase 3 (Fragment).

GN ADH3

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

CX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20082971; PubMed=10613847;

RA Caetano A.R.; Shue Y.L.; Lyons L.A.; O'Brien S.J.; Laughlin T.F.;

RA Bowling A.T.; Murray J.D.;

RT "A comparative gene map of the horse (Equus caballus).";

RL Genome Res. 9:1239-1249(1999).

DR EMBL; AF134056; AAF31299.1; -

FT NON\_TER 1 1

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B0D6DD CRC64;

Query Match

20.0%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEP 11  
DB 5 VEP 7

RESULT 20

Q8WBR7

ID Q8WBR7 PRELIMINARY; PRT; 10 AA.

AC Q8WBR7

DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DE Cytochrome oxidase subunit I (Fragment).

GN COI

OS Chaitophorus leucomelas.

OC Mitochondrion.

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

CC Aphidoidea; Drepanosiphidae; Chaitophorus.

OX NCBI\_TaxID=136351;

RN [1]

RP SEQUENCE FROM N.A.

RA Shingleton A.W.; Stern D.L.;

RT "Molecular phylogenetic evidence for multiple origins of ant mutualism

RT within the aphid genus Chaitophorus.";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF444288; AAL38565.1; -

KW Mitochondrion.

FT NON\_TER 1 1

SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match

20.0%; Score 3; DB 8; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
DB 4 LPV 6

RESULT 21

Q9QVJ5

ID Q9QVJ5 PRELIMINARY; PRT; 10 AA.

AC Q9QVJ5

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Myo-inositol hexakisphosphate phosphohydrolase (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CX NCBI\_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=91370007; PubMed=1654110;

RA Yang W.J.; Matsuda Y.; Sano S.; Masutani H.; Nakagawa H.;

RT "Purification and characterization of phytase from rat intestinal

RT mucosa.";

RL Biochim. Biophys. Acta 1075:75-82(1991).

FT NON\_TER 1 1

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1086 MW; 37A8EA4B1B02D7 CRC64;

Query Match

20.0%; Score 3; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10  
DB 3 PVE 5

```

RESULT 22
Q63389 PRELIMINARY; PRT; 10 AA.
AC Q63389;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Ornithine decarboxylase (ODC).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=SPRague-Dawley; Tissue=Testis;
RX MEDLINE=8925378; PubMed=2722815;
RA Wen L., Huang J.K., Blackshear F.J.;
RT "Rat ornithine decarboxylase gene. Nucleotide sequence, potential
regulatory elements, and comparison to the mouse gene.";
RL J. Biol. Chem. 264:9016-9021(1989).
DR EMBL; J04791; AAA66163.1; -.
SQ SEQUENCE 10 AA; 1074 MW; 30F6BE69D415BDC7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 8 PVL 10

RESULT 23
Q9QVJ6 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYO-inositol hexakisphosphate phosphohydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE
RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
mucosa.";
RL Biochim. Biophys. Acta 1075:75-82(1991).
SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10
DB 3 PVE 5

RESULT 24
Q9ESU5 PRELIMINARY; PRT; 10 AA.
AC Q9ESU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).

```

---

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
Yonish-Rouach E., Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
p53-responsive element that is activated by p53 mutants unable to
induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 7 VLP 9

RESULT 25
Q8JFE7 PRELIMINARY; PRT; 10 AA.
AC Q8JFE7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]_TaxID=59894;
RP SEQUENCE FROM N.A.
RC STRAIN=Bc5; and Bc8;
RX MEDLINE=21918460; PubMed=11918793;
RA Finner C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
limited available sequence information: high nucleotide diversity
revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAM22903.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 20.0%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 5 VLP 7

RESULT 26
Q8JFJ3 PRELIMINARY; PRT; 10 AA.
AC Q8JFJ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



OC Archosauia; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
 CX NCBI\_TaxID=46689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Op86;  
 RX MEDLINE=21918460; PubMed=11918793;  
 RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;  
 RT "Single-nucleotide polymorphism characterization in species with  
 RT limited available sequence information: high nucleotide diversity  
 RT revealed in the avian genome.";  
 RL Mol. Ecol. 11:603-612(2002).  
 DR EMBL: AF454216; AM22902.1; --  
 FT NON\_TER 1  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;  
 Query Match 20.0%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 VLP 8  
 Db |||  
 5 VLP 7  
 RESULT 27  
 P82700  
 ID P82700 PRELIMINARY; PRT; 11 AA.  
 AC Q82700;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Periviscerokinin-3 (LEM-PVK-3).  
 OS Periviscerae maderae (Madeira cockroach),  
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
 OS Blaberus craniifer,  
 OS Blaberus dubia (Argentinian wood cockroach), and  
 OS Gomphadorina portentosa (Cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberridae; Leucophaea.  
 CX NCBI\_TaxID=6988, 6990, 6982, 132935, 36953;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.  
 RC TISSUE-ABDOMINAL PERISYMPATHETIC ORGANS;  
 RX MEDLINE=20307624; PubMed=10845066;  
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;  
 RT "Identification of novel periviscerokinin from single neurohaemal  
 RT release sites in insects. MS/MS fragmentation complemented by Edman  
 RT degradation.";  
 RL Eur. J. Biochem. 267:3869-3873(2000).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11  
 FT MOD\_RES 11  
 SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;  
 Query Match 20.0%; Score 3; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 PPP 13  
 Db |||  
 7 FFF 9  
 RESULT 28  
 Q9S829  
 ID Q9S829 PRELIMINARY; PRT; 11 AA.  
 AC Q9S829;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE W1 peptide (Fragment).  
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 CX NCBI\_TaxID=3891;  
 RN [1]  
 RP SEQUENCE  
 EX MEDLINE=92232221; PubMed=1368037;  
 RA Hirano H., Kagawa H., Okubo K.;  
 RL Phytochemistry 31:731-735(1992).  
 FT NON\_TER 1  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1120 MW; 8391BACD77772D1 CRC64;  
 Query Match 20.0%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 PVL 7  
 Db |||  
 7 PVL 9  
 RESULT 29  
 Q9HB04  
 ID Q9HB04 PRELIMINARY; PRT; 12 AA.  
 AC Q9HB04;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Caspase 8 isoform 1 (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Eckhart L., Fischer H., Bach J., Henry M., Ban J., Tschachler E.;  
 RT "Identification and characterization of novel splice variants of human  
 RT caspase-8".  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL: AF207672; AAC10682.1; --  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1343 MW; 80F055095B6B02D1 CRC64;  
 Query Match 20.0%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 VEP 11  
 Db |||  
 6 VEP 8  
 RESULT 30  
 Q9UGS1  
 ID Q9UGS1 PRELIMINARY; PRT; 12 AA.  
 AC Q9UGS1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE DJ796117.4 (Novel protein similar to GS2) (fragment).  
 GN DJ796117.4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barlow K.;

```

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;
Query Match 20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LEM 4
Db 3 LEM 5

RESULT 31
Q9GI96 PRELIMINARY; PRT; 12 AA.
ID Q9GI96;
AC Q9GI96;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
DE RBGS.
GN Sargassum polycystum.
OC Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OC NCBI_TaxID=127578;
OX NCBI_TaxID=127578;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=nepl27;
EC Phillips N.E.;
RA "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=nepl27;
RA Phillips N.E.; Smith C.M., Morden C.W.;
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
KW NON_TER 12
SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;
Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 PFF 14
Db 8 PFF 10

RESULT 32
Q9S8F0 PRELIMINARY; PRT; 12 AA.
ID Q9S8F0;
AC Q9S8F0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.19) (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
OX NCBI_TaxID=4577;
RN [1] SEQUENCE.
RP MEDLINE=95322859; PubMed=7599527;

```

---

```

RA Holt D.C., Lay V.J., Clarke E.D., Dinmore A., Jepson I., Bright S.W.,
RA Greenland A.J.;
RT "Characterization of the safener-induced glutathione S-transferase
RT isoform II from maize.";
RL Planta 196:295-302(1995).
SQ SEQUENCE 12 AA; 1382 MW; C28977F65975B05D CRC64;
Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PFF 15
Db 8 PFF 10

RESULT 33
P82441 PRELIMINARY; PRT; 12 AA.
ID P82441;
AC P82441;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 26 kDa cell wall protein (Fragment).
DE Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
OX NCBI_TaxID=4097;
RN [1] SEQUENCE.
RP STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
KW NON_TER 12
SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;
Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 PFF 15
Db 5 PFF 7

RESULT 34
Q96Q66 PRELIMINARY; PRT; 13 AA.
ID Q96Q66;
AC Q96Q66;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial ribosomal protein L38 (Fragment).
GN MRP238.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=21439115; PubMed=11543634;
RX Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RA "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).

```

DR EMBL; AB051345; BAB54935.1; -.  
 KW Ribosomal protein. 13  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1440 MW; 22C088BAFDF21448 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPV 6  
 DB 1 MPV 3  
 |||

## RESULT 35

Q9TWR4 PRELIMINARY; PRT; 13 AA.

AC Q9TWR4; 2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DE Peptide T-BRADYKININ potentiator.  
 OS Tityus serrulatus (Brazilian scorpion).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Buthoidea; Buthidae; Tityus.  
 OX NCBI\_TaxID=6887;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94024945; PubMed=8212046;  
 RA Ferreira L.A., Alves E.W., Henriques O.B.;  
 RT "Peptide T, a novel bradykinin potentiator isolated from Tityus  
 serrulatus scorpion venom.";  
 RL Toxicon 31:941-947(1993).  
 SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10  
 DB 6 PVE 8  
 |||

## RESULT 36

Q33417 PRELIMINARY; PRT; 13 AA.

AC Q33417; 1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-MAY-1998 (TRENBLrel. 10, Last annotation update)  
 DE Rps19, protein (Fragment).  
 GN Rps19.  
 OS Digitalis purpurea (Common foxglove).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Lamiales; Antirrhinaceae; Digitalis.  
 OX NCBI\_TaxID=4164;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96397499; PubMed=8804393;  
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;  
 RT "Ebb and Flow of the Chloroplast Inverted Repeat.";  
 RL Mol. Gen. Genet. 252:195-206(1996).  
 DR EMBL; Z11251; CA94968.1; -.  
 KW Chloroplast.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1518 MW; 4D775A09A55D4333 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15  
 DB 9 PFV 11  
 |||

## RESULT 37

O88176 PRELIMINARY; PRT; 13 AA.

AC O88176; 1998 (TRENBLrel. 08, Created)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM1 OR NCAM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=balb-c; TISSUE=Liver;  
 RX MEDLINE=98250618; PubMed=9582442;  
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
 RT "A cis-acting regulatory element that affects the alternative splicing  
 of a muscle-specific exon in the mouse NCAM gene.";  
 RL Biochim. Biophys. Acta 1397:305-315(1998).  
 DR EMBL; AB001873; BA31275.1; -.  
 DR MGD; MGI:97281; Ncam1  
 FT NON\_TER 13  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 DB 4 LPV 6  
 |||

## RESULT 38

O9QVK6 PRELIMINARY; PRT; 13 AA.

AC O9QVK6; 2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
 DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373341; PubMed=1832670;  
 RA Hoppner W., Beckert L., Buck F., Seitz H.J.;  
 RT "Is the p29 protein involved in the rapid regulation of  
 phosphoenolpyruvate carboxykinase (GTP)?";  
 RL J. Biol. Chem. 266:17257-17260(1991).  
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBA6D2D7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 DB 5 LPV 7  
 |||

## RESULT 39

```

Q9PXB5 .
ID Q9PXB5 PRELIMINARY; PRT; 13 AA.
AC Q9PXB5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 14, Last annotation update)
DE 170 kDa DHRV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retrovirus; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 7 PVL 9

RESULT 40
Q9WNG5 PRELIMINARY; PRT; 13 AA.
AC Q9WNG5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE 3 protein (fragment).
GN GENE 3.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212481; PubMed=8384742;
RA Teninges D., Bris F., Dezelee S.;
RT "Genome organization of the sigma rhabdovirus: six genes and a gene
RT overlap.";
RL Virology 193:1018-1023(1993).
DR EMBL; S57850; AAD40700.1; -.
FT NON TER 13
SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 7 VLP 9

RESULT 41
P82830 PRELIMINARY; PRT; 13 AA.
AC P82830;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE Temporin-11A.
OS Rana luteiventris.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

Q9PXB5 .
ID Q9PXB5 PRELIMINARY; PRT; 13 AA.
AC Q9PXB5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE 170 kDa DHRV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retrovirus; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
DB 1 VLP 3

RESULT 42
P83159 PRELIMINARY; PRT; 14 AA.
AC P83159;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
DE rod (fragment).
OS Anabaena sp. (strain L311).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apke S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (Oct-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS
CC -!- ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
KW Phycobilisome; Photosynthesis.
FT NON TER 14
SQ SEQUENCE 14 AA; 1405 MW; 96823844F60A3115 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
DB 12 EPF 14

RESULT 43
Q9TWW0 PRELIMINARY; PRT; 14 AA.
AC Q9TWW0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

```

```

DE Histone C (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;
RX MEDLINE=93064852; PubMed=1437281;
RA Bender K., Betschart B., Schaller J., Kampfer U., Hecker H.;
RT "Sequence differences between histones of procyclic Trypanosoma brucei
RT brucei and higher eukaryotes.";
RL Parasitology 105:97-104(1992).
SQ SEQUENCE 14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
Db 8 VLP 10

RESULT 44
ID O70599 PRELIMINARY; PRT; 14 AA.
AC O70599;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Thymidine kinase (EC 2.7.1.21) (Fragment).
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sauer M.;
RL Thesis (1999), University of Vienna. Inst. of Molecular Biology.
DR EMBL; A006455; CAA07030.1; -.
KW Kinase; Transferase.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8
Db 9 VLP 11

RESULT 45
Q9EON0 PRELIMINARY; PRT; 14 AA.
ID Q9EON0
AC Q9EON0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელიj A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1.";

```

```

RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290018; AAG3134.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEM 4
Db 5 LEM 7

RESULT 46
Q9EON1 PRELIMINARY; PRT; 14 AA.
ID Q9EON1
AC Q9EON1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელიj A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1.";
RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290017; AAG3133.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEM 4
Db 5 LEM 7

RESULT 47
Q9EON2 PRELIMINARY; PRT; 14 AA.
ID Q9EON2
AC Q9EON2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21119878; PubMed=11273067;
RA Osterhaus A.D.M.E.;
RA Osterhaus A.D.M.E.;
RT "Herpes simplex virus type 1 transmission through corneal
RT transplantation.";
RL Lancet 357:442-442(2001).
DR EMBL; AF324428; AAK12110.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

```

```
Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
 |||
 5 LEM 7

Db

RESULT 48
ID Q9R5Z5 PRELIMINARY; PRT; 15 AA.
AC Q9R5Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Streptolysin O (Fragment).
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273535; PubMed=8500915;
RA Gerlach D., Kohler W., Gunther E., Mann K.;
RT "Purification and characterization of streptolysin O secreted by
RT Streptococcus equisimilis (group C).";
RL Infect. Immun. 61:2727-2731(1993).
SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5
 |||
 4 EMP 6

Db

RESULT 49
ID Q9JF39 PRELIMINARY; PRT; 15 AA.
AC Q9JF39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE HrpK (Fragment).
GN HRPK.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=61;
RA MEDLINE=97348579; PubMed=9204563;
RA Alfano J.R., Kim H.S., Delaney T.P., Collmer A.;
RT "Evidence that the Pseudomonas syringae pv. syringae hrp-linked hrpA
RT gene encodes an Avr-like protein that acts in an hrp-dependent manner
RT within tobacco cells.";
RL Mol. Plant Microbe Interact. 10:580-588(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=61;
RA MEDLINE=20243785; PubMed=10781092;
RA Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L.,
RA Petnicki-Ocwieja T., van Dijk K., Collmer A.;
RT "The Pseudomonas syringae Hrp pathogenicity island has a tripartite
RT mosaic structure composed of a cluster of type III secretion genes
RT bounded by exchangeable effector and conserved effector loci that
RT contribute to parasitic fitness and pathogenicity in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4856-4861(2000).
RL EMBL; AF232003; AAF71482.1; -.
```

```
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1696 MW; C0E7FAC1E44B4B20 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
 |||
 4 PVL 6

Db

RESULT 50
ID Q8RKN0 PRELIMINARY; PRT; 15 AA.
AC Q8RKN0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transposase ORF1005 (Fragment).
GN ORF1005.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex sull-type integrin in Escherichia coli carrying the
RT bla(CIX-M-9) gene.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092058; AAM15719.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1751 MW; 2D706E3A12001249 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
 |||
 10 LPV 12

Db

RESULT 51
ID Q9BXX4 PRELIMINARY; PRT; 15 AA.
AC Q9BXX4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Transcription factor PAX 5 (PAX5) (Fragment).
GN PAX5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirabayashi Y., Rahman M., Sasaki T.;
RT "Identification of a novel repressor element in the 5'UTR of human
RT BSAP/FoxSA.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354098; PubMed=11460166;
RA Paqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT "Hypermethylation of multiple proto-oncogenes in B-cell diffuse large-
RT cell lymphomas.";
RL Nature 412:341-346(2001).
```

DR EMBL; AF268279; AAK25737.1; -;  
 DR EMBL; AF386790; AAK70869.1; -;  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLE 3  
 DB 2 DLE 4

RESULT 52  
 Q9HCX8 PRELIMINARY; PRT; 15 AA.

AC Q9HCX8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE CAMP-specific phosphodiesterase 4D.  
 GN PDE4DN1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20374482; PubMed=10913353;  
 RA Miro X., Casacuberta J.M., Gutierrez-Lopez M.D., Landazuri M.O.,  
 RA Puigdomenech P.;  
 RT "Phosphodiesterases 4D and 7A splice variants in the response of HUVEC  
 RT cells to TNP-alpha1.";  
 RL Biochem. Biophys. Res. Commun. 274:415-421(2000).  
 DR EMBL; AJ250852; CAC03756.1; -;  
 SQ SEQUENCE 15 AA; 1972 MW; 36C1CF0521236FEE CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFF 14  
 DB 7 PFF 9

RESULT 53  
 Q9BXQ0 PRELIMINARY; PRT; 15 AA.

AC Q9BXQ0;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE Tissue transglutaminase (EC 2.3.2.13) (Fragment).  
 GN TGM2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Festoff B.W.;  
 RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau  
 RT aggregation in Alzheimer's disease.";  
 RL J. Biol. Chem. 0:0-0(2001).  
 DR EMBL; AF311286; AAK15272.1; -;  
 KW Acyltransferase; Transferrase.  
 FT NON TER 1

SQ SEQUENCE 15 AA; 1641 MW; C340982AFBFBF851 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PFF 12  
 DB 2 PFF 4

RESULT 54

Q28822 PRELIMINARY; PRT; 15 AA.  
 AC Q28822;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE Voltage-dependent dihydropyridine-sensitive calcium channel alpha 1  
 DE subunit 155 kDa isoform (Rabbit).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92265303; PubMed=1316766;  
 RA Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;  
 RT "A two-motif isoform of the major calcium channel subunit in skeletal  
 RT muscle.";  
 RL Neuron 8:899-906(1992).  
 DR EMBL; S36895; AAB22180.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1796 MW; 841B2D08BFE99DB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4  
 DB 13 LEM 15

RESULT 55

Q8HZ79 PRELIMINARY; PRT; 15 AA.  
 AC Q8HZ79;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Alpha-synuclein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OX NCBI\_TaxID=9913;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;  
 RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine  
 RT adrenal medullary chromaffin cells.";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY124580; AAM94359.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1774 MW; 1715433C9115DADA CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
 DB 1 EMP 3

## RESULT 58

Q9TN05 PRELIMINARY; PRT; 15 AA.  
 AC Q9TN05;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Major histocompatibility complex class II bound peptide  
 DE (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94082939; PubMed=8260091;  
 RA Freed J.H., Marrack P.;  
 RT "tissue-specific expression of self peptides bound by major  
 RT histocompatibility complex class II molecules.";  
 RL Chem. Immunol. 57:88-112(1993).  
 KW MHC.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1607 MW; CBE93F7E8C5E7425 CRC64;  
 Query Match 20.0%; Score 3; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db 10 LPV 12

## RESULT 57

Q9TN01 PRELIMINARY; PRT; 15 AA.  
 AC Q9TN01;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex  
 DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin  
 DE (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94240094; PubMed=8183884;  
 RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;  
 RT "Characterization of an incompletely assembled major  
 RT histocompatibility class I molecule (H-2Kb) associated with unusually  
 RT long peptides: implications for antigen processing and presentation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).  
 KW MHC.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;  
 Query Match 20.0%; Score 3; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

Db 7 LPV 9

## RESULT 58

Q9T2G9 PRELIMINARY; PRT; 15 AA.  
 ID Q9T2G9

AC Q9T2G9;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE Carbonic anhydrase (EC 4.2.1.1) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96327808; PubMed=8680307;  
 RA Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;  
 RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum  
 RT L. leaves: characterization of two compartment-specific isoforms.";  
 RL Planta 199:79-88(1996).  
 SQ SEQUENCE 15 AA; 1647 MW; CA587063CDD32976 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVE 10

Db 10 PVE 12

## RESULT 59

Q37016 PRELIMINARY; PRT; 15 AA.  
 ID Q37016;  
 AC Q37016;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
 DE RPS19, protein (Fragment).  
 GN RPS19.  
 OS Nicotiana glauca (Winged tobacco) (Persian tobacco),  
 OS Nicotiana tabacum (Common tobacco), and  
 OS Nicotiana glutinosa (Tobacco).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Aceridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4087, 4097, 35889;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;  
 RL Mol. Gen. Genet. 0:0-0(1996).  
 DR EMBL; 271239; CAA94944.1; -;  
 DR EMBL; 271236; CAA94937.1; -;  
 DR EMBL; 271238; CAA94942.1; -;  
 DR InterPro; IPR002222; Ribosomal\_S19.  
 DR Pfam; PF00203; Ribosomal\_S19; I.  
 KW Chloroplast.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1756 MW; 09DE1D775A138C5D CRC64;

Query Match 20.0%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15

Db 9 PFV 11

## RESULT 60

Q78794 PRELIMINARY; PRT; 15 AA.  
 ID Q78794  
 AC Q78794;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)



DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE Mitochondrial ribosomal protein S14 (Fragment).  
 GN RPS14.  
 OS Pylaiella littoralis.  
 OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;  
 OC Acinetosporaceae; Pylaiella.  
 OX NCBI\_TaxID=2885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ROSCOFF;  
 RX MEDLINE=98239704; PubMed=9571021;  
 RA Rousvoal S., Oudot M.-P., Fontaine J.-M., Kloareg B.,  
 RA Loiseaux-De Goer S.L.,  
 RT "Witnessing the evolution of transcription in mitochondria: the  
 mitochondrial genome of the primitive brown alga Pylaiella littoralis  
 (L.) Kjellm. encodes a T7-like RNA polymerase.";  
 RL J. Mol. Biol. 277:1047-1057(1998).  
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 CC -!- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
 DR EMBL; AF034976; AAC23952.1; -;  
 DR InterPro; IPR001209; Ribosomal S14.  
 DR PROSITE; PS00527; RIBOSOMAL S14; PARTIAL.  
 KW Ribosomal protein; Mitochondrion; Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1599 MW; 2D406410C588731B CRC64;  
 Query Match 20.0%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VLP 8  
 DB |||  
 6 VLP 8  
 RESULT 61  
 Q9S8F1 PRELIMINARY; PRT; 15 AA.  
 AC Q9S8F1;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
 DE Glutathione S-transferase isoform II (SC 2.5.1.18) (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95322859; PubMed=7599527;  
 RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,  
 RA Greenland A.J.;  
 RT "Characterization of the safener-induced glutathione S-transferase  
 isoform II from maize.";  
 RL Planta 196:295-302(1995).  
 SQ SEQUENCE 15 AA; 1530 MW; 2F105C48F7DD3A56 CRC64;  
 Query Match 20.0%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MPV 6  
 DB |||  
 5 MPV 7  
 RESULT 62  
 Q9QV34 PRELIMINARY; PRT; 15 AA.  
 ID Q9QV34  
 AC Q9QV34;

DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DE CHOLIC acid transport protein P50 (Fragment).  
 DE CHOLIC acid transport protein P50 (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94183413; PubMed=8136027;  
 RA Hoffmann A., Mulliner S., Ziegler K., Rasold H.;  
 RT "Purification and partial sequence of proteins involved in the cholic  
 acid transport into rat liver hepatocytes.";  
 RL J. Protein Chem. 12:765-769(1993).  
 SQ SEQUENCE 15 AA; 1597 MW; D719DFB7C75AC0B CRC64;  
 Query Match 20.0%; Score 3; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PVL 7  
 DB |||  
 3 PVL 5  
 RESULT 63  
 Q8KM54 PRELIMINARY; PRT; 16 AA.  
 ID Q8KM54;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Transposase (Fragment).  
 GN TNPA.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82137098; PubMed=6277510;  
 RA Casadaban M.J., Chou J., Cohen S.N.;  
 RT "Overproduction of the Tn3 transposition protein and its role in DNA  
 transposition.";  
 RL Cell 28:345-354(1982).  
 DR EMBL; J01833; AAM54741.1; -;  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1821 MW; 4E376F4D2E554F8 CRC64;  
 Query Match 20.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MPV 6  
 DB |||  
 12 MPV 14  
 RESULT 64  
 P82597 PRELIMINARY; PRT; 16 AA.  
 ID P82597;  
 AC P82597;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE Thermolabile monoacylglycerol lipase (MGUP) (24 kDa) (SC 3.1.1.23)  
 DE (Fragment).  
 OS Bacillus sp.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1409;  
 RN [1]  
 RP SEQUENCE.

```

RC STRAIN=H-257;
RX MEDLINE=20196254; PubMed=10731713;
RA Inamura S., Kitaara S.;
RT "Purification and characterization of a monoacylglycerol lipase from
RL the moderately thermophilic Bacillus sp. H-257.";
RJ J. Biochem. 127:419-425(2000).
CC -1- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
CC OCCURRING WITH 1-MONOLAUROYLGLYCEROL.
CC -1- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
CC TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -1- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
CC OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER. 16 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVL 7
DB 5 PVL 7
|||
|||

RESULT 65
Q9UCD4 PRELIMINARY; PRT; 16 AA.
ID Q9UCD4 PRELIMINARY; PRT; 16 AA.
AC Q9UCD4 PRELIMINARY; PRT; 16 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94028977; PubMed=8215410;
RX Wrighton S.A., Stevens J.C., Becker G.W., VandenBranden M.;
RT "Isolation and characterization of human liver cytochrome P450 2C19:
RT correlation between 2C19 and S-mephenytoin 4'-hydroxylation.";
RL Arch. Biochem. Biophys. 306:240-245(1993).
SQ SEQUENCE 16 AA; 1792 MW; 68C719F62D2C7EEC CRC64;

Query Match 20.0%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFV 15
DB 3 PFV 5
|||
|||

RESULT 66
Q9TRK9 PRELIMINARY; PRT; 16 AA.
ID Q9TRK9 PRELIMINARY; PRT; 16 AA.
AC Q9TRK9 PRELIMINARY; PRT; 16 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)
DE Casein kinase II=24 kDa polypeptide (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RA MEDLINE=93054738; PubMed=1331100;

```

```

RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin.";
RL J. Biol. Chem. 267:23789-23796(1992).
FT NON TER. 16 16
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;

Query Match 20.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPF 12
DB 6 EPF 8
|||
|||

RESULT 67
Q9TNN9 PRELIMINARY; PRT; 16 AA.
ID Q9TNN9 PRELIMINARY; PRT; 16 AA.
AC Q9TNN9 PRELIMINARY; PRT; 16 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 20S proteasome subunit X (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94215713; PubMed=8163024;
RX Akiyama K., Kagawa S., Tamura T., Shimbara N., Takashina M.,
RX Kristensen P., Hendil K.B., Tanaka K., Ichihara A.;
RT "Replacement of proteasome subunits X and Y by LMP7 and LMP2 induced
RT by interferon-gamma for acquisition of the functional diversity
RT responsible for antigen processing.";
RL FEBS Lett. 343:85-88(1994).
KW MHC.
SQ SEQUENCE 16 AA; 1892 MW; BB869802A16657F1 CRC64;

Query Match 20.0%; Score 3; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLB 3
DB 5 DLB 7
|||
|||

RESULT 68
Q36789 PRELIMINARY; PRT; 16 AA.
ID Q36789 PRELIMINARY; PRT; 16 AA.
AC Q36789 PRELIMINARY; PRT; 16 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Rps19, protein (Fragment).
OS Solanum nigrum (Black nightshade).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4112;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96397499; PubMed=8804393;
RX Goulding S.E., Olmsstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.";
RL Mol. Gen. Genet. 252:195-206(1996).
DR EMBL; Z71249; CAA94964.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; I.

```



## Q9Y3F6

ID Q9Y3F6 PRELIMINARY; PRT; 17 AA.  
 AC Q9Y3F6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE EST00098 protein (Fragment).  
 GN EST00098.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99299247; PubMed=10369878;  
 RX Gilley J., Fried M.;  
 RT "Extensive gene order differences within regions of conserved synteny  
 between the Fugu and human genomes: implications for chromosomal  
 RT volution and the cloning of disease genes";  
 RL Hum. Mol. Genet. 8:1313-1320(1999).  
 DR EMBL: Y17449; CAB4366.1; -.  
 FT NON-TER 17  
 SQ SEQUENCE 17 AA; 1695 MW; 1EA4692B032AF8D0 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPV 6  
 Db 1 MPV 3

## RESULT 74

OSUC43  
 ID Q9UC43 PRELIMINARY; PRT; 17 AA.

AC Q9UC43;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Interferon-alpha-induced protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96132854; PubMed=8557639;  
 RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;  
 RT "Purification, microsequencing, and immunolocalization of p36, a new  
 RT interferon-alpha-induced protein that is associated with human lupus  
 RT inclusions";  
 RL J. Biol. Chem. 271:1118-1126(1996).  
 SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 20.0%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL 7  
 Db 8 PVL 10

## RESULT 75

Q9TRH5  
 ID Q9TRH5 PRELIMINARY; PRT; 17 AA.

AC Q9TRH5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Alpha-S1-casein homolog (Fragment).  
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93231344; PubMed=1299613;  
 RA Neuteboom B., Giuffrida M.G., Conti A.;  
 RT "Isolation of a new ligand-carrying casein fragment from bovine  
 RT mammary gland microsomes";  
 RL FEBS Lett. 305:189-191(1992).  
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF068EA0537F CRC64;

Query Match 20.0%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPF 13  
 Db 4 PPF 6

Search completed: November 25, 2003, 18:25:19  
 Job time : 38.1936 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48.5904 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15

Sequence: 1 DLEMPVLPVEPPFV 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03:\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 15    | 100.0       | 15     | AA872250 | Colostrinin derive |
| 2          | 15    | 100.0       | 15     | AA872504 | Colostrinin peptid |
| 3          | 15    | 100.0       | 15     | AA872536 | Colostrinin peptid |
| 4          | 15    | 100.0       | 15     | AA859322 | Ewe colostrinin pe |
| 5          | 15    | 100.0       | 15     | AA859322 | Colostrinin consti |
| 6          | 15    | 100.0       | 15     | AA851040 | Colostrinin consti |
| 7          | 15    | 100.0       | 15     | AA851040 | Neural cell regula |
| 8          | 15    | 100.0       | 16     | AA859352 | Ewe colostrinin pe |
| 9          | 10    | 66.7        | 10     | AA807187 | Colostrinin peptid |

|    |   |      |    |    |          |                    |
|----|---|------|----|----|----------|--------------------|
| 10 | 9 | 60.0 | 10 | 22 | AA807197 | Modified colostrin |
| 11 | 6 | 40.0 | 10 | 22 | AA875678 | HLA class I bindin |
| 12 | 5 | 33.3 | 6  | 17 | AAW03289 | CNS-inhibiting pep |
| 13 | 5 | 33.3 | 6  | 23 | ABG32212 | Sheep colostrinin  |
| 14 | 5 | 33.3 | 8  | 13 | AA821263 | N-terminal of gene |
| 15 | 5 | 33.3 | 10 | 24 | ABR47208 | Staphylococcus aur |
| 16 | 5 | 33.3 | 10 | 24 | ABR47319 | Staphylococcus aur |
| 17 | 5 | 33.3 | 11 | 17 | AAW03290 | CNS-inhibiting pep |
| 18 | 5 | 33.3 | 13 | 17 | AAW03291 | CNS-inhibiting pep |
| 19 | 5 | 33.3 | 15 | 16 | AA879630 | Endocarditis speci |
| 20 | 5 | 33.3 | 18 | 22 | AA872267 | Colostrinin derive |
| 21 | 5 | 33.3 | 18 | 22 | AA872520 | Colostrinin peptid |
| 22 | 5 | 33.3 | 18 | 22 | AA872522 | Colostrinin peptid |
| 23 | 5 | 33.3 | 18 | 22 | AA859330 | Ewe colostrinin pe |
| 24 | 5 | 33.3 | 18 | 23 | AA820249 | Colostrinin consti |
| 25 | 5 | 33.3 | 18 | 23 | AAW51056 | Colostrinin consti |
| 26 | 5 | 33.3 | 18 | 23 | AA814598 | Neural cell regula |
| 27 | 5 | 33.3 | 20 | 11 | AA804512 | Transposon phoA pr |
| 28 | 4 | 26.7 | 4  | 20 | AAW78500 | Dioxin-binding pep |
| 29 | 4 | 26.7 | 5  | 19 | AAW65791 | Polyprolyl inhibi  |
| 30 | 4 | 26.7 | 5  | 22 | AA873397 | Human gene 9-encod |
| 31 | 4 | 26.7 | 5  | 23 | ABG64291 | Human albumin fusi |
| 32 | 4 | 26.7 | 5  | 24 | ABU12265 | Chymotrypsin inhib |
| 33 | 4 | 26.7 | 5  | 24 | ABU12267 | Chymotrypsin inhib |
| 34 | 4 | 26.7 | 6  | 17 | AA895892 | Angiotensin conver |
| 35 | 4 | 26.7 | 7  | 17 | AAW04273 | Milk derived anti- |
| 36 | 4 | 26.7 | 7  | 17 | AA895891 | Angiotensin conver |
| 37 | 4 | 26.7 | 7  | 19 | AAW59314 | Non-polio enterovi |
| 38 | 4 | 26.7 | 7  | 20 | AAV50072 | Coxsackievirus A v |
| 39 | 4 | 26.7 | 7  | 20 | AAV16900 | Heat shock protein |
| 40 | 4 | 26.7 | 7  | 21 | AA196209 | Arabidopsis AHAS s |
| 41 | 4 | 26.7 | 7  | 22 | AAU72042 | Melanoma antigen,  |
| 42 | 4 | 26.7 | 7  | 22 | ABG97087 | Human leukocyte an |
| 43 | 4 | 26.7 | 7  | 23 | AAU80592 | Javelin peptide #2 |
| 44 | 4 | 26.7 | 8  | 15 | AAW58331 | Hypotensive polype |
| 45 | 4 | 26.7 | 8  | 17 | AAW05539 | Peptide fragment # |
| 46 | 4 | 26.7 | 8  | 18 | AAW36802 | Synthetic peptide  |
| 47 | 4 | 26.7 | 8  | 19 | AAW59334 | Non-polio enterovi |
| 48 | 4 | 26.7 | 8  | 22 | AAW98148 | Human peptide #142 |
| 49 | 4 | 26.7 | 8  | 22 | AAW98149 | Human peptide #142 |
| 50 | 4 | 26.7 | 8  | 22 | AA847584 | Ag85 complex deriv |
| 51 | 4 | 26.7 | 8  | 22 | AAU05199 | Peptide released f |
| 52 | 4 | 26.7 | 8  | 24 | ABG73074 | Ag85 complex deriv |
| 53 | 4 | 26.7 | 9  | 17 | AAW07056 | Ag85 complex deriv |
| 54 | 4 | 26.7 | 9  | 18 | AAW36804 | Synthetic peptide  |
| 55 | 4 | 26.7 | 9  | 18 | AAW36804 | Synthetic peptide  |
| 56 | 4 | 26.7 | 9  | 22 | AA847585 | Ag85 complex deriv |
| 57 | 4 | 26.7 | 9  | 22 | AAW59364 | Vaccine related MH |
| 58 | 4 | 26.7 | 9  | 22 | AA82787  | Epitope of mycobac |
| 59 | 4 | 26.7 | 9  | 22 | AA807191 | Colostrinin peptid |
| 60 | 4 | 26.7 | 9  | 22 | AA875912 | Hepatitis B virus  |
| 61 | 4 | 26.7 | 9  | 22 | AA875913 | Hepatitis B virus  |
| 62 | 4 | 26.7 | 9  | 23 | AAU99719 | Mouse WNC Ld/beta2 |
| 63 | 4 | 26.7 | 9  | 23 | ABP61737 | Human KRPI tryptic |
| 64 | 4 | 26.7 | 9  | 23 | AAU98288 | M. tuberculosis Ag |
| 65 | 4 | 26.7 | 9  | 23 | AAU94070 | Human novel protei |
| 66 | 4 | 26.7 | 9  | 23 | AAU94117 | Human novel protei |
| 67 | 4 | 26.7 | 9  | 23 | AAU94489 | Human novel protei |
| 68 | 4 | 26.7 | 9  | 23 | AAU94707 | Human novel protei |
| 69 | 4 | 26.7 | 9  | 23 | AAU95042 | Human novel protei |
| 70 | 4 | 26.7 | 9  | 24 | ABR10368 | Human cancer-relat |
| 71 | 4 | 26.7 | 9  | 24 | ABR10399 | Human cancer-relat |
| 72 | 4 | 26.7 | 9  | 24 | ABR10408 | Human cancer-relat |
| 73 | 4 | 26.7 | 9  | 24 | ABR10438 | Human cancer-relat |
| 74 | 4 | 26.7 | 9  | 24 | ABR10455 | Human cancer-relat |
| 75 | 4 | 26.7 | 9  | 24 | ABR10580 | Human cancer-relat |
| 76 | 4 | 26.7 | 9  | 24 | ABR10595 | Human cancer-relat |
| 77 | 4 | 26.7 | 9  | 24 | ABR10599 | Human cancer-relat |
| 78 | 4 | 26.7 | 9  | 24 | ABR10794 | Human cancer-relat |
| 79 | 4 | 26.7 | 9  | 24 | ABR10800 | Human cancer-relat |
| 80 | 4 | 26.7 | 9  | 24 | ABR10809 | Human cancer-relat |
| 81 | 4 | 26.7 | 9  | 24 | ABR10853 | Human cancer-relat |
| 82 | 4 | 26.7 | 9  | 24 | ABR10996 | Human cancer-relat |

83 4 26.7 9 24 ABR11038 Human cancer-relat  
 84 4 26.7 9 24 ABR11059 Human cancer-relat  
 85 4 26.7 9 24 ABR11193 Human cancer-relat  
 86 4 26.7 9 24 ABR11222 Human cancer-relat  
 87 4 26.7 9 24 ABR11235 Human cancer-relat  
 88 4 26.7 9 24 ABR11265 Human cancer-relat  
 89 4 26.7 9 24 ABR11376 Human cancer-relat  
 90 4 26.7 9 24 ABR11404 Human cancer-relat  
 91 4 26.7 9 24 ABR11431 Human cancer-relat  
 92 4 26.7 9 24 ABR11444 Human cancer-relat  
 93 4 26.7 9 24 ABR11592 Human cancer-relat  
 94 4 26.7 9 24 ABR11632 Human cancer-relat  
 95 4 26.7 9 24 ABR11664 Human cancer-relat  
 96 4 26.7 9 24 ABR20170 Human cancer-relat  
 97 4 26.7 9 24 ABR20224 Human cancer-relat  
 98 4 26.7 9 24 ABR21366 Human cancer-relat  
 99 4 26.7 9 24 ABR21569 Human cancer-relat  
 100 4 26.7 9 24 ABR21616 Human cancer-relat

## ALIGNMENTS

## RESULT 1

AAB72250  
 ID AAB72250 standard; peptide; 15 AA.

AC AAB72250;

DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 5.

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

PR 17-AUG-1999; 99US-0149311.

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

PS Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLVEPPFPV 15  
 |||||||  
 DB 1 DLEMPVLVEPPFPV 15  
 |||||||

## RESULT 2

AAB72504

ID AAB72504 standard; Peptide; 15 AA.

XX AC AAB72504;

XX 09-MAY-2001 (first entry)

DE Colostrinin peptide #5.

KW Dermatological; oxidative stress regulator; colostrinin.  
 XX Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22665.

PR 17-AUG-1999; 99US-0149310.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 15 AA;

XX Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVEPPFPV 15  
 |||||||

DB 1 DLEMPVLVEPPFPV 15  
 |||||||

## RESULT 3

AAB72536

ID AAB72536 standard; Peptide; 15 AA.

XX AC AAB72536;

XX 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #5.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrinum.  
 XX Unidentified.  
 OS WO200112651-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22774.  
 XX 17-AUG-1999; 99US-0149633.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Boldogh I;  
 XX WPI; 2001-228545/23.  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DLEMPVLVPEPPFV 15  
 Db 1 DLEMPVLVPEPPFV 15  
 RESULT 4  
 AAB59322  
 ID AAB59322 standard; Peptide; 15 AA.  
 AC AAB59322;  
 XX 21-MAR-2001 (first entry)  
 DE Ewe colostrinin peptide fragment B-7.  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX Ovis sp.  
 OS WO2000075173-A2.  
 XX 14-DEC-2000.  
 XX 02-JUN-2000; 2000WO-GB02128.  
 XX 02-JUN-1999; 99GB-0012852.  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX Georgiades JA;  
 XX WPI; 2001-071058/08.  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX Claim 7; Page 27; 63pp; English.  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DLEMPVLVPEPPFV 15  
 Db 1 DLEMPVLVPEPPFV 15  
 RESULT 5  
 AAE20232  
 ID AAE20232 standard; peptide; 15 AA.  
 AC AAE20232;  
 XX 18-JUN-2002 (first entry)  
 XX Colostrinin constituent peptide #5.  
 DE Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FT Modified-site 15 /note= "Optionally C-terminal amide"  
 FT WO200213850-A1.  
 XX 21-FEB-2002.  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2002-269151/31.  
 XX Composition useful for the modulation of blood cell proliferation in a  
 FT patient comprises a blood cell regulator selected from colostrinin, its  
 FT constituent peptide and/or analog -  
 XX Claim 6; Page 25; 51pp; English.  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

QY 1 DLEMPVLVEPPFV 15  
 |||||  
 Db 1 DLEMPVLVEPPFV 15

RESULT 6  
 AAM51040  
 ID AAM51040 standard; Peptide; 15 AA.

XX AAM51040;

AC AAM51040;

XX 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

XX blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10.

SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVEPPFV 15  
 |||||  
 Db 1 DLEMPVLVEPPFV 15

RESULT 7  
 AAO14581

ID AAO14581 standard; peptide; 15 AA.

XX AAO14581;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 5.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for



CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLVPEPFFV 15  
 |||||  
 Db 1 DLEMPVLVPEPFFV 15  
 |||||  
 RESULT 8  
 AAB59352  
 ID AAB59352 standard; Peptide; 16 AA.  
 XX  
 AC AAB59352;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment derived sequence #12.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 XX  
 PR 02-JUN-1999; 99GB-0012852.  
 XX  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 8; Page 27; 53pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEMPVLVPEPFFV 15  
 |||||  
 Db 2 DLEMPVLVPEPFFV 16  
 |||||  
 RESULT 9  
 AAE07187

ID AAE07187 standard; peptide; 10 AA.  
 XX  
 AC AAE07187;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Colostrinin peptide 3.  
 XX  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200155199-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-GB00329.  
 XX  
 PR 26-JAN-2000; 2000GB-0001825.  
 XX  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-488775/53.  
 XX  
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -  
 XX  
 PS Claim 1; Page 15; 40pp; English.  
 XX  
 CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g., psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 3 related to the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 66.7%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FVLPEPFFV 14  
 |||||  
 Db 1 FVLPEPFFV 10  
 |||||  
 RESULT 10  
 AAE07197  
 ID AAE07197 standard; peptide; 10 AA.  
 XX



```

XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 2 PVEPF 6
RESULT 13
ABG32212
ID ABG32212 standard; peptide; 6 AA.
AC ABG32212;
XX 05-NOV-2002 (first entry)
DE Sheep colostrin derived peptide #6.
XX Sheep: colostrin; colostrum; cytokine inducer; antigen; dementia;
XX central nervous system disorder; neurological disorder;
XX mental disorder; psychosis; neurodegenerative disorder;
XX Alzheimer's disease; motor neuron disease; immune system disorder;
XX acquired immunological deficiency; bacterial infection; viral infection;
XX amyloid plaque; dietary supplement; cachexia; weight loss;
XX senile dementia; Parkinson's disease; emotional disturbance; depression;
XX drug addiction; drug withdrawal.
XX Ovis aries.
XX WO200246211-A2.
XX 13-JUN-2002.
XX 05-DEC-2001; 2001WO-GB05376.
XX 06-DEC-2000; 2000GB-0029777.
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 2 PVEPF 6
RESULT 13
ABG32212
ID ABG32212 standard; peptide; 6 AA.
AC ABG32212;
XX 05-NOV-2002 (first entry)
DE Sheep colostrin derived peptide #6.
XX Sheep: colostrin; colostrum; cytokine inducer; antigen; dementia;
XX central nervous system disorder; neurological disorder;
XX mental disorder; psychosis; neurodegenerative disorder;
XX Alzheimer's disease; motor neuron disease; immune system disorder;
XX acquired immunological deficiency; bacterial infection; viral infection;
XX amyloid plaque; dietary supplement; cachexia; weight loss;
XX senile dementia; Parkinson's disease; emotional disturbance; depression;
XX drug addiction; drug withdrawal.
XX Ovis aries.
XX WO200246211-A2.
XX 13-JUN-2002.
XX 05-DEC-2001; 2001WO-GB05376.
XX 06-DEC-2000; 2000GB-0029777.
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 1 PVEPF 5
RESULT 14
AAR21263
ID AAR21263 standard; Peptide; 8 AA.
AC AAR21263;
XX 21-MAY-1992 (first entry)
DE N-terminal of gene III-PhoA fusion product.
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package;
XX alkaline phosphatase.
XX Synthetic.
XX WO9201047-A.
XX 23-JAN-1992.
XX 10-JUL-1991; 91WO-GB011134.
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.

```

```

XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 2 PVEPF 6
RESULT 13
ABG32212
ID ABG32212 standard; peptide; 6 AA.
AC ABG32212;
XX 05-NOV-2002 (first entry)
DE Sheep colostrin derived peptide #6.
XX Sheep: colostrin; colostrum; cytokine inducer; antigen; dementia;
XX central nervous system disorder; neurological disorder;
XX mental disorder; psychosis; neurodegenerative disorder;
XX Alzheimer's disease; motor neuron disease; immune system disorder;
XX acquired immunological deficiency; bacterial infection; viral infection;
XX amyloid plaque; dietary supplement; cachexia; weight loss;
XX senile dementia; Parkinson's disease; emotional disturbance; depression;
XX drug addiction; drug withdrawal.
XX Ovis aries.
XX WO200246211-A2.
XX 13-JUN-2002.
XX 05-DEC-2001; 2001WO-GB05376.
XX 06-DEC-2000; 2000GB-0029777.
XX (REG-) REGEN THERAPEUTICS PLC.
XX
XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 1 PVEPF 5
RESULT 14
AAR21263
ID AAR21263 standard; Peptide; 8 AA.
AC AAR21263;
XX 21-MAY-1992 (first entry)
DE N-terminal of gene III-PhoA fusion product.
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package;
XX alkaline phosphatase.
XX Synthetic.
XX WO9201047-A.
XX 23-JAN-1992.
XX 10-JUL-1991; 91WO-GB011134.
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.

```

```

XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 1 PVEPF 5
RESULT 14
AAR21263
ID AAR21263 standard; Peptide; 8 AA.
AC AAR21263;
XX 21-MAY-1992 (first entry)
DE N-terminal of gene III-PhoA fusion product.
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package;
XX alkaline phosphatase.
XX Synthetic.
XX WO9201047-A.
XX 23-JAN-1992.
XX 10-JUL-1991; 91WO-GB011134.
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.

```

```

XX OS Synthetic.
XX PN JF08269090-A.
XX PD 15-OCT-1996.
XX PF 28-MAR-1995; 95JP-0094516.
XX PR 28-MAR-1995; 95JP-0094516.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX DR WPI; 1996-515013/51.
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative
XX PS Claim 1; Page 2; 11pp; Japanese.
XX CC Acid casein was prepared from raw milk by acid precipitation, and
XX CC beta casein was formed by the product by the method of Hipp et al.
XX CC This material was digested with porcine pepsin. The digested protein
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The
XX CC product was further digested with bovine pancreatin, trypsin and porcine
XX CC kidney-derived LAP and then subjected to reverse phase chromatography
XX CC to provide the present peptide.
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,
XX CC analgesic and sedative activities
XX SQ Sequence 6 AA;
Query Match 33.3%; Score 5; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PVEPF 12
Db 1 PVEPF 5
RESULT 14
AAR21263
ID AAR21263 standard; Peptide; 8 AA.
AC AAR21263;
XX 21-MAY-1992 (first entry)
DE N-terminal of gene III-PhoA fusion product.
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package;
XX alkaline phosphatase.
XX Synthetic.
XX WO9201047-A.
XX 23-JAN-1992.
XX 10-JUL-1991; 91WO-GB011134.
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.

```

```

PR 06-MAR-1991; 91CB-0004744.
PA (CAMP-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GF, Bonfert TP;
XX
DR WPI; 1992-056862/07.
DR N-PSDB; AAQ21099.
XX
PT Producing members of specific binding pairs - By expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 11; Fig 15; 209pp; English.
XX
CC The sequence is the N-terminal of alkaline phosphatase encoded by
CC a PCR amplified DNA fragment comprising the PhoA gene (Chang et al.
CC Gene 44, 121-125, 1986). The template used for the PCR was pK66
CC which contains a phoA gene encoding an alkaline phosphatase which
CC differs from that of Chang et al by a mutation which converts
CC arginine to alanine at position 166. The PCR prod. was ligated
CC into the fd gene III confg. vector, fdCAT2 derived from fdTPS/Xh
CC which was in turn derived from fd-tet (Zacher, AN et al., 1980,
CC Gene 9, 127-140), a tetracycline resistant version of the fd
CC bacteriophage (ATCC No.37000). (Prepn. of fdTPS/Xh is described in
CC AAQ21095.) The clone having the PhoA gene fused in frame to gene III
CC was designated fd-phoA 166. The first five amino acids of the
CC mature fusion come from gene III. The phage expressed active
CC alkaline phosphatase enzyme from the phoA-gene III fusion, on the
CC phage surface.
CC N.B. fdCAT2 is also referred to as fd-tet-D031 and fdDOG1.
CC See also AAR21260-307, 309-311; AAR22450, 565-581.
XX
SQ Sequence 8 AA;
XX
Query Match 33.3%; Score 5; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EMPVL 7
DB 4 EMPVL 8
XX
RESULT 15
ABR47208
ID ABR47208 standard; Peptide; 10 AA.
AC ABR47208;
XX
DT 10-JUN-2003 (first entry)
XX
DE Staphylococcus aureus CHIPS-related peptide #2397.
XX
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
PN WO2003006048-A1.
XX
PD 23-JAN-2003.
XX
PF 11-JUL-2001; 2001WO-EP08004.
XX
PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
XX

```

```

XX
PR 11-JUL-2001; 2001WO-EP08004.
XX
PA (JARI-) JARI PHARM BV.
XX
PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
DR WPI; 2003-247783/25.
XX
PT Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
PS Example 1; Page 55; 89pp; English.
XX
CC The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (PPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
SQ Sequence 10 AA;
XX
Query Match 33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EPFPP 14
DB 4 EPFPP 8
XX
RESULT 16
ABR47319
ID ABR47319 standard; Peptide; 10 AA.
AC ABR47319;
XX
DT 10-JUN-2003 (first entry)
XX
DE Staphylococcus aureus CHIPS-related peptide #2508.
XX
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
PN WO2003006048-A1.
XX
PD 23-JAN-2003.
XX
PF 11-JUL-2001; 2001WO-EP08004.
XX
PR 11-JUL-2001; 2001WO-EP08004.
XX
PA (JARI-) JARI PHARM BV.
XX
PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX

```

DR WPI; 2003-247783/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases

XX

PS Example 1; Page 56; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and

CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)

CC from Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the

CC CSA-receptor (CSAR) and/or formylated peptide receptor (FPR) or

CC neutrophils, monocytes and endothelial cells or involving acute or

CC chronic inflammation reactions. The diseases or disorders include

CC cardiovascular diseases, disease of the central nervous system,

CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint

CC diseases, respiratory diseases and HIV infection.

XX

SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VERPP 13

DB 3 VERPP 7

RESULT 17

AAW03290

ID AAW03290 standard; peptide; 11 AA.

AC AAW03290;

XX

XX 23-MAR-1997 (first entry)

XX

DE CNS-inhibiting peptide from casein.

DE

XX casein; central nervous system; CNS inhibiting; antitussive;

XX analgesic; sedative.

XX

OS Synthetic.

XX

PN JP08269090-A.

XX

PD 15-OCT-1996.

XX

PP 28-MAR-1995; 95JP-0094516.

XX

PR 28-MAR-1995; 95JP-0094516.

XX

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX

DR WPI; 1996-515013/51.

XX

XX New peptide(s) obtd. by digestion of casein - useful as drugs

XX displaying e.g. CNS inhibiting, antitussive, analgesic and sedative

XX activities

XX

PS Claim 1; Page 2; 11pp; Japanese.

XX

CC Acid casein was prepared from raw milk by acid precipitation, and

CC beta casein was formed by the product by the method of Hipp et al.

CC This material was digested with porcine pepsin. The digested protein

CC was neutralised with NaOH, then heated to inactivate the enzyme. The

CC product was further digested with bovine pancreatin, trypsin and porcine

CC kidney-derived IAP and then subjected to reverse phase chromatography

CC to provide the present peptide.

CC The peptide is useful as a drug having CNS inhibiting, antitussive,

CC analgesic and sedative activities

XX SQ Sequence 11 AA;

Query Match 33.3%; Score 5; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12

DB 2 PVEPP 6

RESULT 18

AAW03291

ID AAW03291 standard; peptide; 13 AA.

XX

XX AAW03291;

AC AAW03291;

XX

XX 23-MAR-1997 (first entry)

XX

DE CNS-inhibiting peptide from casein.

DE

XX casein; central nervous system; CNS inhibiting; antitussive;

XX analgesic; sedative.

XX

OS Synthetic.

XX

PN JP08269090-A.

XX

PD 15-OCT-1996.

XX

PP 28-MAR-1995; 95JP-0094516.

XX

PR 28-MAR-1995; 95JP-0094516.

XX

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX

DR WPI; 1996-515013/51.

XX

XX New peptide(s) obtd. by digestion of casein - useful as drugs

XX displaying e.g. CNS inhibiting, antitussive, analgesic and sedative

XX activities

XX

PS Claim 1; Page 2; 11pp; Japanese.

XX

CC Acid casein was prepared from raw milk by acid precipitation, and

CC beta casein was formed by the product by the method of Hipp et al.

CC This material was digested with porcine pepsin. The digested protein

CC was neutralised with NaOH, then heated to inactivate the enzyme. The

CC product was further digested with bovine pancreatin, trypsin and porcine

CC kidney-derived IAP and then subjected to reverse phase chromatography

CC to provide the present peptide.

CC The peptide is useful as a drug having CNS inhibiting, antitussive,

CC analgesic and sedative activities

XX

SQ Sequence 13 AA;

Query Match 33.3%; Score 5; DB 17; Length 13;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPP 12

DB 2 PVEPP 6

RESULT 19

AAAR79630

ID AAR79630 standard; Protein; 15 AA.

XX

XX AAR79630;

AC

XX

DT 18-APR-1996 (first entry)

XX DE Endocarditis specific antigen fragment.  
 XX KW Streptococci; enterococci; sera; antibodies; diagnosis;  
 XX KW prophylaxis; treatment; therapy; infection; endocarditis;  
 XX KW septicemia.  
 XX OS Streptococcus oralis.  
 XX PN WO9520658-A2.  
 XX PD 03-AUG-1995.  
 XX PF 30-JAN-1995; 95WO-0500186.  
 XX PR 28-JAN-1994; 94GB-0001689.  
 XX PA (UYMA-) UNIV VICTORIA MANCHESTER.  
 XX PI Burnie JP, Matthews RC;  
 XX DR MPI; 1995-275443/36.  
 XX XX New purified bacterial protein - used to develop prods. for the  
 PT diagnosis and treatment of infections due to streptococci and  
 PT enterococci  
 XX XX  
 PS Claim 7; Page 75; 92pp; English.  
 CC Purified bacterial proteins expressed during infection by  
 CC Streptococci or enterococci and isolated from human sera may be used  
 CC to develop products e.g. antibodies, for use in the diagnosis,  
 CC prophylaxis and treatment of infections caused by these organisms,  
 CC especially endocarditis and septicemia. Fragments of the proteins  
 CC may also be used. This is an endocarditis specific antigen fragment  
 CC and was isolated from Streptococcus oralis (See AAR79626-633).  
 XX XX  
 SQ Sequence 15 AA;  
 Query Match 33.3%; Score 5; DB 16; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPVEP 11  
 Db 10 LPVEP 14  
 RESULT 20  
 AAB72267  
 ID AAB72267 standard; peptide; 18 AA.  
 XX AC AAB72267;  
 XX XX  
 DT 14-MAY-2001 (first entry)  
 XX DE Colostatin derived cytokine inducing peptide SEQ ID 22.  
 KW Colostatin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX OS Synthetic.  
 XX XX  
 PN WO200111937-A2.  
 XX PD 22-FEB-2001.  
 XX PF 17-AUG-2000; 2000WO-US22818.  
 XX PR 17-AUG-1999; 99US-0149311.  
 XX XX

PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX MPI; 2001-202804/20.  
 XX DR  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX XX  
 SQ Sequence 18 AA;  
 Query Match 33.3%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PVEPF 12  
 Db 10 PVEPF 14  
 RESULT 21  
 AAB72520  
 ID AAB72520 standard; Peptide; 18 AA.  
 XX AC AAB72520;  
 XX XX  
 DT 09-MAY-2001 (first entry)  
 XX DE Colostrinin peptide #21.  
 XX KW Dermatological; oxidative stress regulator; colostrinin.  
 XX OS Unidentified.  
 XX XX  
 PN WO200112650-A2.  
 XX PD 22-FEB-2001.  
 XX PF 17-AUG-2000; 2000WO-US22665.  
 XX PR 17-AUG-1999; 99US-0149310.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PI Stanton GJ, Hughes TK, Boldogh I;  
 XX MPI; 2001-218342/22.  
 XX DR  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX XX  
 PS Claim 6; Page 26; 48pp; English.  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,

CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12  
 |||||  
 Db 10 PVEPF 14

## RESULT 22

AAB72552  
 ID AAB72552 standard; Peptide; 18 AA.

XX AC AAB72552;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #21.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 XX colostrinum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX FT Use of colostrinin, its constituent peptide or analog as a neural cell  
 XX regulator, for promoting neural cell differentiation and treating  
 XX damaged neural cells in a patient -

XX PS Claim 6; Page 21; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell  
 XX differentiation and treating damaged neural cells, using colostrinin and  
 XX colostrinin constituent peptides (e.g. the present peptide) as a neural  
 XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12  
 |||||  
 Db 10 PVEPF 14

## RESULT 23

AAB59330  
 ID AAB59330 standard; Peptide; 18 AA.

XX AC AAB59330;

XX DT 21-MAR-2001 (first entry)  
 XX DE Ewe colostrinin peptide fragment C-5.  
 XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG- ) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from  
 XX colostrinin for treating e.g. disorders of the central nervous system  
 XX and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -

XX PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides  
 XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 XX fragment of colostrum. These peptides can be used in the treatment of  
 XX central nervous system disorders such as senile dementia, Parkinson's  
 XX disease, Alzheimer's disease, psychosis and neurosis, immune system  
 XX disorders such as bacterial and viral infections, to improve the  
 XX development of a child's immune system, as a dietary supplement, and to  
 XX promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12  
 |||||  
 Db 10 PVEPF 14

## RESULT 24

AAE20249  
 ID AAE20249 standard; peptide; 18 AA.

XX AC AAE20249;

XX DT 18-JUN-2002 (first entry)

XX DE Colostrinin constituent peptide #21.

XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 XX transplantation; implantation; dermatological; vulnery.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 18 /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.  
 XX PF 17-AUG-2000; 2000WO-US22776.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PR 17-AUG-2000; 2000WO-US22776.  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WI; 2002-269151/31.  
 XX PT Modulation of blood cell proliferation in a patient involves use of  
 XX PT blood cell regulator selected from colostrinin, its constituent peptide  
 XX PT and/or analogue -  
 XX PS Claim 1; Page 34; 54pp; English.  
 XX CC The invention relates to a composition which comprises a blood cell  
 XX CC regulator selected from colostrinin, its constituent peptide and/or  
 XX CC analogue. The invention is used for modulating the oxidative stress  
 XX CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 XX CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 XX CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 XX CC after a premature birth or normal birth, preventing/delaying aging in a  
 XX CC patient, enhancing wound healing, and the reduction of side effects of  
 XX CC cosmetic procedures. The method changes the level of an oxidizing species  
 XX CC in the cell, such as decreases or prevents increase in the level of  
 XX CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 XX CC lipid, compared to the same conditions when the oxidative stress  
 XX CC regulator is not present. The modulation of oxidative stress results in  
 XX CC enhanced repair, regeneration, and replacement of cells, tissues and  
 XX CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 XX CC external organs), as well as enhanced preservation of such organs for  
 XX CC transplantation, implantation, or scientific research. The present  
 XX CC sequence is a colostrinin constituent peptide.  
 XX SQ Sequence 18 AA;  
 Query Match 33.3%; Score 5; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PVEPFF 12  
 Db 10 PVEPFF 14  
 RESULT 25  
 AAM51056  
 ID AAM51056 standard; Peptide; 18 AA.  
 XX AC AAM51056;  
 XX DT 30-MAY-2002 (first entry)  
 XX DE Colostrinin constituent peptide (casein amino acids 121-138).  
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 XX KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 18  
 XX FT /note= "optional C-terminal amidation"  
 XX PN WO200213849-A1.  
 XX XX 21-FEB-2002.  
 XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WI; 2002-269150/31.  
 XX PT Modulation of blood cell proliferation in a patient involves use of  
 XX PT blood cell regulator selected from colostrinin, its constituent peptide  
 XX PT and/or analogue -  
 XX PS Claim 1; Page 34; 54pp; English.  
 XX CC The present sequence is that of a colostrinin constituent peptide  
 XX CC that is preferred for use as an immunological regulator and as a  
 XX CC blood cell regulator in claimed methods of the invention. It is  
 XX CC classified as having a beta-casein homologue precursor, and  
 XX CC corresponds to casein amino acids 121-138. Methods are claimed  
 XX CC for: inducing a cytokine in a cell by contact with an immunological  
 XX CC regulator, where the cell is present in a cell culture, a tissue,  
 XX CC an organ or an organism, and the cell is mammalian, including human;  
 XX CC modulating an immune response in a cell by contact with the  
 XX CC immunological regulator under conditions effective to induce a  
 XX CC cytokine; modulating an immune response in a patient by administering  
 XX CC a cytokine, where the immunological regulator is administered topically  
 XX CC or as part of a dietary supplement, and where the immune response is  
 XX CC specific or non specific, an interferon response or an antibody  
 XX CC response; modulating blood cell proliferation by contacting blood  
 XX CC cells with a blood cell regulator, where the blood cells are present  
 XX CC in a cell culture or an organism, are mammalian or human, and where  
 XX CC the blood cells are increased in number or differentiated; and a  
 XX CC method for modulating blood cell proliferation in a patient. A  
 XX CC claimed cytokine-inducing composition comprises a pharmaceutical  
 XX CC carrier and an active agent such as the present peptide. Cytokines  
 XX CC induced by this peptide in human leucocyte cultures include  
 XX CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.  
 XX SQ Sequence 18 AA;  
 Query Match 33.3%; Score 5; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PVEPFF 12  
 Db 10 PVEPFF 14  
 RESULT 26  
 AAO14598  
 ID AAO14598 standard; peptide; 18 AA.  
 XX AC AAO14598;  
 XX DT 27-MAY-2002 (first entry)  
 XX DE Neural cell regulatory colostrinin peptide 21.  
 XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX KW neural cell treatment.  
 XX OS Unidentified.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 18  
 XX FT /note= "Optional C-terminal amide"  
 XX PN WO200213851-A1.



```

XX PD 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22777.
XX PR 17-AUG-2000; 2000WO-US22777.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Boldogh I, Stanton JG, Hughes TK;
XX DR WPI; 2002-269152/31.
XX PT Promoting cell differentiation in a patient involves use of blood cell
XX PT regulator selected from colostrinin, its constituent peptide and/or
XX PS analog -
XX PS Claim 7; Page 21; 37pp; English.
XX CC The invention comprises a method for promoting cell differentiation (e.g.
XX CC neural cell differentiation). The method involves contacting cells with a
XX CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
XX CC cells in morphology to form neural cells. Colostrinin is a proline-rich
XX CC polypeptide aggregate that is present in colostrum. The method of the
XX CC invention is useful for promoting the differentiation of cells and for
XX CC treating damaged neural cells in a patient. The present amino acid
XX CC sequence represents a specifically claimed colostrinin peptide used in
XX CC the method of the invention.
XX SQ Sequence 18 AA;
 Query Match 33.3%; Score 5; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 PVPEPF 12
Db 10 PVPEPF 14
 |||||
 |||||

RESULT 27
AAR04512
ID AAR04512 standard; protein; 20 AA.
AC AAR04512;
DT 25-MAR-2003 (updated)
DE 20-SEP-1990 (first entry)
DE Transposon phoA product.
KW Transposon; Tn5; alkaline phosphatase; phoA; export DNA.
XX E.coli.
XX Key Location/Qualifiers
XX Region 1..17
XX /label=Tn product
XX Region 18..20
XX /label=first three aa of alkaline phosphatase
XX US4914025-A.
XX 03-APR-1990.
XX 05-DEC-1985; 85US-0805486.
XX 05-DEC-1985; 85US-0805486.
XX (MANO/) MANOIL C.
XX Manoil C, Beckwith J, Syvanen M, Isbert RR, Hoffman CS, Wright A;
XX
```

```

DR WPI; 1990-147416/19.
DR N-PSDB; AAR04280.
XX Identification of export DNA sequences in transformed bacteria -
XX using transposon contg.-structural gene for alkaline phosphatase
XX PT which requires export DNA for expression.
XX PS Disclosure; Page ?; ?pp; English.
XX CC Xl-Ser, Pro, Thr or Ala.
XX CC Pref the transposon is Tn5 and the detectable gene product is
XX CC alkaline phosphatase. Transformants containing an export DNA
XX CC sequence and where transposition has occurred can be screened
XX CC for their ability to secrete alkaline phosphatase.
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 20 AA;
 Query Match 33.3%; Score 5; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 10 EPFPP 14
Db 12 EPFPP 16
 |||||
 |||||

RESULT 28
AAR78500
ID AAR78500 standard; peptide; 4 AA.
AC AAR78500;
DT 21-MAY-1999 (first entry)
DE Dioxin-binding peptide.
KW Dioxin; random peptide phage display library; identification; ligand;
KW affinity; molecular target; drug; toxin.
XX Synthetic.
XX WO9902733-A1.
XX 21-JAN-1999.
XX 07-JUL-1998; 98WO-US14082.
XX 07-JUL-1997; 97US-0051781.
XX 07-JUL-1997; 97US-0051780.
XX (UYFL) UNIV FLORIDA STATE.
XX Makowski DR, Makowski L, Sanganee HJ;
XX WPI; 1999-120933/10.
XX Identifying protein that binds to small ligands - by screening
XX against a peptide library in which each member is coupled to nucleic
XX acid encoding it, sequencing in selected library members, deducing
XX peptide sequence and searching proteins for the sequence
XX Example 3; Page 48; 52pp; English.
XX This sequence represents a dioxin-binding peptide generated by a random
XX peptide phage display library. The invention relates to a method of
XX identifying a protein (P) that binds to a ligand (L), of molecular weight
XX below 5 kD, other than a nucleic acid, peptide or protein, by:
XX (a) screening (L) against a peptide or protein library consisting of
XX genetic packages in which each peptide or protein member is coupled to
XX nucleic acid encoding it; (b) separating library members with greatest
XX affinity for (L); (c) determining the nucleic acid sequences encoding the
XX separated library members and translating these to peptide sequences,
XX
```

CC and (d) identifying proteins that contain a portion of the translated  
 CC sequence or which correspond to consensus peptide sequences derived by  
 CC statistical analysis of the translated sequences. The method is used  
 CC to identify molecular targets for drugs and toxins, particularly for  
 CC determining their mode of action and to identify secondary targets  
 CC associated with side effects.

XX SQ Sequence 4 AA;  
 Query Match 26.7%; Score 4; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPFF 13  
 Db 1 EPFF 4  
 |||||

RESULT 29  
 AAW65791  
 ID AAW65791 standard; peptide; 5 AA.

XX AC AAW65791;  
 XX DT 19-OCT-1998 (first entry)  
 XX DE Polypyrrol inhibitor of cyclophilin.

XX KW polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPI;  
 KW pectidyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;  
 KW neuronal damage.

XX OS Synthetic.  
 XX PN WO9825950-A1.  
 XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US23102.  
 XX PR 09-DEC-1996; 96US-0761902.

XX PA (GUIL-) GUILFORD PHARM INC.  
 XX PI Hamilton GS, Steiner JP, Wei L;  
 XX DR WPI; 1998-348444/30.

XX PT Effecting neuronal activity in mammals - by administering tetra-  
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,  
 XX useful in treatment of neuronal damage or degeneration disorders

XX PS Claim 11; Page 40; 70pp; English.

XX CC The invention relates to a method of effecting a neuronal activity. It  
 CC comprises administering a neurotrophic compound with an affinity for a  
 CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl  
 CC isomerase (rotamase) activity. The neurotrophic compound achieves the  
 CC stimulation of damaged neurons, promotion of neuronal regeneration or  
 CC prevention of neurodegeneration, and treatment of neurological disorder.

XX CC The neurotrophic compounds are potent peptidyl-proline isomerase  
 CC (rotamase) inhibitors. They are of use in disorders which include  
 CC peripheral neuropathy caused by physical injury or disease state, i.e.  
 CC physical injury to the brain or spinal cord, stroke, or neurological  
 CC disorder leading to neurodegeneration, notably Alzheimer's and  
 CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic  
 CC compounds avoid the side effects of immunosuppressant drugs including  
 CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,  
 CC involuntary tremors, headaches, and hypertension. They are also free from  
 CC the difficulties in delivery and bioavailability of large molecular  
 CC weight proteins. The present sequence represents a specifically claimed  
 CC neurotrophic compound.

XX CC

SQ Sequence 5 AA;  
 Query Match 26.7%; Score 4; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPFF 14  
 Db 2 PPFF 5  
 |||||

RESULT 30  
 AAG73397  
 ID AAG73397 standard; peptide; 5 AA.

XX AC AAG73397;  
 XX DT 10-AUG-2001 (first entry)

XX DE Human gene 9-encoded secreted protein HETAM53, SEQ ID NO:168.  
 XX KW Human; secreted protein; proliferative disorder; cancer; chromosome 4;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;  
 KW endocrine disorder; infection; wound healing; vulnerability;  
 KW cell culture; chemotaxis; food additive;  
 KW binding partner identification.

XX OS Homo sapiens.  
 XX PN WO200134628-A1.  
 XX PD 17-MAY-2001.

XX PF 08-NOV-2000; 2000WO-US30653.  
 XX PR 12-NOV-1999; 99US-0164735.  
 XX PR 27-JUL-2000; 2000US-0221193.

XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Ruben SM, Komatoulis GA, Birse CE, Ni J, Moore PA;  
 XX DR WPI; 2001-329066/34.  
 XX DR N-PSDB; AAH32573.

XX PT Nucleic acids encoding 35 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 XX disease and diabetic retinopathy -

XX PS Claim 11; Page 537; 604pp; English.

XX CC AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted  
 CC protein genes, and AAG73346-AAG73448 represent the proteins they encode.  
 CC AAG73449-AAG73519 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 52 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,



CC identifying a superstructure encompassing alternative beta-strand  
 CC arrangements, representing the superstructure by an integer-linear  
 CC programming mathematical model, with the model maximising the total  
 CC hydrophobic contact energy, and then solving the model. The method can  
 CC also apply energy modelling with a full atom force field potential to  
 CC generate a constrained global optimisation problem, optionally applying a  
 CC torsion angle dynamics algorithm and then solving the constrained global  
 CC optimisation problem to determine the three-dimensional structure of the  
 CC polypeptide. The method is useful for determining the tertiary structure  
 CC of a polypeptide and is accurate and reliable. The sequences presented in  
 CC ABU12237-ABU12295 are the pentapeptides of the chymotrypsin inhibitor,  
 CC 3C12, which were used to predict the alpha-helical regions in an example  
 CC of the method of the invention.

XX Sequence 5 AA;  
 CC Query Match 26.7%; Score 4; DB 24; Length 5;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 DB 2 VLPV 5  
 |||||

RESULT 33  
 ABU12267  
 ID ABU12267 standard; Peptide; 5 AA.  
 XX AC ABU12267;  
 XX DT 18-FEB-2003 (first entry)  
 XX DE Chymotrypsin inhibitor 2, 3C12, alpha helix prediction pentapeptide #31.  
 XX KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;  
 XX KM atomistic modelling; low energy conformation; entropic energy;  
 XX KW free energy; equilibrium probability; helical cluster; integer-linear;  
 XX KW mathematical model; hydrophobic contact energy;  
 XX KW atom force field potential; global optimisation; torsion angle;  
 XX KW dynamic algorithm; three-dimensional structure; tertiary structure;  
 XX KW chymotrypsin inhibitor; 3C12.  
 XX OS Hordeum vulgare.  
 XX PN WO200279872-A2.  
 XX PD 10-OCT-2002.  
 XX PF 19-FEB-2002; 2002WO-US04644.  
 XX PR 16-FEB-2001; 2001US-0788006.  
 XX PA (UYPR-) UNIV PRINCETON.  
 XX PI Floudas CA, Klepeis JL;  
 XX DR WPI; 2003-058449/05.  
 XX PT Determining helix regions, and beta sheets of polypeptide, involves  
 PT partitioning peptide, atomistic modeling by selected force, generating  
 PT ensemble low energy, and calculating free energies for each peptide -  
 XX Example 1; Page 62; 147pp; English.

CC The invention discloses a ASTRO-FOLD approach for the ab initio  
 CC prediction method for determining the existence and location of  
 CC alpha-helix regions and arrangement of beta-sheets and disulphide bridges  
 CC of a polypeptide. The method comprises defining the first segment of the  
 CC amino acid sequence, performing atomistic modelling upon each segment,  
 CC generating an ensemble of low energy conformations, determining the  
 CC entropic and free energy for each segment and then ascertaining the  
 CC equilibrium probabilities for helical clusters. The segments consist of

CC pentapeptides, with each further segment including a majority of the  
 CC amino acid residues of the first segment, together with an additional  
 CC amino acid residue(s), adjacent to the first amino acid sequence. The  
 CC beta-sheets and disulphide bridges of a polypeptide are determined by  
 CC identifying a superstructure encompassing alternative beta-strand  
 CC arrangements, representing the superstructure by an integer-linear  
 CC programming mathematical model, with the model maximising the total  
 CC hydrophobic contact energy, and then solving the model. The method can  
 CC also apply energy modelling with a full atom force field potential to  
 CC generate a constrained global optimisation problem, optionally applying a  
 CC torsion angle dynamics algorithm and then solving the constrained global  
 CC optimisation problem to determine the three-dimensional structure of the  
 CC polypeptide. The method is useful for determining the tertiary structure  
 CC of a polypeptide and is accurate and reliable. The sequences presented in  
 CC ABU12237-ABU12295 are the pentapeptides of the chymotrypsin inhibitor,  
 CC 3C12, which were used to predict the alpha-helical regions in an example  
 CC of the method of the invention.

XX Sequence 5 AA;  
 CC Query Match 26.7%; Score 4; DB 24; Length 5;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 DB 1 VLPV 4  
 |||||

RESULT 34  
 AAR95892  
 ID AAR95892 standard; peptide; 6 AA.  
 XX AC AAR95892;  
 XX DT 18-NOV-1996 (first entry)  
 XX DE Angiotensin converting enzyme inhibitor #2.  
 XX KW Angiotensin converting enzyme; inhibitor; ACE; hypotensive; health food;  
 XX KW animal milk; drug; proteinase; carboxypeptidase.  
 XX OS Synthetic.  
 XX PN JP08039994-A.  
 XX PD 16-APR-1996.  
 XX PF 28-APR-1995; 95JP-0105262.  
 XX PR 02-AUG-1994; 94JP-0181653.  
 XX PA (CALV) CALFIS SHOKUHIN KOGYO KK.  
 XX DR WPI; 1996-246958/25.  
 XX PT New ACE-inhibiting peptide derived from animal milk - useful as  
 PT hypotensive drug or health food component  
 XX Claim 1; Page 6; 7pp; Japanese.

CC AAR95891 and AAR95892 represent angiotensin converting enzyme (ACE)  
 CC inhibitors. These sequences have hypotensive activity, and can be used  
 CC in drugs and health foods. These sequences are prepared by treating  
 CC animal milk with a proteinase and then a carboxypeptidase. These  
 CC peptides are highly safe, and can be easily prepared at low cost.

XX Sequence 6 AA;  
 CC Query Match 26.7%; Score 4; DB 17; Length 6;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



XX The peptide sequences AAW59298-W59344 are amplified by primers to detect  
 CC the presence of a non-polio enterovirus (NPEV) in a sample. The primers  
 CC and assays are used to detect NPEVs in a sample, to serotype these  
 CC viruses, to diagnose enteroviral diseases and medical conditions, and to  
 CC correlate (or disprove a correlation between) specific symptoms or  
 CC combinations of symptoms with the presence of a particular enterovirus.  
 CC They can be used for diseases such as aseptic meningitis. The detection  
 CC of NPEV infections and their correlation with medical conditions will  
 CC make possible vaccines and methods of treatment.

XX SQ Sequence 7 AA;  
 Query Match 26.7%; Score 4; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7  
 DB 1 MPVL 4

RESULT 38  
 AAY50072  
 ID AAY50072 standard; peptide; 7 AA.  
 XX AC AAY50072;  
 XX DT 19-JAN-2000 (first entry)  
 XX DE Cocksackievirus A VPI conserved epitope 38.  
 XX KW Virus; epitope; target; degenerate; PCR; primer; amplification;  
 KW VPI; nonstructural protein 2A; conserved; base analogue; inosine;  
 KW predetermined nucleotide; diagnosis; enterovirus; poliovirus.  
 XX OS Synthetic.  
 OS Cocksackievirus.  
 PN WO9953097-A2.  
 PD 21-OCT-1999.  
 XX PF 06-APR-1999; 99WO-US07513.  
 XX PR 15-APR-1998; 98US-0081944.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Kilpatrick DR;  
 XX WPI; 1999-620444/53.  
 XX N-PSDB; AA230991.  
 XX Designing degenerate polymerase chain reaction primers -  
 XX Example 3; Page 18; 30pp; English.

XX This sequence represents a conserved Cocksackievirus A  
 CC (serotype A9) VPI epitope. The invention relates to a novel  
 CC method for designing degenerate PCR primers (AA230975-231000, AA232601-  
 CC AA232611) for amplifying target polynucleotides. This method comprises  
 CC identifying uniquely conserved amino acid sequences (e.g., this  
 CC epitope) in target proteins; synthesizing degenerate polynucleotides  
 CC encoding the conserved sequences; and substituting the synthesised  
 CC polynucleotides with up to four predetermined nucleotides (e.g.,  
 CC inosine) at degenerate nucleotide positions. The nucleic acids  
 CC comprise no more than 7 degenerate positions. Have no more  
 CC than 2 adjacent predetermined nucleotides and the predetermined  
 CC nucleotides are 3 bases away from the 3' end of the synthesised strand.  
 CC The degenerate primers are useful for amplifying target polynucleotides  
 CC by the polymerase chain reaction (PCR). The use of the method of  
 CC designing degenerate primers useful for the detection of polioviruses

CC in clinical samples is described in US585477. The degenerate primers  
 CC facilitate PCR amplification of unknown polynucleotides, where the amino  
 CC acid sequence encoded is known. The primers also allow for the  
 CC correlation of the subsequent molecular based diagnosis with a  
 CC serologically derived diagnosis.

XX SQ Sequence 7 AA;  
 Query Match 26.7%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7  
 DB 1 MPVL 4

RESULT 39  
 AAY16900  
 ID AAY16900 standard; peptide; 7 AA.  
 XX AC AAY16900;  
 XX DT 20-JUL-1999 (first entry)  
 XX DE Heat shock protein (hsp) binding peptide.  
 XX KW Conjugate peptide; heat shock protein; hsp; phase display library; virus;  
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;  
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;  
 KW acquired immune deficiency; autoimmune disease.  
 XX OS Synthetic.  
 XX PN WO9922761-A1.  
 XX PD 14-MAY-1999.  
 XX PF 22-OCT-1996; 98WO-US222335.  
 XX PR 31-OCT-1997; 97US-0961707.  
 XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;  
 XX Overfell O, Rothman JE;  
 XX WPI; 1999-313177/26.  
 XX Identifying peptides which bind heat shock proteins  
 XX Examples; Page 20; 155pp; English.

XX The invention relates to conjugate peptides engineered to noncovalently  
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding  
 CC peptide comprises (a) contacting a phase display library having  
 CC bacteriophage expressing, in a surface protein, inserted peptides with a  
 CC hsp target and bound to a benzimidazole ansamycin antibiotic (BAA), in a  
 CC physiologic binding buffer; (b) isolating a phase binding to the hsp  
 CC target; and (c) identifying the inserted peptide expressed. The peptides  
 CC which bind to a hsp can be used as tethering peptides for a hsp which may  
 CC serve as an accessory in a chaperone process and/or may comprise a  
 CC cytokine. Such compositions can be used for inducing an immune  
 CC response. Such compositions can be used for treating neoplastic disease,  
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,  
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a  
 CC disease of the immune system, e.g. acquired immune deficiencies or  
 CC autoimmune diseases.

XX SQ Sequence 7 AA;  
 Query Match 26.7%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
 Db 4 MPVL 7

RESULT 40  
 AAY96209  
 ID AAY96209 standard; Peptide; 7 AA.  
 AC AAY96209;  
 XX  
 DT 11-AUG-2000 (first entry)  
 DE Arabidopsis AHAS small subunit F3 gene fragment N-terminal sequence.  
 XX  
 DE Herbicide-resistance; acetohydroxy-acid synthase; AHAS;  
 KW acetolactate synthase; imidazolinone; sulfonyleurea;  
 KW triazopyrimidine sulfonamide; sulfamoylurea; enzyme;  
 KW pyrimidyl-oxy-benzoic acid; sulfonyleurea; transgenic plant;  
 KW branched-chain amino acid synthesis.  
 XX  
 OS Arabidopsis.  
 XX  
 PN WO2000026390-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 28-OCT-1999; 99WO-US25452.  
 XX  
 PR 29-OCT-1998; 98US-0106239.  
 XX  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Kakefuda G, Costello C, Sun M, Hu W;  
 XX  
 DR WPI; 2000-365633/31.  
 XX  
 PT New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase  
 PT small subunit protein for producing transgenic herbicide resistant  
 PT plants and identifying mutations affecting enzymatic activity of the  
 PT synthetase -  
 XX  
 PS Disclosure; Page 25; 57pp; English.  
 XX  
 CC Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed  
 CC for branched-chain amino acid synthesis and so is essential for life.  
 CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme  
 CC in plants would lead to plant death and therefore inhibitors would be  
 CC potential herbicides. Certain herbicides are known to inhibit AHASs:  
 CC imidazolinones, sulfonyleureas, triazopyrimidine sulfonamides,  
 CC pyrimidyl-oxy-benzoic acids, sulfamoylureas and sulfonyleureas.  
 CC Mutant AHAS may be resistant to these herbicides and may be used to  
 CC create herbicide resistant transgenic plants e.g. dicot and monocot crop  
 CC plants. A thrombin cleavage site was incorporated into an AHAS small  
 CC subunit gene. The AHAS small subunit gene fragments were cloned into  
 CC plasmid expression vectors, and were expressed as glutathione  
 CC transferase/ AHAS small subunit fusion proteins. The glutathione  
 CC transferase was then cleaved via the thrombin cleavage site. Cleavage  
 CC however modifies the N-terminal sequence of the AHAS small subunit gene  
 CC fragments, in that the glycine and serine residues of the cleavage site  
 CC are maintained on the AHAS protein. The present sequence details the  
 CC N-terminal sequence of one such AHAS small subunit gene fragment,  
 CC F3, which is a near full length AHAS small subunit gene, with the  
 CC modification due to cleavage.  
 XX  
 SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
 Db 4 MPVL 7

RESULT 42  
 ABG97087  
 ID ABG97087 standard; Peptide; 7 AA.  
 XX  
 AC ABG97087;

Qy 9 VEPF 12  
 Db 3 VEPF 6

RESULT 41  
 AAU72042  
 ID AAU72042 standard; Peptide; 7 AA.  
 AC AAU72042;  
 XX  
 DT 26-FEB-2002 (first entry)  
 DE Melanoma antigen, javelin peptide #28.  
 XX  
 DE Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;  
 KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYE01; GM2;  
 KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;  
 KW javelin molecule; melanoma antigen recognised by T cells-1; human.  
 XX  
 OS Bacteriophage M13.  
 XX  
 PN WO200178655-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 17-APR-2001; 2001WO-US12449.  
 XX  
 PR 17-APR-2000; 2000US-197462P.  
 XX  
 PA (HOUG/) HOUGHTON A.  
 PA (LIVL/) LIVINGSTON P.  
 PA (ALAW/) AL-AWQATI Q.  
 PA (MAYH/) MAYHEW M.  
 PA (HOEN/) HOE M.  
 XX  
 PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;  
 XX  
 DR WPI; 2001-663092/76.  
 XX  
 PT Anti cancer vaccine for the treatment of melanoma comprises a heat  
 PT shock protein and a melanoma antigen i.e. tyrosinase -  
 XX  
 PS Disclosure; Page 16; 150pp; English.  
 XX  
 CC The invention relates to a method of induction of an immune response,  
 CC comprising administration of an immunotherapeutic composition, comprising  
 CC a heat shock protein, and a melanoma antigen, where the melanoma  
 CC antigen is selected from tyrosinase, tyrosinase related protein 1,  
 CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,  
 CC NYE01, MART antigens, GM2, antigenic portions and combinations of these.  
 CC The melanoma antigen is covalently bound to a javelin molecule, where the  
 CC melanoma antigen bound to the javelin molecule is non-covalently bound to  
 CC the heat shock protein. The composition is useful for inducing an immune  
 CC response for the treatment of melanoma. AAU71980-AAU72481 represent  
 CC melanoma antigen peptides of the invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 26.7%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
 Db 4 MPVL 7

RESULT 42  
 ABG97087  
 ID ABG97087 standard; Peptide; 7 AA.  
 XX  
 AC ABG97087;

XX DT 16-DEC-2002 (first entry)  
 XX DE Human leukocyte antigen (HLA) B15 ligand #416.  
 XX KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;  
 XX KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;  
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;  
 KW major histocompatibility complex; diagnostic development;  
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.  
 XX OS Homo sapiens.  
 XX PN WO200262846-A2.  
 XX PD 15-AUG-2002.  
 XX PF 18-DEC-2001; 2001WO-US49744.  
 XX PR 18-DEC-2000; 2000US-256409P.  
 XX PR 18-DEC-2000; 2000US-256410P.  
 XX PR 10-OCT-2001; 2001US-0974366.  
 XX (HIL/) HILDEBRAND W H.  
 XX PA (PRIL/) PRILLMAN K R.  
 XX PI Hildebrand WH, Prillman KR;  
 XX DR WPI; 2002-698563/75.  
 XX PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful  
 PT for studies of peptide loading for characterizing human immune  
 PT responses involves using HLA allelic cDNA or genomic DNA as starting  
 PT material -  
 XX PS Disclosure; Page 184; 300pp; English.  
 XX CC The invention describes a method of producing soluble human leukocyte  
 CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA  
 CC allelic DNA by PCR using a locus specific primer to produce truncated a  
 CC PCR product (P1), inserting P1 into mammalian expression vector;  
 CC electroporating the plasmid into a host cell; inoculating the cell pharm  
 CC with the host cell such that cell pharm produces sHLA. A multimeric HLA  
 CC complex (I) is useful for testing functionality of peptide ligands bound  
 CC by at least two soluble HLA molecules. (I) can be tested for its ability  
 CC to serve as ligands for cytotoxic T lymphocytes (CTL) and induce immune  
 CC responses in humans. (I) is useful for studying T cell responses to  
 CC pathological conditions such as viral infections and cancer, and for  
 CC modulating the human immune system to induce tolerance in autoimmune  
 CC diseases. The individual secreted major histocompatibility complex (MHC)  
 CC molecules produced are useful for studies of peptide loading (i.e., in  
 CC vaccine development) and to the development of diagnostics. With the  
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the  
 CC MHC molecule and characterised. The secreted MHC molecules allow the  
 CC assessment of structural and functional impact of HLA class I  
 CC polymorphism. The molecules are also useful to generate ligands and hence  
 CC ligand maps from the peptide pools extracted from series of distinct yet  
 CC related class I HLA-B15 allotypes; compare the different ligand maps to  
 CC identify potentially shared elements; and characterise the elements  
 CC identified to positively or negatively validate the occurrence of  
 CC overlapping ligands. The truncated version of (MHC) can be produced in  
 CC mammalian or insect/bacterial cells such that milligram or greater  
 CC quantities of an individual class I or class II molecule can be obtained.  
 CC This sequence represents a HLA (human leukocyte antigen) peptide  
 XX ligand.  
 XX SQ Sequence 7 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 12 PPFV 15  
 QY

DB 3 PPFV 6  
 RESULT 43  
 AAU80592  
 ID AAU80592 standard; peptide; 7 AA.  
 XX AC AAU80592;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Javelin peptide #22 for conjugation to multi-component viral particles.  
 XX KW Immunogenic complex; non-pathogenic multi-component viral particle;  
 KW Javelin; heat shock protein; humoral immunity; cellular immunity;  
 KW anti-viral immune response; viral infection; hepatitis; influenza;  
 KW mumps; HIV infection; human immunodeficiency virus; polio;  
 KW tick-borne encephalitis; ebola virus infection.  
 XX OS Synthetic.  
 XX PN WO200178772-A1.  
 XX PD 25-OCT-2001.  
 XX PF 17-APR-2001; 2001WO-US12568.  
 XX PR 17-APR-2000; 2000US-197462P.  
 XX PA (MOJA-) MOJAVE THERAPEUTICS INC.  
 XX PI Hoe M, Landsberger F;  
 XX DR WPI; 2002-049177/06.  
 XX PT New heat shock protein-based viral vaccines, useful for enhancing  
 PT anti-viral immune response in an organism, particularly as a vaccine  
 PT for preventing or ameliorating viral infections, e.g. hepatitis,  
 PT influenza or HIV infection -  
 XX PS Disclosure; Page 10; 75pp; English.  
 XX CC The present invention relates to the use of an immunogenic complex,  
 CC comprising a non-pathogenic multi-component viral particle covalently  
 CC linked to a Javelin molecule (preferably a peptide) that selectively  
 CC binds to a heat shock protein. The immunogenic complex is useful for  
 CC inducing both humoral and cellular immunity, especially for enhancing  
 CC the anti-viral immune response, in a human or non-human subject. The  
 CC immunogenic complex is particularly useful as a vaccine for preventing  
 CC or ameliorating viral infections, e.g. hepatitis, influenza, mumps,  
 CC HIV (human immunodeficiency virus) infection, polio, tick-borne  
 CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent  
 CC Javelin peptides which may be covalently conjugated to multi-component  
 CC viral particles.  
 XX SQ Sequence 7 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 4 MPVL 7  
 QY 4 MPVL 7  
 DB 4 MPVL 7  
 RESULT 44  
 AAR58331  
 ID AAR58331 standard; peptide; 8 AA.  
 XX AC AAR58331;  
 XX



DT 22-SEP-1994 (first entry)  
 XX Hypotensive polypeptide.  
 DE Hypotensive; antioxidant; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 KW Lactobacillus helveticus.  
 XX JP06041191-A.  
 XX 15-FEB-1994.  
 PD 03-MAR-1993; 93JP-0043047.  
 PF 04-MAR-1992; 92JP-0047340.  
 PR (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 PA WPI; 1994-089332/11.  
 DR New polypeptide - used in physiologically active agents having  
 XX e.g. hypotensive antioxidant and calcium absorption promoting  
 PT activity  
 PT Claim 1-2; Page 8; 10pp; Japanese.  
 XX Sequences (AA058319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidant activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX SQ Sequence 8 AA;  
 Query Match 26.7%; Score 4; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VLPV 9  
 DB |||||  
 3 VLPV 6  
 RESULT 45  
 AAW05539  
 ID AAW05539 standard; peptide; 8 AA.  
 AC AAW05539;  
 XX 17-JUN-1997 (first entry)  
 DT Peptide fragment #1 of aminopeptidase of the invention.  
 DE Aminopeptidase; aspergillus oryzae; enzyme; protein hydrolysate; gluten;  
 KW protease; N-terminus.  
 XX Aspergillus oryzae.  
 OS WO9628542-A1.  
 PN 19-SEP-1996.  
 PD 15-MAR-1996; 96WO-DK00104.  
 PF 16-MAR-1995; 95DK-000262.  
 PR (NOVO ) NOVO-NORDISK AS.  
 PA Dambmann C, Halkier T, Kauppinen S, Ostergaard PR;  
 PI Si JQ, Spendler T;  
 XX WPI; 1996-464617/46.  
 DR

XX Enzyme with aminopeptidase activity - used in bread or  
 PT dough-improving compans., and to reduce the bitter taste of proteins  
 PT or protein hydrolysates for foodstuffs, partic. cheese or cocoa  
 XX Claim 7; Page 56; 75pp; English.  
 XX AAW05538-W05543 represent fragments of the Aspergillus oryzae  
 CC aminopeptidase (see AAW05589) of the invention. Aminopeptidases are  
 CC capable of removing one or more amino terminal residues from  
 CC polypeptides. The enzyme is used in a preparation to reduce the bitter  
 CC taste of proteins or protein hydrolysates for foodstuffs, particularly  
 CC cheese or cocoa, so improving their flavour. It is also useful in a bread  
 CC or dough-improving composition, and in the preparation of baked products  
 CC from a flour dough or frozen dough. The enzyme is also useful to improve  
 CC dough stickiness, crumb structure or crust colour of a baked product. The  
 CC enzyme preparation can also be used to clean contact lenses and in  
 CC brewing. The enzyme does not degrade the network of the gluten normally  
 CC seen when proteases are used in the preparation of baked products. Thus,  
 CC the dough characteristics and crumb structure are unaffected.  
 XX SQ Sequence 8 AA;  
 Query Match 26.7%; Score 4; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VEPP 12  
 DB |||||  
 4 VEPP 7  
 RESULT 46  
 AAW36802  
 ID AAW36802 standard; peptide; 8 AA.  
 AC AAW36802;  
 XX 20-APR-1998 (first entry)  
 DT Synthetic peptide p2Ca.  
 DE Immune response; modulation; regulation; T-cell receptor;  
 KW immunoglobulin; selective; target.  
 XX Synthetic.  
 OS WO9735991-A1.  
 PN 02-OCT-1997.  
 PD 28-MAR-1997; 97WO-US04694.  
 PF 28-MAR-1996; 96US-0014367.  
 PR (UYJO ) UNIV JOHNS HOPKINS.  
 PA O'Herrin S, Schneek JP;  
 XX WPI; 1997-489652/45.  
 DR New soluble recombinant divalent and multivalent proteins - used for  
 PT modulating immune responses for treating e.g. transplant rejection,  
 PT auto-immune disorders, tumours or viral infection  
 XX Example 4; Page 38; 80pp; English.  
 XX Peptides AAW36802-W36810 are used in a novel method which regulates the  
 CC immune response and involves a soluble recombinant divalent or  
 CC multivalent protein composition comprising the extracellular domains of  
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and  
 CC light chain polypeptides. Peptide p2Ca is loaded into H-2 Ld on RMA-S Ld  
 CC cells and used to assay the reactivity of the soluble divalent TCR

CC chimera 2C TCR/Ig. The protein compositions are capable of specifically  
 CC binding target molecules and can selectively increase or decrease  
 CC cellular activation, proliferation, anergy or deletion of specific  
 CC T cell subsets. They can also be used for selectively inhibiting or  
 CC decreasing an immune response. If the heterodimeric protein is a MHC  
 CC class II molecule comprising an antigenic peptide, the protein  
 CC compositions can be used for stimulating an antigen-specific T-cell  
 CC response. If the protein is a T cell receptor (TCR) molecule it can be  
 CC used for identifying and purifying an unknown peptide/MHC complex. The  
 CC compositions can also be used for destroying viral-infected or tumour  
 CC cells and for treating autoimmune diseases. The compositions have high  
 CC affinity for their target molecules and allows selective immune  
 CC modulation without compromising the general performance of the immune  
 CC system.  
 XX  
 XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14  
 Db 3 PFPF 6

RESULT 47  
 AAW59334  
 ID AAW59334 standard; peptide; 8 AA.

XX AC AAW59334;

XX DT 24-SEP-1998 (first entry)

XX DE Non-polio enterovirus peptide fragment 73A.

XX KW Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;  
 KW vaccination.

XX OS Enterovirus sp.

XX PN WO9814611-A2.

XX PD 09-APR-1998.

XX PF 01-OCT-1997; 97WO-US17734.

XX PR 02-OCT-1996; 96US-0027353.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kilpatrick D;

XX WPI; 1998-240106/21.

XX PT Identifying non-polio enteroviruses - using primers which hybridise  
 PT to sense and antisense strands that encode conserved non-polio  
 PT enterovirus peptide sequences

XX PS Claim 4; Page 23; 47pp; English.

XX CC The peptide sequences AAW59298-W59344 are amplified by primers to detect  
 CC the presence of a non-polio enterovirus (NPEV) in a sample. The primers  
 CC and assays are used to detect NPEVs in a sample, to serotype these  
 CC viruses, to diagnose enteroviral diseases and medical conditions, and to  
 CC correlate (or disprove a correlation between) specific symptoms or  
 CC combinations of symptoms with the presence of a particular enterovirus.  
 CC They can be used for diseases such as aseptic meningitis. The detection  
 CC of NPEV infections and their correlation with medical conditions will  
 CC make possible vaccines and methods of treatment.  
 XX  
 XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 26.7%; Score 4; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
 Db 3 MPVL 6

RESULT 48

AAW98148

ID AAW98148 standard; Peptide; 8 AA.

XX AC AAW98148;

XX DT 24-JAN-2002 (first entry)

XX DE Human peptide #1423 encoded by a SNP oligonucleotide.

XX KW Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US-0173419.

XX PR 27-DEC-2000; 2000US-0173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -

XX PS Disclosure; Page 3980; 4143pp; English.

XX CC The present invention relates to oligonucleotides (see AAL26793-AAJ34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.

XX Sequence 8 AA;

Query Match 26.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LPVE 10  
 ||||  
 Db 4 LPVE 7

## RESULT 49

AA098149  
 ID AAM98149 standard; Peptide; 8 AA.

XX AC  
 XX DT 24-JAN-2002 (first entry)  
 XX DE  
 XX DE Human peptide #1424 encoded by a SNP oligonucleotide.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX OS Homo sapiens.  
 XX PN WO200147944-A2.  
 XX PD 05-JUL-2001.  
 XX PF 28-DEC-2000; 2000WO-US35498.  
 XX PR 28-DEC-1999; 99US-0173419.  
 XX PR 27-DEC-2000; 2000US-0173419.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Shimketa RA, Leach M;  
 XX WPT; 2001-465210/50.  
 XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX PS Disclosure; Page 3980; 4143pp; English.

XX CC The present invention relates to oligonucleotides (see AA026793-AA034659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.

XX SQ Sequence 8 AA;  
 Query Match 26.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LPVE 10  
 ||||

Db 4 LPVE 7

## RESULT 50

AA047584  
 ID AAB47584 standard; peptide; 8 AA.

XX AC  
 XX DT 13-DEC-2001 (first entry)  
 XX DE  
 XX DE Ag85 complex derived peptide #15.  
 XX KW Antigen 85; CD8 T-cell; vaccine; mycobacterium; detection; epitope;  
 KW lysis.

XX OS Mycobacterium tuberculosis.  
 XX PN WO200170991-A1.  
 XX PD 27-SEP-2001.  
 XX PF 20-MAR-2001; 2001WO-GB01210.  
 XX PR 20-MAR-2000; 2000GB-0006693.  
 XX PA (GLAX ) GLAXO GROUP LTD.  
 XX PI Klein MR;  
 XX WPT; 2001-611506/70.  
 XX PT Use of a polypeptide comprising CD8 T-cell groups derived from  
 PT Mycobacterium tuberculosis antigen 85 in manufacture of a medicament  
 PT for vaccinating prophylactically or therapeutically against  
 PT mycobacterial infection -  
 XX PS Disclosure; Fig 1; 56pp; English.

XX CC The sequences given in AAB47570-86 are polypeptides derived from M.  
 CC tuberculosis antigen 85 which can be recognized by a CD8 T-cell and  
 CC which may be used in the manufacture of agent for vaccinating  
 CC prophylactically or therapeutically against infection by a  
 CC mycobacterium by stimulating a CD8 T cell response.  
 CC These polypeptides are useful for vaccinating a pre-selected host to  
 CC stimulate a CD8 T cell response against a Mycobacterial infection. They  
 CC are also useful for detecting in a population of T cells the presence or  
 CC absence of CD8 T cells that recognize an epitope sequence by contacting  
 CC the population of cells comprising CD8 T-cells with the peptide in  
 CC question and detecting whether the CD8 T-cells recognizing the peptide  
 CC by detecting the expression of a substance by the T cell which indicates  
 CC that the T cell have recognized the peptide or by detecting lysis by T  
 CC cells of cells that present the peptide on their surface, the detection  
 CC of lysis indicating that the T cells have recognized the peptide.

XX SQ Sequence 8 AA;  
 Query Match 26.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LPVE 10  
 ||||  
 Db 4 LPVE 7

## RESULT 51

AA05399  
 ID AA05399 standard; peptide; 8 AA.

XX AC  
 XX DT 24-OCT-2001 (first entry)

```

XX DE Peptide released from alphaKG after cleavage of peptide P1.
XX KW Heat shock protein; hsp; CD8+ cytotoxic T lymphocyte; alphaKG;
XX KW CTL; CD4+ T cell; AIDS; acquired immunodeficiency syndrome; murine;
XX KW human immunodeficiency virus; HIV; pathogen; cancer;
XX KW alpha-ketoglutaraldehyde dehydrogenase.
XX OS Mus sp.
XX PN WO200151081-A1.
XX PD 19-JUL-2001.
XX PF 01-DEC-2000; 2000WO-US32831.
XX PR 14-JAN-2000; 2000US-0176143.
XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX PI Huang Q; Richmond JFL, Cho BK, Palliser D, Chen J, Eisen HN;
XX PI Young RA;
XX DR WPI; 2001-451815/48.
XX CC Inducing a CD8+ cytotoxic T lymphocyte immune response in an individual
XX CC for treating diseases such as HIV involves administering a fusion
XX CC molecule comprising a heat shock protein -
XX PS Disclosure; Page 4; 59pp; English.
XX CC The present sequence represents a naturally occurring murine peptide
XX CC which is released from alpha-ketoglutaraldehyde dehydrogenase (alphaKG)
XX CC upon cleavage of peptide P1 (AAU05397). The present sequence is described
XX CC in an invention relating to a novel method of inducing a CD8+ cytotoxic
XX CC T lymphocyte (CTL) response to a molecule in an individual by
XX CC administering a fusion molecule joined to a hsp, or an adenosine
XX CC triphosphate (ATP) binding domain of a hsp. The method is particularly
XX CC useful in inducing a CD8+ CTL response in an individual deficient in
XX CC CD4+ T cells e.g. for treating an AIDS acquired immunodeficiency
XX CC syndrome patient carrying the human immunodeficiency virus (HIV). The
XX CC method is also useful for treating diseases that are caused by or
XX CC associated with intracellular pathogens, and for treating cancer.
XX SQ Sequence 8 AA;
XX CC Query Match 26.7%; Score 4; DB 22; Length 8;
XX CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 11 PFPF 14
XX DB 3 PFPF 6
XX RESULT 52
XX ABG73074
XX ID ABG73074 standard; peptide; 8 AA.
XX AC ABG73074;
XX DT 02-APR-2003 (first entry)
XX DE MHC Class I peptide p2Ca.
XX KW Antigen-specific T lymphocyte; MHC-antigen complex; MHC Class I peptide;
XX KW major histocompatibility complex; tumour-specific killer T cell;
XX KW virus-specific killer T cell; cytostatic; virucide; p2Ca.
XX OS Synthetic.
XX PN US2002151690-A1.

```

```

XX PD 17-OCT-2002.
XX PF 05-NOV-1999; 99US-0434965.
XX PR 12-AUG-1997; 97US-0909549.
XX PA (LUKE/) LUXEMBURG A T.
XX PA (JACK/) JACKSON M R.
XX PA (PETE/) PETER P A.
XX PI Luxembourg AT, Jackson MR, Peter PA;
XX DR WPI; 2003-182532/18.
XX PT Enriching antigen-specific T lymphocytes, for purifying or expanding in
XX PT vitro tumour- or virus-specific killer T cells for cell therapy,
XX PT comprises capture of the lymphocytes on a substrate coated with
XX PT antigenic peptide-MHC complexes -
XX PS Example 2; Page 5; 40pp; English.
XX CC The invention relates to a method for enriching antigen-specific T
XX CC lymphocytes, comprising contacting a heterogeneous population of
XX CC antigen-specific T lymphocytes with a matrix comprising MHC-antigen
XX CC complexes for a period of time sufficient to allow the antigen-specific T
XX CC lymphocytes to interact with the matrix, and eluting the antigen-specific
XX CC T lymphocytes from the matrix to provide an enriched population of
XX CC antigen-specific T lymphocytes. The MHC-antigen complexes comprise one or
XX CC more antigens. Also claimed is a matrix for capturing antigen-specific T
XX CC lymphocytes, comprising a support having on its surface an immobilised
XX CC Class I peptide and a predetermined amount of an antigen, or for
XX CC capturing antigens, comprising a support having on its surface an
XX CC immobilised empty Class I peptide which is capable of binding one or more
XX CC antigens, and isolating antigen-specific T lymphocytes from a
XX CC heterogeneous population of cells from a patient. The methods are useful
XX CC for enriching antigen-specific T lymphocytes to purify and expand in
XX CC vitro tumour- and virus-specific killer T cells for cell therapy. The
XX CC methods are also useful for isolating or preparing a population of
XX CC antigen-specific T lymphocytes from a patient for treatment of the
XX CC patient's disease or condition. This sequence represents an MHC Class I
XX CC peptide used in the method of the invention.
XX SQ Sequence 8 AA;
XX CC Query Match 26.7%; Score 4; DB 24; Length 8;
XX CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 11 PFPF 14
XX DB 3 PFPF 6
XX RESULT 53
XX AAU07056
XX ID AAU07056 standard; peptide; 9 AA.
XX AC AAU07056;
XX DT 21-JAN-1997 (first entry)
XX DE Synthetic peptide used in GalNac-transferase activity SPA.
XX KW SPA; scintillation proximity assay; antigen; bead coating; capture;
XX KW antibody; N-acetyl galactosamine transferase; GalNac transferase;
XX KW activity; enzyme; O-linked glycosylation.
XX OS Synthetic.
XX PN WO9615258-A1.
XX PD 23-MAY-1996.

```

XX PF 08-NOV-1995; 95WO-US13483.  
 XX PR 16-NOV-1994; 94US-0340283.  
 XX PA (UPJO ) UPJOHN CO.  
 XX PI Elhammer AP;  
 XX DR WPI; 1996-268220/27.  
 XX PT Scintillation proximity assay for N-acetyl-galactosaminyl activity  
 PT - esp. for large scale screening of cpds. for their effect on enzyme  
 PT activity  
 XX PS Claim 14; Page 17; 29pp; English.  
 XX AAW06985-W07180 are antigenic peptides derived from either the  
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDPK).  
 CC The peptides are useful for coating beads used in a scintillation  
 CC proximity assay for N-acetylgalactosamine (GalNAc)-transferase (GNT)  
 CC activity. The assay involves fewer steps than known assays and is  
 CC quicker, producing excellent signal-to-noise ratios. The  
 CC assay is capable of screening large numbers of cpds. for their  
 CC ability to affect GNT activity and is thus useful for identifying  
 CC inhibitors and promoters of glycosylation (in partic. O-linked  
 CC glycosylation).  
 XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLIP 8  
 DB 1 PVLIP 4

RESULT 54  
 AAW36803  
 ID AAW36803 standard; peptide; 9 AA.  
 XX AC AAW36803;  
 XX DT 20-APR-1998 (first entry)  
 XX DE Synthetic peptide QL9.  
 XX KW Immune response; modulation; regulation; T-cell receptor;  
 KW immunoglobulin; selective; target.  
 XX OS Synthetic.  
 XX PN WO9735991-A1.  
 XX PD 02-OCT-1997.  
 XX PF 28-MAR-1997; 97WO-US04694.  
 XX PR 28-MAR-1996; 96US-0014367.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI O'Herrin S, Schneck JP;  
 XX DR WPI; 1997-489652/45.  
 XX PT New soluble recombinant divalent and multivalent proteins - used for  
 PT modulating immune responses for treating e.g. transplant rejection,  
 PT auto-immune disorders, tumours or viral infection  
 XX PS Example 4; Page 38; 80pp; English.

XX CC Peptides AAW36802-W36810 are used in a novel method which regulates the  
 CC immune response and involves a soluble recombinant divalent or  
 CC multivalent protein composition comprising the extracellular domains of  
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and  
 CC light chain polypeptides. Peptide Q99 is loaded into H-2 Ld on RMA-S Ld  
 CC cells and used to assay the reactivity of the soluble divalent TCR  
 CC chimera 2C TCR/1g. The protein compositions are capable of specifically  
 CC binding target molecules and can selectively increase or decrease  
 CC cellular activation, proliferation, anergy, or deletion of specific  
 CC T cell subsets. They can also be used for selectively inhibiting or  
 CC decreasing an immune response. If the heterodimeric protein is a MHC  
 CC class II molecule comprising an antigenic peptide, the protein  
 CC compositions can be used for stimulating an antigen-specific T-cell  
 CC response. If the protein is a T cell receptor (TCR) molecule it can be  
 CC used for identifying and purifying an unknown peptide/MHC complex. The  
 CC compositions can also be used for destroying viral-infected or tumour  
 CC cells and for treating autoimmune diseases. The compositions have high  
 CC affinity for their target molecules and allows selective immune  
 CC modulation without compromising the general performance of the immune  
 CC system.  
 XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14  
 DB 4 PPPF 7

RESULT 55  
 AAW36804  
 ID AAW36804 standard; peptide; 9 AA.  
 XX AC AAW36804;  
 XX DT 20-APR-1998 (first entry)  
 XX DE Synthetic peptide SL9.  
 XX KW Immune response; modulation; regulation; T-cell receptor;  
 KW immunoglobulin; selective; target.  
 XX OS Synthetic.  
 XX PN WO9735991-A1.  
 XX PD 02-OCT-1997.  
 XX PF 28-MAR-1997; 97WO-US04694.  
 XX PR 28-MAR-1996; 96US-0014367.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI O'Herrin S, Schneck JP;  
 XX DR WPI; 1997-489652/45.  
 XX PT New soluble recombinant divalent and multivalent proteins - used for  
 PT modulating immune responses for treating e.g. transplant rejection,  
 PT auto-immune disorders, tumours or viral infection  
 XX PS Example 4; Page 38; 80pp; English.

XX CC Peptides AAW36802-W36810 are used in a novel method which regulates the  
 CC immune response and involves a soluble recombinant divalent or  
 CC multivalent protein composition comprising the extracellular domains of  
 CC a heterodimeric protein operatively linked to immunoglobulin heavy and  
 CC light chain polypeptides. Peptide S99 is loaded into H-2 Ld on RMA-S Ld

CC cells and used to assay the reactivity of the soluble divalent TCR  
 CC chimera 2C TCR/Ig. The protein compositions are capable of specifically  
 CC binding target molecules and can selectively increase or decrease  
 CC cellular activation, proliferation, energy, or deletion of specific  
 CC T cell subsets. They can also be used for selectively inhibiting or  
 CC decreasing an immune response. If the heterodimeric protein is a MHC  
 CC class II molecule comprising an antigenic peptide, the protein  
 CC compositions can be used for stimulating an antigen-specific T-cell  
 CC response. If the protein is a T cell receptor (TCR) molecule it can be  
 CC used for identifying and purifying an unknown peptide/MHC complex. The  
 CC compositions can also be used for destroying viral-infected or tumour  
 CC cells and for treating autoimmune diseases. The compositions have high  
 CC affinity for their target molecules and allows selective immune  
 CC modulation without compromising the general performance of the immune  
 CC system.

XX  
 XX  
 SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PFPP 14  
 DB 3 PFPP 6

RESULT 56  
 AAB47585  
 ID AAB47585 standard; peptide; 9 AA.  
 XX  
 AC AAB47585;  
 XX  
 DT 13-DEC-2001 (first entry)  
 XX  
 XX Ag85 complex derived peptide #16.  
 XX  
 XX Antigen 85; CD8 T-cell; vaccine; mycobacterium; detection; epitope;  
 KW lysis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WC200170991-A1.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 20-MAR-2001; 2001WO-GB01210.  
 XX  
 XX 20-MAR-2000; 2000GB-0006693.  
 XX  
 XX (GLAXO) GLAXO GROUP LTD.  
 PA  
 XX Klein MR;  
 PI  
 XX WPI; 2001-611506/70.  
 XX  
 XX Use of a polypeptide comprising CD8 T-cell groups derived from  
 PT Mycobacterium tuberculosis antigen 85 in manufacture of a medicament  
 PT for vaccinating prophylactically or therapeutically against  
 PT mycobacterial infection -  
 XX  
 XX Disclosure; Fig 1; 56pp; English.

CC The sequences given in AAB47570-86 are polypeptides derived from M.  
 CC tuberculosis antigen 85 which can be recognized by a CD8 T-cell and  
 CC which may be used in the manufacture of agent for vaccinating  
 CC prophylactically or therapeutically against infection by a  
 CC mycobacterium by stimulating a CD8 T cell response.  
 CC These polypeptides are useful for vaccinating a pre-selected host to  
 CC stimulate a CD8 T cell response against a Mycobacterial infection. They  
 CC are also useful for detecting in a population of T cells the presence or  
 CC absence of CD8 T cells that recognize an epitope sequence, by contacting  
 CC the population of cells comprising CD8 T-cells with the peptide in

CC question and detecting whether the CD8 T-cells recognize the peptide,  
 CC by detecting the expression of a substance by the T cell which indicates  
 CC that the T cell have recognized the peptide or by detecting lysis by T  
 CC cells of cells that present the peptide on their surface, the detection  
 CC of lysis indicating that the T cells have recognized the peptide.

XX  
 SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LPVE 10  
 DB 4 LPVE 7

RESULT 57  
 AAM99364  
 ID AAM99364 standard; Peptide; 9 AA.  
 XX  
 AC AAM99364;  
 XX  
 DT 07-DEC-2001 (first entry)  
 XX  
 XX Vaccine related MHC ligand peptide SEQ ID NO:467.  
 XX  
 XX Glutamic acid; glutamine; vaccine; major histocompatibility complex;  
 KW MHC; immunomodulator; antiallergic; endocrine; neuroprotectant;  
 KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;  
 KW medicine; pharmaceutical; immune disorder; immune deficiency;  
 KW autoimmune; hypersensitivity; allergy; graft rejection; infection;  
 KW hormonal disorder; central nervous system disease; cancer; melanoma;  
 KW anti-melanoma vaccine; human immunodeficiency virus.  
 XX  
 OS Mus musculus.  
 XX  
 XX WO200170772-A2.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 22-MAR-2001; 2001WO-FR00872.  
 XX  
 XX 23-MAR-2000; 2000FR-0003711.  
 XX  
 XX (FABR) FABRE MEDICAMENT SA PIERRE.  
 XX  
 XX Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;  
 FI WPI; 2001-611470/70.  
 DR  
 XX Stabilized pharmaceutical containing N-terminal glutamic acid or  
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
 PT with strong acid -  
 PT  
 XX Claim 9; Page 111; 149pp; French.

CC The present invention describes a pharmaceutical compound (I) that  
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue  
 CC in the form of an addition salt with a strong, physiologically  
 CC acceptable acid (II), also described are: (a) a pharmaceutical  
 CC composition containing at least one (I); (b) a vaccine containing at  
 CC least one (I) where this is a major histocompatibility complex (MHC)  
 CC ligand (Ia); (c) a method for in vitro diagnosis of diseases associated  
 CC with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);  
 CC and (e) a process for preparing (I). (I) has immunomodulator, endocrine,  
 CC antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic,  
 CC fungicidal and cytostatic activities. (I) are useful, in human or  
 CC veterinary medicine, in pharmaceutical compositions (for treating immune  
 CC disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,  
 CC allergy, graft rejection, infection, hormonal disorders and central  
 CC nervous system diseases), also, where (I) is a MHC ligand (Ia), in  
 CC vaccines for treatment or prevention of: (i) viral, bacterial, parasitic

CC or fungal infections; or (ii) of cancers. A particular application is in  
 CC anti-melanoma vaccines. (i) are also useful for in vitro diagnosis of  
 CC diseases associated with interactions between MHC and (ii), e.g. melanoma  
 CC and human immunodeficiency virus infection. AAM9898 to AAM99592  
 CC represent peptides which can be used in pharmaceutical compounds from  
 CC the present invention.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14  
 DB 4 PPF 7

RESULT 58  
 AAB82787  
 ID AAB82787 standard; Peptide; 9 AA.

XX AC AAB82787;  
 XX DT 29-OCT-2001 (first entry)  
 XX DE Epitope of mycobacterial antigen 85A.  
 XX KW Mycobacterial antigen 85A; Ag85A; infection; vaccine; diagnosis;  
 XX therapy.

OS Mycobacterium tuberculosis.

XX WO200158461-A1.

PN 16-AUG-2001.

PD 12-FEB-2001; 2001WO-GB00561.

PF 10-FEB-2000; 2000GB-0003082.

PR (GLAXO) GLAXO GROUP LTD.

PA Dockrell HM, Smith SM, Brookes R;

PI WPI; 2001-536505/59.

XX Use of polypeptides comprising groups of mycobacterial antigen 85A  
 PT protein and expression vectors comprising polynucleotides encoding the  
 PT polypeptide for vaccination against Mycobacterium infection -

XX Disclosure; Page 5; 49pp; English.

XX The present sequence is that of an epitope peptide comprising amino  
 CC acid residues 48-56 of Mycobacterium tuberculosis antigen 85A  
 CC (Ag85A). Epitopes, including the present sequence, have been  
 CC found in Ag85A which cause the generation of a strong CD8 T-cell  
 CC response in humans. The CD8 T-cells which recognise the epitopes  
 CC are able to lyse macrophages infected with live Mycobacterium  
 CC tuberculosis. A polypeptide which comprises an epitope structure  
 CC of Ag85A, or an expression vector comprising a polynucleotide  
 CC encoding such a polypeptide, is used in the manufacture of a  
 CC medicament for vaccinating prophylactically or therapeutically  
 CC against infection by a mycobacterium stimulating a CD8 T-cell  
 CC response. The polypeptide or expression vector may be within an  
 CC antigen-presenting cell. A claimed vaccine composition comprises  
 CC the polypeptide or expression vector and an adjuvant or delivery  
 CC system capable of stimulating a CD8 T-cell response. Also claimed  
 CC are methods of detecting in a population of T-cells the presence  
 CC or absence of CD8 T-cells that recognise the epitope sequence, a  
 CC method of diagnosing mycobacterial infection or of testing the  
 CC effectiveness of a vaccination, and a method of treating a  
 CC mycobacterium infection by administering T-cells capable of

CC recognising the epitope.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10  
 DB 2 LEVE 5

RESULT 59

AAE07191  
 ID AAE07191 standard; peptide; 9 AA.

XX AC AAE07191;

XX DT 06-NOV-2001 (first entry)

XX DE Colostriin peptide 7.

XX KW Colostriin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.

XX OS Unidentified.

XX WO200155199-A1.

PN 02-AUG-2001.

PD 26-JAN-2001; 2001WO-GB00329.

PF 26-JAN-2000; 2000GB-0001825.

PR (REGG) REGEN THERAPEUTICS PLC.

PA Georgiades JA;

PI WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT Colostriin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostriin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostriin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostriin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostriin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostriin peptides improve the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostriin peptide 7 related to the invention.  
 CC Colostriin peptide 7 corresponds to position 182-200 of beta-caesin.

XX Sequence 9 AA;  
SQ

Query Match 26.7%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9  
|  
|  
|  
|  
Db 4 VLPV 7

RESULT 60

AAB75912  
ID AAB75912 standard; Peptide; 9 AA.

XX

AC AAB75912;

XX

DT 10-APR-2001 (first entry)

XX

DE Hepatitis B virus env HLA-A2 binding peptide.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
KW human immunodeficiency virus; protozoacide; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
KW condyloma acuminatum.

XX

OS Hepatitis B virus.

XX

PN WO200100225-A1.

XX

PD 04-JAN-2001.

XX

XX 28-JUN-2000; 2000WO-US17842.

XX

PF 29-JUN-1999; 99US-0141422.

XX

XX (EPIM-) EPIMUNE INC.

XX

XX Sette A, Sidney J, Southwood S;

XX

XX WPI; 2001-112389/12.

XX

XX Composition comprising human leukocyte antigen binding peptide which  
XX comprises isolated, prepared epitope useful for treating viral  
XX infections such as acquired immunodeficiency syndrome, and cancer -

XX

XX Claim 1; Page 43; 58pp; English.

XX

XX The present invention describes a composition (I) which comprises at  
XX least one human leukocyte antigen (HLA) binding peptide comprising an  
XX isolated, prepared epitope comprising one of 547 8-11 residue amino acid  
XX sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,  
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human  
XX immunodeficiency virus) and protozoacide activities, which can be used  
XX in vaccine production and is an inducer of cytotoxic T-cell response.  
XX (I) is useful for inducing a cytotoxic T cell response against a  
XX preselected antigen in a patient expressing a specific major  
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
XX treat and/or prevent viral infection and cancer such as prostate cancer,  
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
XX acuminatum.

XX Sequence 9 AA;

SQ

Query Match

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLV 8  
|  
|  
|  
|  
Db 1 PVLV 4

RESULT 61

AAB75913  
ID AAB75913 standard; Peptide; 9 AA.

XX

AC AAB75913;

XX

DT 10-APR-2001 (first entry)

XX

DE Hepatitis B virus env HLA-A2 binding peptide.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
KW human immunodeficiency virus; protozoacide; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
KW condyloma acuminatum.

XX

OS Hepatitis B virus.

XX

PN WO200100225-A1.

XX

PD 04-JAN-2001.

XX

XX 28-JUN-2000; 2000WO-US17842.

XX

PF 29-JUN-1999; 99US-0141422.

XX

XX (EPIM-) EPIMUNE INC.

XX

XX Sette A, Sidney J, Southwood S;

XX

XX WPI; 2001-112389/12.

XX

XX Composition comprising human leukocyte antigen binding peptide which  
XX comprises isolated, prepared epitope useful for treating viral  
XX infections such as acquired immunodeficiency syndrome, and cancer -

XX

XX Claim 1; Page 43; 58pp; English.

XX

XX The present invention describes a composition (I) which comprises at  
XX least one human leukocyte antigen (HLA) binding peptide comprising an  
XX isolated, prepared epitope comprising one of 547 8-11 residue amino acid  
XX sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,  
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human  
XX immunodeficiency virus) and protozoacide activities, which can be used  
XX in vaccine production and is an inducer of cytotoxic T-cell response.  
XX (I) is useful for inducing a cytotoxic T cell response against a  
XX preselected antigen in a patient expressing a specific major  
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
XX treat and/or prevent viral infection and cancer such as prostate cancer,  
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
XX acuminatum.

XX Sequence 9 AA;

SQ

Query Match 26.7%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 5 FVLP 8  
 Db 1 FVLP 4

RESULT 62  
 AAU99719 ID AAU99719 standard; Peptide; 9 AA.  
 XX AC AAU99719;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Mouse MHC Ld/beta2m specific peptide sequence.  
 XX KW Mutant major histocompatibility complex class I chimeric protein; MHC;  
 KW lymphocyte; T-cell receptor; tissue sample; biopsy material; pathogen;  
 KW bodily fluid; T lymphocyte; neoplastic cell; tumour cell; MHC antigen;  
 KW virus; protozoan; bacteria; fungi; nematode; immune response; activator;  
 KW enhancer; T cell activator; mouse; recombinant yeast cell; Kb; OVA; Ld;  
 KW beta2m; dEV8.  
 XX OS Mus sp..  
 XX PN WC200246399-A2.  
 XX PD 13-JUN-2002.  
 XX PF 10-DEC-2001; 2001WO-US47817.  
 XX PR 08-DEC-2000; 2000US-254495P.  
 XX PA (UNII) UNIV ILLINOIS FOUND.  
 XX PI Kranz DM, Brophy S;  
 XX DR WPI; 2002-527916/56.  
 XX PT New isolated mutant major histocompatibility complex class I chimeric  
 PT protein displayed on surfaces of recombinant yeast cells, has improved  
 PT stability, and is useful for activating immune response -  
 XX PS Disclosure; Page 7; 96pp; English.  
 XX CC The present invention relates to a new mutant major histocompatibility  
 CC complex (MHC) class I chimeric protein. The protein of the invention  
 CC comprises a portion mediating binding to surfaces of recombinant yeast  
 CC cells and a portion comprising peptide binding region of MHC class I  
 CC protein, where the invention is improved in stability as compared with  
 CC MHC class I chimeric protein which is not a mutant chimeric protein.  
 CC The protein, further comprising a detectable label, is useful for  
 CC detecting a lymphocyte having a T-cell receptor protein in a biological  
 CC sample such as cells, tissue sample, biopsy material or bodily fluids.  
 CC The method is useful for detecting a T lymphocyte that is specific for  
 CC a neoplastic cell, a tumour cell, a virus-infected cell, a protozoan-  
 CC infected cell, a bacterium-infected cell or a fungus-infected cell. The  
 CC protein of the invention can be used to directly activate T cells, in  
 CC order to identify/screen for peptide-MHC antigens. The protein is also  
 CC useful in activating T cells that participate in the removal of target  
 CC cells including neoplastic cells and cells infected with pathogenic  
 CC agents including viruses, protozoans, bacteria, fungi or nematodes.  
 CC The invention is improved in stability as compared with MHC class I  
 CC protein which is not a mutant chimeric protein. The present amino acid  
 CC sequence represents a mouse MHC peptide of the invention, as described  
 CC above.  
 XX SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 BPFF 14  
 Db 4 BPFF 7

RESULT 63  
 ABP61737 ID ABP61737 standard; Peptide; 9 AA.  
 XX AC ABP61737;  
 XX DT 02-OCT-2002 (first entry)  
 XX DE Human KRPI tryptic digest peptide #170.  
 XX KW Human; tryptic digest peptide; KRPI; kidney response; KR; nephrotropic  
 KW kidney response-associated protein isoform; gene therapy; renal failure;  
 KW antitense therapy; kidney function; tubular nephritis; glomerular necrosis;  
 KW nephron cell metabolic pathway modulation; glomerular necrosis;  
 KW papillary necrosis.  
 XX OS Homo sapiens.  
 XX PN WC200254081-A2.  
 XX PD 11-JUL-2002.  
 XX PF 24-DEC-2001; 2001WO-GB05777.  
 XX PR 29-DEC-2000; 2000US-260392P.  
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX PI Holt GD, Kelly MD, Kennedy SJ, Moyses C;  
 XX DR WPI; 2002-583637/62.  
 XX PT Screening, diagnosis or prognosis of kidney response in subject, by  
 PT detecting kidney response-associated features or kidney  
 PT response-associated protein isoforms in body fluid or tissue from  
 PT subject -  
 XX PS Disclosure; Page 46; 169pp; English.  
 XX CC The invention relates to a novel method for the screening, diagnosis or  
 CC prognosis of kidney response (KR). The method of the invention has  
 CC nephrotropic activity, and may have a use in gene therapy or antitense  
 CC therapy. The method is useful for the screening, diagnosis or prognosis  
 CC of KR in a subject, for determining the stage or severity of KR in a  
 CC subject, for identifying a subject at risk of developing KR, or for  
 CC monitoring the effect of therapy administered to a subject with KR. An  
 CC alternative method of the invention is useful for screening agents that  
 CC interact with one or more of the kidney response-associated protein  
 CC isoforms (KRPIs). The kidney response includes alterations in kidney  
 CC function, any phase of nephron cell metabolic pathway modulation,  
 CC glomerular/proximal tubular nephritis, glomerular/papillary necrosis,  
 CC acute and chronic renal failure, and end stage renal disease. The  
 CC sequences shown in ABP61514-ABP61787 represent tryptic digest peptides of  
 CC the KRPIs of the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10  
 Db 2 LPVE 5

RESULT 64  
 AAU98288

ID AAU98288 standard; peptide; 9 AA.  
 XX AAU98288;  
 AC 15-AUG-2002 (first entry)  
 DT M. tuberculosis Ag85 derived immunodominant T cell epitope #15.  
 DE Ag85; epitope; vaccine; tuberculosis; mycolyltransferase; HLA-A\*02001;  
 XX Mycobacterium tuberculosis; Mycobacterium leprae; Mycobacterium bovis;  
 KW Mycobacterium ulcerans; Mycobacterium avium; antibacterial;  
 XX MHC class I-restricted CD8+ T cell; human leukocyte antigen.  
 OS Mycobacterium tuberculosis.  
 XX Key Location/Qualifiers  
 XX 2  
 FT /note= "Amino acid contributing to the HLA-A\*02001  
 FT binding motif"  
 FT 9  
 FT Region  
 FT /note= "Amino acid contributing to the HLA-A\*02001  
 FT binding motif"  
 FT EP1211260-A1.  
 XX 05-JUN-2002.  
 XX 30-NOV-2000; 2000EP-0204268.  
 XX 30-NOV-2000; 2000EP-0204268.  
 XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
 XX Ottenhof THM, Geluk A;  
 XX WPI; 2002-464923/50.  
 XX Peptide of 8-11 amino acids derived from the Ag85 protein of  
 PT mycobacterium induce proliferation of MHC class I-restricted CD8+ T  
 PT cells and are useful to vaccinate against infection by mycobacterium  
 PS Claim 1; Page 7; 20pp; English.  
 XX The invention relates to peptide (P1) derived from an Ag85 protein of  
 CC mycobacterium (which is associated with mycolyltransferase activity  
 CC and is involved in cell wall synthesis), comprising 8-11 amino acids, and  
 CC capable of inducing proliferation of MHC class I-restricted CD8+ T cells  
 CC in vivo. Also included are (1) a peptide comprising P1 flanked by amino  
 CC acids representing antigen processing sites; (2) a polypeptide comprising  
 CC at least two of the peptides in (1); (3) a nucleic acid encoding one of  
 CC the claimed peptides or polypeptides; (4) a vector comprising the above  
 CC nucleic acid; (5) a host cell comprising the above nucleic acid or  
 CC vector; and (6) detecting and/or enumerating CD8+ T cells against  
 CC mycobacterium, comprising tetrameric complexes of MHC (major  
 CC histocompatibility group) class I and one of the claimed peptides or  
 CC polypeptides. The molecules of the invention are used to prepare a  
 CC vaccine against mycobacterium (e.g. Mycobacterium tuberculosis,  
 CC Mycobacterium leprae, Mycobacterium bovis, Mycobacterium ulcerans,  
 CC Mycobacterium avium) and thus protect against diseases such as  
 CC tuberculosis. The present sequence is an M. tuberculosis Ag85  
 CC derived immunogenic peptide of the invention binding to HLA-A\*02001  
 CC (human leukocyte antigen).  
 XX Sequence 9 AA;  
 SQ

Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPVE 10  
 DB 2 LPVE 5

RESULT 65  
 AAU94070  
 ID AAU94070 standard; Peptide; 9 AA.  
 XX AAU94070;  
 AC 02-JUL-2002 (first entry)  
 DT Human novel protein CatrP2E11 HLA binding peptide #3.  
 DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CatrP2E11;  
 XX calcium transport protein; cancer; prostate cancer; cytostatic;  
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
 XX Homo sapiens.  
 OS WO200214361-A2.  
 XX 21-FEB-2002.  
 XX 17-AUG-2001; 2001WO-US25782.  
 XX 17-AUG-2000; 2000US-226329P.  
 XX (AGEN-) AGENSYS INC.  
 XX Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;  
 PI Levin B, Hubert RS, Ge W, Jakobovits A;  
 XX WPI; 2002-269179/31.  
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 FT in a subject, comprises determining the status of 83P2H3 gene products  
 FT in a tissue sample from the subject and comparing it to a normal sample  
 FT -  
 XX Example 11; Page 164; 270pp; English.  
 PS The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related, protein CatrP2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence

CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 DLEM 4  
 |||||  
 Db 1 DLEM 4  
 RESULT 66  
 AAU94117  
 ID AAU94117 standard; Peptide; 9 AA.  
 XX  
 AC AAU94117;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human novel protein CaTrF2E11 HLA binding peptide #50.  
 XX  
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
 KW calcium transport protein; cancer; prostate cancer; cytostatic;  
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200214361-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US25782.  
 XX  
 PR 17-AUG-2000; 2000US-226329P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;  
 PI Levin E, Hubert RS, Ge W, Jakobovits A;  
 XX  
 DR WPI; 2002-269179/31.  
 XX  
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products  
 PT in a tissue sample from the subject and comparing it to a normal sample  
 XX  
 PS Example 11; Page 166; 270pp; English.  
 CC  
 CC The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method

CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 DLEM 4  
 |||||  
 Db 3 DLEM 6  
 RESULT 67  
 AAU94489  
 ID AAU94489 standard; Peptide; 9 AA.  
 XX  
 AC AAU94489;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human novel protein CaTrF2E11 HLA binding peptide #222.  
 XX  
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
 KW calcium transport protein; cancer; prostate cancer; cytostatic;  
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200214361-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US25782.  
 XX  
 PR 17-AUG-2000; 2000US-226329P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Raitano AB, Challita-Bid PM, Faris M, Saffran DC, Afar DEH;  
 PI Levin E, Hubert RS, Ge W, Jakobovits A;  
 XX  
 DR WPI; 2002-269179/31.  
 XX  
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products  
 PT in a tissue sample from the subject and comparing it to a normal sample  
 XX  
 PS Example 11; Page 179; 270pp; English.  
 CC  
 CC The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against

CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEM 4  
 ||||  
 Db 1 DLEM 4

RESULT 68

AAU94707  
 ID AAU94707 standard; Peptide; 9 AA.

XX AAU94707;

XX 02-JUL-2002 (first entry)

XX Human novel protein CaTrF2E11 HLA binding peptide #340.

XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
 XX calcium transport protein; cancer; prostate cancer; cytostatic;  
 XX chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
 XX Levin E, Hubert RS, Ge W, Jakobovits A;

XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products

PT in a tissue sample from the subject and comparing it to a normal sample  
 FS Example 11; Page 187; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having the  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEM 4  
 ||||  
 Db 1 DLEM 4

RESULT 69

AAU95042  
 ID AAU95042 standard; Peptide; 9 AA.

XX AAU95042;

XX 02-JUL-2002 (first entry)

XX Human novel protein CaTrF2E11 HLA binding peptide #475.

XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
 XX calcium transport protein; cancer; prostate cancer; cytostatic;  
 XX chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

PF 17-AUG-2001; 2001WO-US25782.  
 XX  
 PR 17-AUG-2000; 2000US-226329P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Raitano AB, Challita-Eid PM, Faris M, Safran DC, Afar DBH;  
 PI Levin E, Hubert RS, Ge W, Jakobovits A;  
 XX  
 DR WPI; 2002-269179/31.  
 XX  
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products  
 PT in a tissue sample from the subject and comparing it to a normal sample  
 PT  
 XX  
 PS Example 11; Page 201; 270pp; English.  
 XX  
 CC The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related protein CanrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CanrF2E11.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLEM 4  
 DB 5 DLEM 8  
 RESULT 70  
 ABR10368  
 ID ABR10368 standard; Peptide; 9 AA.  
 XX  
 AC ABR10368;  
 XX  
 DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 154P2A8 HLA peptide #3.  
 DE  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 XX 10-APR-2002; 2002WO-US11654.  
 PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR  
 PR 10-APR-2001; 2001US-283112P.  
 PR  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison KK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients  
 XX  
 PS Claim 13; Page 216; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 26.7%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VLPV 9  
 DB 4 VLPV 7  
 RESULT 71  
 ABR10399  
 ID ABR10399 standard; Peptide; 9 AA.  
 XX  
 AC ABR10399;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 XX Human cancer-related protein 154P2A8 HLA peptide #34.  
 DE  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX

```

PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 216; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 VLPV 9
XX ||||
XX 2 VLPV 5
XX
XX RESULT 72
XX ABR10408
XX AC ABR10408 standard; Peptide; 9 AA.
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 154P2A8 HLA peptide #43.
XX
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO200283921-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX 10-APR-2001; 2001US-283112P.
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 216; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 VLPV 9
XX ||||
XX 2 VLPV 5
XX
XX RESULT 73
XX ABR10438
XX ID ABR10438 standard; Peptide; 9 AA.
XX
XX AC ABR10438;
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 154P2A8 HLA peptide #73.
XX
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO200283921-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX 10-APR-2001; 2001US-283112P.
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 216; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 VLPV 9
XX ||||
XX 6 VLPV 9
XX
XX Db

```

PS Claim 13; Page 216; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

DB 3 VLPV 6

RESULT 74

ABR10455

ID ABR10455 standard; Peptide; 9 AA.

XX AC ABR10455;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 154P2A8 HLA peptide #90.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 216; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

DB 1 VLPV 4

RESULT 75

ABR10580

ID ABR10580 standard; Peptide; 9 AA.

XX AC ABR10580;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 154P2A8 HLA peptide #215.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX DR WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of

XX PT proteins and polynucleotides, useful for therapeutic, prognostic and

XX PT diagnostic reagents for eliciting cellular or humoral immune response

XX PT in cancer patients -

XX PS Claim 13; Page 218; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            6 VLPV 9  
             ||||  
Db            3 VLPV 6

Search completed: November 25, 2003, 18:15:45  
Job time : 50.5904 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 29.8404 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-5

Perfect score: 15  
Sequence: 1 DLEMPVLVPEFFPV 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW PUB. pep.\*  
2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW PUB. pep.\*  
3: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB. pep.\*  
4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB. pep.\*  
5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW PUB. pep.\*  
6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB. pep.\*  
7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW PUB. pep.\*  
8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB. pep.\*  
9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB. pep.\*  
10: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB. pep.\*  
11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB. pep.\*  
12: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB. pep.\*  
13: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB. pep.\*  
14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB. pep.\*  
15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB. pep.\*  
16: /cgn2\_6/ptodata/1/pubaa/US10\_NEW PUB. pep.\*  
17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW PUB. pep.\*  
18: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB. pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID              | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 15    | 100.0       | 15     | US-10-281-652-5    | Sequence 5, Appli  |
| 2          | 5     | 33.3        | 18     | US-10-281-652-22   | Sequence 22, Appli |
| 3          | 4     | 26.7        | 5      | US-09-788-006-138  | Sequence 138, Appl |
| 4          | 4     | 26.7        | 5      | US-09-788-006-140  | Sequence 140, Appl |
| 5          | 4     | 26.7        | 7      | US-09-997-900-11   | Sequence 11, Appli |
| 6          | 4     | 26.7        | 7      | US-10-052-578-170  | Sequence 170, Appl |
| 7          | 4     | 26.7        | 7      | US-10-022-066-506  | Sequence 506, Appl |
| 8          | 4     | 26.7        | 7      | US-10-053-520-170  | Sequence 170, Appl |
| 9          | 4     | 26.7        | 7      | US-10-118-708-2    | Sequence 2, Appli  |
| 10         | 4     | 26.7        | 7      | US-10-053-498B-170 | Sequence 170, Appl |
| 11         | 4     | 26.7        | 7      | US-10-305-346-8    | Sequence 8, Appli  |
| 12         | 4     | 26.7        | 8      | US-09-954-166-12   | Sequence 12, Appli |
| 13         | 4     | 26.7        | 8      | US-09-761-534A-3   | Sequence 3, Appli  |
| 14         | 4     | 26.7        | 8      | US-09-434-965-2    | Sequence 2, Appli  |
| 15         | 4     | 26.7        | 8      | US-10-266-463A-46  | Sequence 46, Appli |

|    |   |      |    |    |                    |                    |
|----|---|------|----|----|--------------------|--------------------|
| 16 | 4 | 26.7 | 8  | 15 | US-10-145-396-2    | Sequence 2, Appli  |
| 17 | 4 | 26.7 | 8  | 15 | US-10-046-801-25   | Sequence 25, Appli |
| 18 | 4 | 26.7 | 8  | 15 | US-10-046-801-28   | Sequence 28, Appli |
| 19 | 4 | 26.7 | 8  | 15 | US-10-046-801-33   | Sequence 33, Appli |
| 20 | 4 | 26.7 | 9  | 10 | US-09-954-166-13   | Sequence 13, Appli |
| 21 | 4 | 26.7 | 9  | 10 | US-09-954-166-14   | Sequence 14, Appli |
| 22 | 4 | 26.7 | 9  | 10 | US-09-434-965-1    | Sequence 1, Appli  |
| 23 | 4 | 26.7 | 9  | 10 | US-09-434-965-3    | Sequence 3, Appli  |
| 24 | 4 | 26.7 | 9  | 12 | US-09-932-165-53   | Sequence 53, Appli |
| 25 | 4 | 26.7 | 9  | 12 | US-09-932-165-100  | Sequence 100, Appl |
| 26 | 4 | 26.7 | 9  | 12 | US-09-932-165-472  | Sequence 472, Appl |
| 27 | 4 | 26.7 | 9  | 12 | US-09-932-165-690  | Sequence 690, Appl |
| 28 | 4 | 26.7 | 9  | 12 | US-09-932-165-1025 | Sequence 1025, Ap  |
| 29 | 4 | 26.7 | 9  | 12 | US-10-266-463A-47  | Sequence 47, Appli |
| 30 | 4 | 26.7 | 9  | 12 | US-10-062-109A-4   | Sequence 4, Appli  |
| 31 | 4 | 26.7 | 9  | 12 | US-10-062-109A-44  | Sequence 44, Appli |
| 32 | 4 | 26.7 | 9  | 12 | US-10-239-313A-467 | Sequence 467, Appl |
| 33 | 4 | 26.7 | 9  | 12 | US-10-005-480A-4   | Sequence 4, Appli  |
| 34 | 4 | 26.7 | 9  | 12 | US-10-005-480A-44  | Sequence 44, Appli |
| 35 | 4 | 26.7 | 9  | 14 | US-10-093-200A-13  | Sequence 13, Appli |
| 36 | 4 | 26.7 | 9  | 15 | US-10-015-535-4    | Sequence 4, Appli  |
| 37 | 4 | 26.7 | 9  | 15 | US-10-046-801-29   | Sequence 29, Appli |
| 38 | 4 | 26.7 | 9  | 15 | US-10-093-248-13   | Sequence 13, Appli |
| 39 | 4 | 26.7 | 10 | 9  | US-09-220-920-111  | Sequence 111, Appl |
| 40 | 4 | 26.7 | 10 | 12 | US-09-932-165-154  | Sequence 154, Appl |
| 41 | 4 | 26.7 | 10 | 12 | US-09-932-165-785  | Sequence 785, Appl |
| 42 | 4 | 26.7 | 10 | 12 | US-10-062-109A-55  | Sequence 55, Appli |
| 43 | 4 | 26.7 | 10 | 12 | US-10-062-109A-71  | Sequence 71, Appli |
| 44 | 4 | 26.7 | 10 | 12 | US-10-005-480A-55  | Sequence 55, Appli |
| 45 | 4 | 26.7 | 10 | 12 | US-10-005-480A-71  | Sequence 71, Appli |
| 46 | 4 | 26.7 | 10 | 15 | US-10-062-710-199  | Sequence 199, Appl |
| 47 | 4 | 26.7 | 11 | 9  | US-09-780-662A-14  | Sequence 14, Appli |
| 48 | 4 | 26.7 | 11 | 12 | US-10-182-303-14   | Sequence 14, Appli |
| 49 | 4 | 26.7 | 11 | 15 | US-10-082-710-173  | Sequence 173, Appl |
| 50 | 4 | 26.7 | 12 | 11 | US-09-934-385-146  | Sequence 146, Appl |
| 51 | 4 | 26.7 | 12 | 11 | US-09-934-385-319  | Sequence 319, Appl |
| 52 | 4 | 26.7 | 12 | 12 | US-10-214-867A-17  | Sequence 17, Appli |
| 53 | 4 | 26.7 | 12 | 12 | US-10-118-708-5    | Sequence 5, Appli  |
| 54 | 4 | 26.7 | 12 | 15 | US-10-057-789-142  | Sequence 142, Appl |
| 55 | 4 | 26.7 | 12 | 15 | US-10-212-628-142  | Sequence 142, Appl |
| 56 | 4 | 26.7 | 12 | 15 | US-10-254-446A-157 | Sequence 157, Appl |
| 57 | 4 | 26.7 | 13 | 9  | US-09-113-924-14   | Sequence 14, Appli |
| 58 | 4 | 26.7 | 13 | 10 | US-09-937-107-72   | Sequence 72, Appli |
| 59 | 4 | 26.7 | 13 | 10 | US-09-943-692-29   | Sequence 29, Appli |
| 60 | 4 | 26.7 | 13 | 15 | US-10-116-846B-5   | Sequence 5, Appli  |
| 61 | 4 | 26.7 | 13 | 15 | US-10-116-846B-45  | Sequence 45, Appli |
| 62 | 4 | 26.7 | 14 | 9  | US-09-113-924-13   | Sequence 13, Appli |
| 63 | 4 | 26.7 | 15 | 9  | US-09-936-010-9    | Sequence 9, Appli  |
| 64 | 4 | 26.7 | 15 | 9  | US-09-947-770-15   | Sequence 15, Appli |
| 65 | 4 | 26.7 | 15 | 10 | US-09-813-333-18   | Sequence 18, Appli |
| 66 | 4 | 26.7 | 15 | 10 | US-09-953-510-37   | Sequence 37, Appli |
| 67 | 4 | 26.7 | 15 | 10 | US-09-953-510-38   | Sequence 38, Appli |
| 68 | 4 | 26.7 | 15 | 11 | US-09-880-505-22   | Sequence 22, Appli |
| 69 | 4 | 26.7 | 15 | 11 | US-09-880-505-24   | Sequence 24, Appli |
| 70 | 4 | 26.7 | 15 | 12 | US-10-349-023-18   | Sequence 18, Appli |
| 71 | 4 | 26.7 | 15 | 12 | US-10-147-255-37   | Sequence 37, Appli |
| 72 | 4 | 26.7 | 15 | 12 | US-10-147-255-38   | Sequence 38, Appli |
| 73 | 4 | 26.7 | 15 | 12 | US-10-161-791-312  | Sequence 312, Appl |
| 74 | 4 | 26.7 | 15 | 14 | US-10-044-703-18   | Sequence 18, Appli |
| 75 | 4 | 26.7 | 15 | 14 | US-10-051-643-22   | Sequence 22, Appli |
| 76 | 4 | 26.7 | 15 | 14 | US-10-051-643-24   | Sequence 24, Appli |
| 77 | 4 | 26.7 | 15 | 15 | US-10-100-957A-104 | Sequence 104, Appl |
| 78 | 4 | 26.7 | 15 | 15 | US-10-186-867-35   | Sequence 35, Appli |
| 79 | 4 | 26.7 | 16 | 11 | US-09-880-748-2228 | Sequence 2228, Ap  |
| 80 | 4 | 26.7 | 16 | 11 | US-09-880-748-2334 | Sequence 2334, Ap  |
| 81 | 4 | 26.7 | 16 | 12 | US-10-094-407A-36  | Sequence 36, Appli |
| 82 | 4 | 26.7 | 16 | 12 | US-10-161-791-200  | Sequence 200, Appl |
| 83 | 4 | 26.7 | 16 | 12 | US-10-161-791-202  | Sequence 202, Appl |
| 84 | 4 | 26.7 | 16 | 12 | US-10-161-791-406  | Sequence 406, Appl |
| 85 | 4 | 26.7 | 16 | 12 | US-10-043-487-442  | Sequence 442, Appl |
| 86 | 4 | 26.7 | 16 | 15 | US-10-034-934-141  | Sequence 141, Appl |
| 87 | 4 | 26.7 | 16 | 15 | US-10-211-088-27   | Sequence 27, Appli |
| 88 | 4 | 26.7 | 16 | 15 |                    |                    |

89 4 26.7 16 15 US-10-028-075B-4 Sequence 4, Appli  
 90 4 26.7 16 15 US-10-029-206A-4 Sequence 4, Appli  
 91 4 26.7 17 9 US-09-864-761-34508 Sequence 34508, A  
 92 4 26.7 17 11 US-09-996-069-30 Sequence 30, Appl  
 93 4 26.7 17 11 US-09-996-069-31 Sequence 31, Appl  
 94 4 26.7 17 12 US-10-161-791-362 Sequence 362, App  
 95 4 26.7 17 15 US-10-091-724-39 Sequence 39, Appl  
 96 4 26.7 17 15 US-10-225-567A-1000 Sequence 1000, Ap  
 97 4 26.7 18 9 US-09-864-761-42763 Sequence 42763, A  
 98 4 26.7 19 11 US-09-880-505-23 Sequence 23, Appl  
 99 4 26.7 19 12 US-10-348-190-9 Sequence 9, Appli  
 100 4 26.7 19 14 US-10-051-643-23 Sequence 23, Appl

## ALIGNMENTS

RESULT 1  
 US-10-281-652-5  
 ; Sequence 5, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: 265.0020101  
 ; CURRENT APPLICATION NUMBER: US/10/281.652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641.803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-5

Query Match 100.0%; Score 15; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1 DLEMPVLVPEFFPV 15  
 |||||  
 Db 1 DLEMPVLVPEFFPV 15

RESULT 2  
 US-10-281-652-22  
 ; Sequence 22, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: 265.0020101  
 ; CURRENT APPLICATION NUMBER: US/10/281.652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641.803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-22

Query Match 33.3%; Score 5; DB 15; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPF 12  
 |||||  
 Db 10 PVEPF 14

RESULT 3  
 US-09-788-006-138  
 ; Sequence 138, Application US/09788006  
 ; Publication No. US20030036093A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 138  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-138

Query Match 26.7%; Score 4; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 |||||  
 Db 2 VLPV 5

RESULT 4  
 US-09-788-006-140  
 ; Sequence 140, Application US/09788006  
 ; Publication No. US20030036093A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 140  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-140

Query Match 26.7%; Score 4; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 |||||

```
Db 1 VLPV 4

RESULT 5
US-09-997-900-11
; Sequence 11, Application US/09997900
; Patent No. US20020053098A1
; GENERAL INFORMATION:
; APPLICANT: Kakefuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; FILE REFERENCE: 043753/241148 (5849-20A)
; CURRENT APPLICATION NUMBER: US/09/997,900
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 09/426,568
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-11

Query Match 26.7%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 ||||
Db 3 VEPF 6

RESULT 6
US-10-052-578-170
; Sequence 170, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPFV 15
 ||||
Db 3 PPFV 6

RESULT 7
US-10-022-066-506
; Sequence 506, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: FRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022.066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 506
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-506

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPFV 15
 ||||
Db 3 PPFV 6

RESULT 8
US-10-053-520-170
; Sequence 170, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 170
```

; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: peptide in m13 coliphage  
 US-10-053-520-170

Query Match 26.7%; Score 4; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7  
 ||||  
 Db 4 MPVL 7

## RESULT 9

US-10-118-708-2  
 ; Sequence 2, Application US/10118708  
 ; Publication No. US20030165991A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hart, L P  
 ; APPLICANT: Pestka, James J  
 ; APPLICANT: Yuan, Qiaoping  
 ; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
 ; FILE REFERENCE: MSU 4.1-447  
 ; CURRENT APPLICATION NUMBER: US/10/118,708  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/146,643  
 ; PRIOR FILING DATE: 1999-07-30  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2  
 ; OTHER INFORMATION: peptide mimotope of deoxynivalenol  
 US-10-118-708-2

Query Match 26.7%; Score 4; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14  
 ||||  
 Db 4 PPPF 7

## RESULT 10

US-10-053-498B-170  
 ; Sequence 170, Application US/10053498B  
 ; Publication No. US20030194409A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloan-Kettering Institute for Cancer Research  
 ; APPLICANT: Rothman, James E.  
 ; APPLICANT: Mayhew, Mark  
 ; APPLICANT: Hoe, Mee H.  
 ; APPLICANT: Houghton, Alan  
 ; APPLICANT: Hartl, Ulrich  
 ; APPLICANT: Ousefelli, Ouathek  
 ; APPLICANT: Morici, Yoichi  
 ; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
 ; FILE REFERENCE: 11746/46002  
 ; CURRENT APPLICATION NUMBER: US/10/053,498B  
 ; CURRENT FILING DATE: 2002-01-17  
 ; PRIOR APPLICATION NUMBER: 08/961,707  
 ; PRIOR FILING DATE: 1997-10-31  
 ; NUMBER OF SEQ ID NOS: 321  
 ; SOFTWARE: WordPerfect 8.0 for Windows  
 ; SEQ ID NO 170

; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: peptide in m13 coliphage  
 US-10-053-498B-170

Query Match 26.7%; Score 4; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7  
 ||||  
 Db 4 MPVL 7

## RESULT 11

US-10-305-346-8  
 ; Sequence 8, Application US/10305346  
 ; Publication No. US20030130195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMIOT, Jean  
 ; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS  
 ; FILE REFERENCE: 6013-57\*US\*-1  
 ; CURRENT APPLICATION NUMBER: US/10/305,346  
 ; CURRENT FILING DATE: 2002-11-27  
 ; PRIOR APPLICATION NUMBER:  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Peptide from enzymatic hydrolyseate of milk proteins  
 US-10-305-346-8

Query Match 26.7%; Score 4; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 ||||  
 Db 1 VLPV 4

## RESULT 12

US-09-954-166-12  
 ; Sequence 12, Application US/09954166  
 ; Patent No. US20020127231A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schneck, Jonathan P.  
 ; O'Herrin, Sean  
 ; TITLE OF INVENTION: Soluble Divalent and Multivalent  
 ; Heterodimeric Analogs of Proteins  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Banner & Witcoff, Ltd.  
 ; STREET: 1001 G Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/954,166  
 ; FILING DATE: 18-Sep-2001  
 ; CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-954-166-12

Query Match 26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 13
US-09-761-534A-3
; Sequence 3, Application US/09761534A
; Patent No. US20020146426A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE OF INVENTION: CD4+T Cell-Independent
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Alpha KG Peptide
US-09-761-534A-3

Query Match 26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 14
US-09-434-965-2
; Sequence 2, Application US/09434965
; Patent No. US20020151690A1
; GENERAL INFORMATION:
; APPLICANT: Luxembourg, Alain T.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,965
; FILING DATE: 05-No. US20020151690A1-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-841
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-2806
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-434-965-2

Query Match 26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 15
US-10-266-463A-46
; Sequence 46, Application US/10266463A
; Publication No. US20030138946A1
; GENERAL INFORMATION:
; APPLICANT: CAI, Zeling
; APPLICANT: SPRENT, Jonathan
; APPLICANT: BRUNMARK, Anders
; APPLICANT: JACKSON, Michael
; APPLICANT: PETERSON, Per A.
; APPLICANT: LUXEMBOURG, Alain
; APPLICANT: LETURCO, Didier Jean
; APPLICANT: MORIARTY, Ann M.
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
; TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
; FILE REFERENCE: TSRI 471.1 Div. 1
; CURRENT APPLICATION NUMBER: US/10/266,463A
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 08/913,612
; PRIOR FILING DATE: 1997-09-08
```

```

; PRIOR APPLICATION NUMBER: PCT/US96/03249
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: US 08/400,338
; PRIOR FILING DATE: 1995-03-08
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mus musculus
US-10-266-463A-46

Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
Db 3 PPPF 6

RESULT 16
US-10-145-396-2
; Sequence 2, Application US/10145396
; Publication No. US2003003485A1
; GENERAL INFORMATION:
; APPLICANT: Uenaka, Akiko
; APPLICANT: Nakayama, Eiichi
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIGENS
; FILE REFERENCE: L00461/70129
; CURRENT APPLICATION NUMBER: US/10/145,396
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/291,125
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-145-396-2

Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
Db 3 PPPF 6

RESULT 17
US-10-046-801-25
; Sequence 25, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequence:
US-10-046-801-25

Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
Db 3 PPPF 6

RESULT 18
US-10-046-801-28
; Sequence 28, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequence:
US-10-046-801-28

Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
Db 3 PPPF 6

RESULT 19
US-10-046-801-33
; Sequence 33, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequence:
US-10-046-801-33

Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPPF 14
Db 3 PPPF 6

```

```

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 20
US-09-954-166-13
; Sequence 13, Application US/09954166
; Patent No. US20020127231A1
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,166
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide QL9
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-954-166-13

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 4 PFPF 7

RESULT 21
US-09-954-166-14
; Sequence 14, Application US/09954166
; Patent No. US20020127231A1
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; Heterodimeric Analogs of Proteins

```

```

; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,166
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide SL9
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-954-166-14

Query Match 26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 22
US-09-434-965-1
; Sequence 1, Application US/09434965
; Patent No. US20020151690A1
; GENERAL INFORMATION:
; APPLICANT: Luxembourg, Alain T.
; Jackson, Michael R.
; Peterson, Per A.
; TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/434,965

```

;; FILING DATE: 05-NO. US20020151690A1-1999  
;; CLASSIFICATION: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wallen, John W.  
;; REGISTRATION NUMBER: 35,403  
;; REFERENCE/DOCKET NUMBER: ORT-841  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 732-524-2806  
;; TELEFAX: 732-524-2808  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ANTI-SENSE: NO  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-434-965-1

Query Match 26.7%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 11 PFPF 14  
|||  
Db 4 PFPF 7

## RESULT 23

US-09-434-965-3  
; Sequence 3, Application US/09434965  
; Patent No. US20020151690A1  
; GENERAL INFORMATION:  
; APPLICANT: Luxembourg, Alain T.  
; Jackson, Michael R.  
; Peterson, Per A.

;; TITLE OF INVENTION: PURIFICATION OF ANTIGEN-SPECIFIC T CELLS  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Johnson & Johnson  
;; STREET: One Johnson & Johnson Plaza  
;; CITY: New Brunswick  
;; STATE: NJ  
;; COUNTRY: USA  
;; ZIP: 08933-7003

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/434,965  
;; FILING DATE: 05-NO. US20020151690A1-1999  
;; CLASSIFICATION: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wallen, John W.  
;; REGISTRATION NUMBER: 35,403  
;; REFERENCE/DOCKET NUMBER: ORT-841  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 732-524-2806  
;; TELEFAX: 732-524-2808  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ANTI-SENSE: NO  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-434-965-3

Query Match 26.7%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 11 PFPF 14  
|||  
Db 2 PFPF 5

## RESULT 24

US-09-932-165-53  
; Sequence 53, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AVA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-53

Query Match 26.7%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 DLEM 4  
|||  
Db 1 DLEM 4

## RESULT 25

US-09-932-165-100  
; Sequence 100, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AVA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CAT-F2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; NUMBER OF SEQ ID NOS: 1508



```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-100

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 3 DLEM 6

RESULT 26
US-09-932-165-472
; Sequence 472, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932.165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-472

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 1 DLEM 4

RESULT 27
US-09-932-165-690
; Sequence 690, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932.165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-472

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 1 DLEM 4

RESULT 28
US-09-932-165-1025
; Sequence 1025, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932.165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1025

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 5 DLEM 8

RESULT 29
US-10-266-463A-47
; Sequence 47, Application US/10266463A
; Publication No. US20030138946A1
; GENERAL INFORMATION:

```

```

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932.165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 690
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-690

```

```

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DLEM 4
 ||||
Db 1 DLEM 4

```

```

RESULT 28
US-09-932-165-1025
; Sequence 1025, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: DETECTION OF CANCER
; CURRENT APPLICATION NUMBER: US/09/932.165
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1025

```

```

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DLEM 4
 ||||
Db 5 DLEM 8

```

```

RESULT 29
US-10-266-463A-47
; Sequence 47, Application US/10266463A
; Publication No. US20030138946A1
; GENERAL INFORMATION:

```

; APPLICANT: CAI, Zeling  
 ; APPLICANT: SPRENT, Jonathan  
 ; APPLICANT: BRUNMARK, Anders  
 ; APPLICANT: JACKSON, Michael  
 ; APPLICANT: PETERSON, Per A.  
 ; APPLICANT: LUXENBOURG, Alain  
 ; APPLICANT: LETURCO, Didier Jean  
 ; APPLICANT: MORIARTY, Ann M.  
 ; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS  
 ; FILE REFERENCE: TSRI 471.1 Div. 1  
 ; CURRENT APPLICATION NUMBER: US/10/266.463A  
 ; PRIOR FILING DATE: 2002-10-08  
 ; PRIOR APPLICATION NUMBER: US 08/913.612  
 ; PRIOR FILING DATE: 1997-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US96/03249  
 ; PRIOR FILING DATE: 1996-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/400.338  
 ; PRIOR FILING DATE: 1995-03-08  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 47  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Mus musculus  
 US-10-266-463A-47

Query Match 26.7%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14  
 DB 4 PPF 7

## RESULT 30

US-10-062-109A-4  
 ; Sequence 4, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Bid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062.109A  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005.480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-4

Query Match 26.7%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12  
 DB 4 VEPF 7

## RESULT 31

US-10-062-109A-44  
 ; Sequence 44, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Bid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062.109A  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005.480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 44  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-44

Query Match 26.7%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12  
 DB 2 VEPF 5

## RESULT 32

US-10-239-313A-467  
 ; Sequence 467, Application US/10239313A  
 ; Publication No. US20030175285A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KLINGUER - HAMOUR, Christine  
 ; APPLICANT: CORVAIA, Nathalie  
 ; APPLICANT: BECK, Alain  
 ; APPLICANT: GOETSCH, Liliane  
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
 ; FILE REFERENCE: 343 727 US  
 ; CURRENT APPLICATION NUMBER: US/10/239.313A  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: FR 00/03711  
 ; PRIOR FILING DATE: 2000-03-23  
 ; PRIOR APPLICATION NUMBER: PCT 01/70772  
 ; PRIOR FILING DATE: 2001-03-22  
 ; NUMBER OF SEQ ID NOS: 697  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 467  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-239-313A-467

Query Match 26.7%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPF 14  
 DB 4 PPF 7

```

RESULT 33
US-10-005-480A-4
; Sequence 4, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Rya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 4 VEPF 7

RESULT 34
US-10-005-480A-44
; Sequence 44, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Rya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-44

Query Match 26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 2 VEPF 5

RESULT 35

```

```

US-10-093-200A-13
; Sequence 13, Application US/10093200A
; Publication No. US20020187521A1
; GENERAL INFORMATION:
; APPLICANT: Duesbery, Nicholas
; APPLICANT: Webb, Craig
; APPLICANT: Leppla, Stephen
; APPLICANT: Vande Woude, George
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the Department
; APPLICANT: of Health and Human Services
; TITLE OF INVENTION: Anthrax Lethal Factor is a MAPK Kinase Protease
; FILE REFERENCE: 015280-345200US
; CURRENT APPLICATION NUMBER: US/10/093,200A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/080,330
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/07126
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/623,104
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal
; OTHER INFORMATION: amino acid residues 1-9 of MAPKK2
US-10-093-200A-13

Query Match 26.7%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLP 8
Db 6 PVLP 9

RESULT 36
US-10-015-535-4
; Sequence 4, Application US/10015535
; Publication No. US20030036506A1
; GENERAL INFORMATION:
; APPLICANT: Kratz, David M.
; APPLICANT: Baskay, Susan
; TITLE OF INVENTION: Mutated Class I Major Histocompatibility proteins and
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: 100-00
; CURRENT APPLICATION NUMBER: US/10/015,535
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/254,495
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-015-535-4

Query Match 26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PPFF 14
Db 4 PPFF 7

```

```

RESULT 37
US-10-046-801-29
; Sequence 29, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/935,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-10-046-801-29

Query Match 26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
 |||||
Db 2 PFPF 5

RESULT 38
US-10-093-248-13
; Sequence 13, Application US/10093248
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Duesbery, Nicholas
; APPLICANT: Webb, Craig
; APPLICANT: Leppla, Stephen
; APPLICANT: Vande Woude, George
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the Department
; APPLICANT: of Health and Human Services
; TITLE OF INVENTION: Anthrax Lethal Factor is a MAPK Kinase Protease
; FILE REFERENCE: 015280-345200US
; CURRENT APPLICATION NUMBER: US/10/093,248
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/080,330
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: WO PCT/US99/07126
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/623,104
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N-terminal
; OTHER INFORMATION: amino acid residues 1-9 of MAPKK2
US-10-093-248-13

Query Match 26.7%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLV 8

```

```

Db |||||
 6 PVLV 9

RESULT 39
US-09-920-920-111
; Sequence 111, Application US/09220920
; Patent No. US20020002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-920-111

Query Match 26.7%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PVLV 9
 |||||
Db 2 PVLV 5

RESULT 40
US-09-932-165-154
; Sequence 154, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CATFE2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51156-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-154

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DLEM 4
 ||||
Db 1 DLEM 4

RESULT 41
US-09-932-165-785
; Sequence 785, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-BID, Pia M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; FILE OF INVENTION: 83P2H3 AND CAT1P2B11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 785
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-785

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 2 DLEM 5

RESULT 42
US-10-062-109A-55
; Sequence 55, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-55

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 ||||
Db 2 DLEM 5

RESULT 43
US-10-062-109A-71
; Sequence 71, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-71

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
 ||||
Db 4 VEPF 7

RESULT 44
US-10-005-480A-55
; Sequence 55, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-55

```

Query Match 26.7%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12  
 ||||  
 Db 2 VEPF 5

## RESULT 45

US-10-005-480A-71  
 ; Sequence 71, Application US/10005480A  
 ; Publication No. US20030191073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Faris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 1612P10B Useful in Treatment and Detection of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: 51158-20062.00  
 ; CURRENT APPLICATION NUMBER: US/10/005,480A  
 ; CURRENT FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 71  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-005-480A-71

Query Match 26.7%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12  
 ||||  
 Db 4 VEPF 7

## RESULT 46

US-10-062-710-199  
 ; Sequence 199, Application US/10062710  
 ; Publication No. US20030049253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Frank Q.  
 ; APPLICANT: Chu, Yong-Liang  
 ; APPLICANT: Qiu, Jian-Tai  
 ; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
 ; TITLE OF INVENTION: MHC-Recognized Epitopes  
 ; TITLE OF INVENTION: Via Peptide Vaccines  
 ; FILE REFERENCE: 3781-001-27  
 ; CURRENT APPLICATION NUMBER: US/10/062,710  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: US 60/310,498  
 ; PRIOR FILING DATE: 2001-09-08  
 ; NUMBER OF SEQ ID NOS: 232  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 199  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: T Cell epitopes  
 US-10-062-710-199

Query Match 26.7%; Score 4; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 PVLP 8  
 ||||  
 Db 1 PVLP 4

## RESULT 47

US-09-780-662A-14  
 ; Sequence 14, Application US/09780662A  
 ; Patent No. US20020076741A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burroughs-Tencza, Sarah  
 ; TITLE OF INVENTION: Biosensor for Anthrax  
 ; FILE REFERENCE: MEH800-126-A  
 ; CURRENT APPLICATION NUMBER: US/09/780,662A  
 ; CURRENT FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Synthetic peptide sequence  
 US-09-780-662A-14

Query Match 26.7%; Score 4; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLP 8  
 ||||  
 Db 4 PVLP 7

## RESULT 48

US-10-182-303-114  
 ; Sequence 114, Application US/10182303  
 ; Publication No. US20030166028A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burroughs-Tencza, Sarah  
 ; TITLE OF INVENTION: Biosensor for Anthrax  
 ; FILE REFERENCE: MEH800-126-US  
 ; CURRENT APPLICATION NUMBER: US/10/182,303  
 ; CURRENT FILING DATE: 2002-11-22  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 114  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Synthetic peptide sequence  
 US-10-182-303-114

Query Match 26.7%; Score 4; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLP 8  
 ||||  
 Db 4 PVLP 7

## RESULT 49

US-10-062-710-173  
 ; Sequence 173, Application US/10062710  
 ; Publication No. US20030049253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Frank Q.

```

; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062.710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-173

```

```

Query Match 26.7%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 PVEP 11
 |||||
DB 1 PVEP 4

```

```

RESULT 50
US-09-954-385-146
; Sequence 146: Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Wintzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-146

```

```

Query Match 26.7%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 PVLP 8
 |||||
DB 8 PVLP 11

```

```

RESULT 51
US-09-954-385-319
; Sequence 319: Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.

```

```

; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Wintzky, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-319

```

```

Query Match 26.7%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 11 PFPF 14
 |||||
DB 7 PFPF 10

```

```

RESULT 52
US-10-214-867A-17
; Sequence 17: Application US/10214867A
; Publication No. US20030148444A1
; GENERAL INFORMATION:
; APPLICANT: ENDU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligopeptide
US-10-214-867A-17

```

```

Query Match 26.7%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 12 FPFV 15
 |||||
DB 8 FPFV 11

```

```

RESULT 53
US-10-118-708-5
; Sequence 5: Application US/10118708
; Publication No. US20030165991A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L. P.
; APPLICANT: Pestka, James J.
; APPLICANT: Yuan, Qiaoping

```

```

; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-1447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-10-118-708-5

Query Match 26.7%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 EPFF 14
Db 4 EPFF 7

RESULT 54
US-10-057-789-142
; Sequence 142, Application US/10057789
; Publication No. US20030082522A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NADII.022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPP 12
Db 2 VEPP 5

RESULT 55
US-10-212-628-142
; Sequence 142, Application US/10212628
; Publication No. US20030087329A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NADII.022A
; CURRENT APPLICATION NUMBER: US/10/057,789
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/264,576
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPP 12
Db 2 VEPP 5

RESULT 56
US-10-254-446A-157
; Sequence 157, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopam
US-10-254-446A-157

Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPFF 13
Db 1 EPFF 4

RESULT 57
US-09-113-924-14
; Sequence 14, Application US/09113924
; Patent No. US20010007019A1

```



GENERAL INFORMATION:  
APPLICANT: Brigstock, David R.  
APPLICANT: Harding, Paul H.  
TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/113,924  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/308,526  
FILING DATE: 07-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A., Ph.D.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 08766/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acids  
LENGTH: 13 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-113-924-14

Query Match 26.7%; Score 4; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10  
DB 8 LEVE 11

RESULT 58  
US-09-897-107-72  
Sequence 72, Application US/09897107  
Patent No. US20020137094A1  
GENERAL INFORMATION:  
APPLICANT: YAMAGISHI, Akihiko  
TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING  
TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODING  
FILE REFERENCE: 210383US0  
CURRENT APPLICATION NUMBER: US/09/897,107  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: JP2000-201920  
PRIOR FILING DATE: 2000-07-04  
PRIOR APPLICATION NUMBER: JP2001-164332  
PRIOR FILING DATE: 2001-05-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 72  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Thermus thermophilus  
US-09-897-107-72

Query Match 26.7%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LEVE 10  
DB 8 LEVE 11

RESULT 58  
US-09-897-107-72  
Sequence 72, Application US/09897107  
Patent No. US20020137094A1  
GENERAL INFORMATION:  
APPLICANT: YAMAGISHI, Akihiko  
TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING  
TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODING  
FILE REFERENCE: 210383US0  
CURRENT APPLICATION NUMBER: US/09/897,107  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: JP2000-201920  
PRIOR FILING DATE: 2000-07-04  
PRIOR APPLICATION NUMBER: JP2001-164332  
PRIOR FILING DATE: 2001-05-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 72  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Thermus thermophilus  
US-09-897-107-72

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPPF 13  
DB 1 EPPF 4

RESULT 59  
US-09-943-692-29  
Sequence 29, Application US/09943692  
Patent No. US20020152496A1  
GENERAL INFORMATION:  
APPLICANT: FISCHHOFF, DAVID A.  
APPLICANT: FUCHS, ROY L.  
APPLICANT: LAVRIK, PAUL B.  
APPLICANT: MCPHERSON, SYLVIA A.  
APPLICANT: PERLAK, FREDERICK J.  
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS  
FILE REFERENCE: MOBT:195--1  
CURRENT APPLICATION NUMBER: US/09/943,692  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 09/027,998  
PRIOR FILING DATE: 1998-02-23  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric toxin  
US-09-943-692-29

Query Match 26.7%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPFV 15  
DB 7 PPFV 10

RESULT 60  
US-10-116-846B-5  
Sequence 5, Application US/10116846B  
Publication No. US20030073102A1  
GENERAL INFORMATION:  
APPLICANT: KWOK, William  
APPLICANT: NEPOM, Gerald  
APPLICANT: GEBE, John  
APPLICANT: REIJONEN, Helena  
APPLICANT: LIU, Andrew  
TITLE OF INVENTION: METHODS OF MHC CLASS II EPIOTOPE MAPPING, DETECTION OF AUTOIMMUNE  
FILE REFERENCE: 20149-000520US  
CURRENT APPLICATION NUMBER: US/10/116,846B  
CURRENT FILING DATE: 2002-09-15  
PRIOR APPLICATION NUMBER: US 60/282,328  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 60/308,962  
PRIOR FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Herpes Simplex Virus 2  
US-10-116-846B-5

Query Match 26.7%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPFV 15  
DB 7 PPFV 10

RESULT 60  
US-10-116-846B-5  
Sequence 5, Application US/10116846B  
Publication No. US20030073102A1  
GENERAL INFORMATION:  
APPLICANT: KWOK, William  
APPLICANT: NEPOM, Gerald  
APPLICANT: GEBE, John  
APPLICANT: REIJONEN, Helena  
APPLICANT: LIU, Andrew  
TITLE OF INVENTION: METHODS OF MHC CLASS II EPIOTOPE MAPPING, DETECTION OF AUTOIMMUNE  
FILE REFERENCE: 20149-000520US  
CURRENT APPLICATION NUMBER: US/10/116,846B  
CURRENT FILING DATE: 2002-09-15  
PRIOR APPLICATION NUMBER: US 60/282,328  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 60/308,962  
PRIOR FILING DATE: 2001-07-30  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Herpes Simplex Virus 2  
US-10-116-846B-5

QY 1 DLEM 4  
|  
|  
|  
|  
Db 2 DLEM 5

## RESULT 61

US-10-116-846B-45  
; Sequence 45, Application US/10116846B  
; Publication No. US20030073102A1  
; GENERAL INFORMATION:  
; APPLICANT: KWOK, William  
; APPLICANT: NEPOM, Gerald  
; APPLICANT: GIBER, John  
; APPLICANT: REIJUNEN, Helena  
; APPLICANT: LIU, Andrew  
; TITLE OF INVENTION: METHODS OF MHC CLASS II EPIOTOPE MAPPING, DETECTION OF AUTOIMMUNE  
; FILE REFERENCE: 20149-000520US  
; CURRENT APPLICATION NUMBER: US/10/116,846B  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 45  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Herpes simplex Virus 2  
US-10-116-846B-45

Query Match 26.7%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 DLEM 4  
|  
|  
|  
|  
Db 2 DLEM 5

## RESULT 62

US-09-113-924-13  
; Sequence 13, Application US/09113924  
; Patent No. US20010007019A1  
; GENERAL INFORMATION:  
; APPLICANT: Brigstock, David R.  
; APPLICANT: Harding, Paul H.  
; TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR (HBGF)  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/09/113,924  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/908,526  
; FILING DATE: 07-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A., Ph.D.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 08766/003001

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-113-924-13

Query Match 26.7%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.8e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 LPVE 10  
|  
|  
|  
|  
Db 9 LPVE 12

## RESULT 63

US-08-996-140-9  
; Sequence 9, Application US/08996140  
; Publication No. US20030190318A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shimpai  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,140  
; FILING DATE: 22-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 356,426/1996  
; FILING DATE: 26-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
US-08-996-140-9

```

Query Match 26.7%; Score 4; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
 |||||
Db 11 VLPV 14

RESULT 64
US-09-759-010-9
; Sequence 9, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Strivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-09-759-010-9

Query Match 26.7%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 |||||
Db 7 DLEM 10

RESULT 65
US-09-947-770-15
; Sequence 15, Application US/09947770
; Patent No. US20020068713A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ruiz, Pedro
; APPLICANT: Garren, Hideki
; TITLE OF INVENTION: DNA Vaccination for Treatment of
; FILE REFERENCE: STAN123CIP
; CURRENT APPLICATION NUMBER: US/09/947,770
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/06233
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/267,590
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HSPV16 P45
US-09-947-770-15

Query Match 26.7%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEM 4
 |||||
Db 12 DLEM 15

```

```

RESULT 66
US-09-813-333-18
; Sequence 18, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-18

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 |||||
Db 1 LPVE 4

RESULT 67
US-09-953-510-37
; Sequence 37, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2019 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids

```

```
;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-953-510-37

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
Db 1 LPVE 4

RESULT 69
US-09-880-505-22
; Sequence 22, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880.505
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-22

Query Match 26.7%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
Db 6 LPVE 9

RESULT 70
US-09-880-505-24
; Sequence 24, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880.505
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-880-505-24
```

```
;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-953-510-37

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10
 ||||
Db 6 LPVE 9

RESULT 68
US-09-953-510-38
; Sequence 38, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; TITLE OF INVENTION: Products and Methods for Their Production and Use
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/POCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
```

Query Match 26.7%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPVE 10  
|  
|  
|  
|  
Db 6 LPVE 9

## RESULT 71

US-10-349-023-18  
; Sequence 18, Application US/10349023  
; Publication No. US20030133919A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; OKURA, Takahori  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/349,023  
; FILING DATE: 23-Jan-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/556,972  
; FILING DATE: 24-Apr-2000  
; APPLICATION NUMBER: US/08/996,338  
; FILING DATE: 22-Dec-1997  
; APPLICATION NUMBER: JP 74,697/1997  
; FILING DATE: 12-Mar-1997  
; APPLICATION NUMBER: JP 215,488/1997  
; FILING DATE: 28-Jul-1997  
; APPLICATION NUMBER: JP 291,837/1997  
; FILING DATE: 09-Oct-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-349-023-18

Query Match 26.7%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 VLPV 9  
|  
|  
|  
|  
Db 11 VLPV 14

## RESULT 72

US-10-147-255-37

; Sequence 37, Application US/10147255  
; Publication No. US20030152584A1  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Marcus A.  
; TITLE OF INVENTION: Abundant Extracellular  
; Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kurt A. MacLean  
STREET: 2029 Century Park East, Suite 3800  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0,  
Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/147,255  
FILING DATE: 15-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/226,539A  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/447,398  
FILING DATE: 23-MAY-1995  
APPLICATION NUMBER: US 08/289,667  
FILING DATE: 12-AUG-1994  
APPLICATION NUMBER: US 08/156,358  
FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: MacLean, Kurt A.  
REGISTRATION NUMBER: 31,118  
REFERENCE/DOCKET NUMBER: 112-272  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (310) 788-5000  
TELEFAX: (310) 277-1297

## INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis  
STRAIN: Erdman  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-10-147-255-37

Query Match 26.7%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10  
|  
|  
|  
|  
Db 6 LPVE 9

## RESULT 73

US-10-147-255-38  
; Sequence 38, Application US/10147255  
; Publication No. US20030152584A1  
; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Marcus A.  
; TITLE OF INVENTION: Abundant Extracellular  
; Products and Methods for Their Production and Use

```
;
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA: Version #1.30
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
;
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
;
; US-10-147-255-38
;
; Query Match 26.7%; Score 4; DB 12; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 LPVE 10
; Db 1 LPVE 4
;
; RESULT 74
; US-10-161-791-312
; Sequence 312, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLER, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
```

```
;
;
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
;
; US-10-161-791-312
;
; Query Match 26.7%; Score 4; DB 12; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 PVL P 8
; Db 8 PVL P 11
;
; RESULT 75
; US-10-044-703-18
; Sequence 18, Application US/10044703
; Publication No. US20020192235A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Mycobacterium tuberculosis
;
; US-10-044-703-18
;
; Query Match 26.7%; Score 4; DB 14; Length 15;
; Best Local Similarity 100.0%; Pred. No. 7.2e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 LPVE 10
; Db 1 LPVE 4
```

Wed Nov 26 09:08:36 2003

us-09-641-801-5.oligo.rapb

Page 23

Search completed: November 25, 2003, 20:25:31  
Job time : 31.8404 secs

---





## ALIGNMENTS

```

RESULT 1
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLVFPFPPFV 15
DB 1 DLEMPVLVFPFPPFV 15

RESULT 2
US-08-687-956A-7
; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773

```

```

; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-7

Query Match 33.3%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVEPF 11
DB 10 LPVEPF 14

RESULT 3
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEPF 12
DB 10 PVEPF 14

RESULT 4
US-08-261-206A-22
; Sequence 22, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting

```

;; TITLE OF INVENTION: with Thrombin  
;; NUMBER OF SEQUENCES: 80  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
;; STREET: 301 N. Washington St.  
;; CITY: Falls Church  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22046-0747  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/261,206A  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/740,492  
;; FILING DATE: 03-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svensson, Leonard R.  
;; REGISTRATION NUMBER: 30330  
;; REFERENCE/DOCKET NUMBER: 216-275P  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-241-1300  
;; TELEFAX: 703-241-2848  
;; TELEX: 248345  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-261-206A-22

Query Match 26.7%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11  
Db 2 PVEP 5

RESULT 5  
US-09-147-933-17  
;; Sequence 17 Application US/09147933A  
;; Patent No. 6168917  
;; GENERAL INFORMATION:  
;; APPLICANT: Kilpatrick, David  
;; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF  
;; FILE OF INVENTION: NON-POLIO ENTEROVIRUSES  
;; FILE REFERENCE: 62242/US  
;; CURRENT APPLICATION NUMBER: US/09/147,933A  
;; CURRENT FILING DATE: 1999-07-09  
;; EARLIER APPLICATION NUMBER: PCT/US97/17734  
;; EARLIER FILING DATE: 1997-10-01  
;; EARLIER APPLICATION NUMBER: U. S. 60/027,353  
;; EARLIER FILING DATE: 1996-10-02  
;; NUMBER OF SEQ ID NOS: 96  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 17  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: peptide  
US-09-147-933-17

Query Match 26.7%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 MPVL 7  
Db 1 MPVL 4

RESULT 6  
US-09-365-581A-2  
;; Sequence 2 Application US/09365581A  
;; Patent No. 6287776  
;; GENERAL INFORMATION:  
;; APPLICANT: Hart, L. P.  
;; APPLICANT: Pestka, James J.  
;; APPLICANT: Yuen, Qiaping  
;; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
;; TITLE OF INVENTION: THEREOF  
;; FILE REFERENCE: MSU 4.1-447  
;; CURRENT APPLICATION NUMBER: US/09/365,581A  
;; CURRENT FILING DATE: 2000-07-27  
;; PRIOR APPLICATION NUMBER: 60/146,643  
;; PRIOR FILING DATE: 1999-07-30  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 2  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: DONPRP.2  
;; OTHER INFORMATION: peptide mimotope of deoxynivalenol  
US-09-365-581A-2

Query Match 26.7%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14  
Db 4 PFPF 7

RESULT 7  
US-09-426-568A-11  
;; Sequence 11 Application US/09426568A  
;; Patent No. 638843  
;; GENERAL INFORMATION:  
;; APPLICANT: Kakefuda, Genichi  
;; APPLICANT: Costello, Colleen  
;; APPLICANT: Sun, Ming  
;; APPLICANT: Hu, Weiming  
;; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance  
;; FILE OF INVENTION: in Plants  
;; FILE REFERENCE: 008103/195497  
;; CURRENT APPLICATION NUMBER: US/09/426,568A  
;; CURRENT FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/106,239  
;; PRIOR FILING DATE: 1998-10-29  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis sp.  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (1)..(7)  
;; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from  
;; OTHER INFORMATION: plasmid F3  
;; NAME/KEY: SITE  
;; LOCATION: (1)..(2)  
;; OTHER INFORMATION: Thrombin cleavage site  
US-09-426-568A-11

Query Match 26.7%; Score 4; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 9 VEPF 12  
 ||||  
 Db 3 VEPF 6

RESULT 8  
 US-09-492-766-8  
 ; Sequence 8, Application US/09492766  
 ; Patent No. 6506732  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMIOT, Jean  
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS  
 ; FILE REFERENCE: 6013-57"US"  
 ; CURRENT APPLICATION NUMBER: US/09/492,766  
 ; CURRENT FILING DATE: 2000-01-27  
 ; EARLIER APPLICATION NUMBER: 60/117,661  
 ; EARLIER FILING DATE: 1999-01-28  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
 ; OTHER INFORMATION: proteins  
 US-09-492-766-8

Query Match 26.7%; Score 4; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 6 VLPV 9  
 ||||  
 Db 1 VLPV 4

RESULT 9  
 US-09-626-821A-2  
 ; Sequence 2, Application US/09626821A  
 ; Patent No. 659762  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hart, L P  
 ; APPLICANT: Pestka, James J  
 ; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
 ; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
 ; FILE REFERENCE: MSU 4.1-447  
 ; CURRENT APPLICATION NUMBER: US/09/626,821A  
 ; CURRENT FILING DATE: 2000-07-27  
 ; PRIOR APPLICATION NUMBER: 60/146,643  
 ; PRIOR FILING DATE: 1999-07-30  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2  
 ; OTHER INFORMATION: peptide mimotope of deoxynivalenol  
 US-09-626-821A-2

Query Match 26.7%; Score 4; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 11 PPF 14

Db 4 PPF 7

RESULT 10  
 US-08-360-239B-2  
 ; Sequence 2, Application US/08360239B  
 ; Patent No. 5801222  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pettit, George R.  
 ; APPLICANT: Tan, Rui  
 ; TITLE OF INVENTION: Isolation and Structure of  
 ; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic  
 ; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Richard R. Mybeck  
 ; STREET: 8010 East Morgan Trail, #10  
 ; CITY: Scottsdale  
 ; STATE: Arizona  
 ; COUNTRY: USA  
 ; ZIP: 85258-1234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: DOS 5  
 ; SOFTWARE: Microsoft Word for Windows  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/360,239B  
 ; FILING DATE: 12/20/94  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Richard R. Mybeck  
 ; REGISTRATION NUMBER: 17,886  
 ; REFERENCE/DOCKET NUMBER: 4997  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (602)-483-1285  
 ; TELEFAX: (602)-483-7452  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acid residues  
 ; TYPE: amino acid  
 ; TOPOLOGY: Cyclic  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: Cyclooctapeptide  
 ; DESCRIPTION: Phakellistatin 11  
 ; HYPOTHEICAL: no  
 ; ANTI-SENSE: no  
 ; FRAGMENT TYPE: circular  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Phakellia sp.  
 ; DEVELOPMENTAL STAGE: whole organism  
 ; FEATURE:  
 ; NAME/KEY: phakellistatin 11  
 ; NAME/KEY: amino acid analysis, high resolution  
 ; NAME/KEY: nuclear magnetic resonance and mass  
 ; NAME/KEY: spectral MS/MS techniques  
 ; OTHER INFORMATION: Phakellistatin is a  
 ; OTHER INFORMATION: cell growth inhibitory peptide with  
 ; OTHER INFORMATION: activity in murine lymphocytic leukemia  
 ; OTHER INFORMATION: cell line of 0.20 mg/ml.  
 US-08-360-239B-2

Query Match 26.7%; Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 11 PPF 14  
 ||||  
 Db 3 PPF 6

RESULT 11

```

US-08-929-922B-7
; Sequence 7, Application US/0892922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dambmann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: stergaard, Peter Rabbek
; APPLICANT: Packat, Shankant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59941130 No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922B
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-08-929-922B-7
; Query Match 26.7%; Score 4; DB 2; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 9 VEPF 12
;
Db 4 VEPF 7
;
RESULT 12
US-08-828-712-12
; Sequence 12, Application US/08828712
; Patent No. 6015884
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.

```

```

; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
; US-08-828-712-12
; Query Match 26.7%; Score 4; DB 3; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 11 PFPF 14
;
Db 3 PFPF 6
;
RESULT 13
US-08-993-165-25
; Sequence 25, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
; US-08-993-165-25
; Query Match 26.7%; Score 4; DB 3; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 11 PFPF 14
;
Db 3 PFPF 6
;
RESULT 14
US-08-993-165-28
; Sequence 28, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:

```

; APPLICANT: Unger, Evan C  
; APPLICANT: Wu, Yungiu  
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use  
; FILE REFERENCE: UNGR1224  
; CURRENT APPLICATION NUMBER: US/08/993,165A  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923a1 Sequence  
US-08-993-165-30  
Query Match 26.7%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PPPF 14  
Db 3 PPPF 6  
RESULT 15  
US-08-993-165-30  
; Sequence 30, Application US/08993165A  
; Patent No. 6123923  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C  
; APPLICANT: Wu, Yungiu  
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use  
; FILE REFERENCE: UNGR1224  
; CURRENT APPLICATION NUMBER: US/08/993,165A  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923a1 Sequence  
US-08-993-165-30  
Query Match 26.7%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PPPF 14  
Db 3 PPPF 6  
RESULT 16  
US-08-993-165-34  
; Sequence 34, Application US/08993165A  
; Patent No. 6123923  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C  
; APPLICANT: Wu, Yungiu  
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use  
; FILE REFERENCE: UNGR1224  
; CURRENT APPLICATION NUMBER: US/08/993,165A  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923a1 Sequence  
US-08-993-165-34  
Query Match 26.7%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PPPF 14  
Db 3 PPPF 6  
RESULT 17  
US-08-993-276-12  
; Sequence 12, Application US/09063276  
; Patent No. 6140113  
; GENERAL INFORMATION:  
; APPLICANT: Schneek, Jonathan  
; APPLICANT: O'Herrin, Sean  
; TITLE OF INVENTION: Molecular Complexes Which  
; TITLE OF INVENTION: Modify Immune Responses  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/063,276  
; FILING DATE: 21-APR-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/828,712  
; FILING DATE: 28-MAR-1997  
; APPLICATION NUMBER: 60/014,367  
; FILING DATE: 28-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A  
; REGISTRATION NUMBER: 32141  
; REFERENCE/DOCKET NUMBER: 01107.74154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6140113e  
US-08-993-276-12  
Query Match 26.7%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 PPPF 14  
Db 3 PPPF 6  
RESULT 18  
US-09-342-394-7  
; Sequence 7, Application US/09342394  
; Patent No. 6143546

```
;
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Pakkar, Shankant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Amino-peptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6143546 No. 6143546disk of No. 6143546th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342,394
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922
; FILING DATE: 15-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-09-342-394-7

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 4 VEPF 7

RESULT 19
US-09-580-064-7
; Sequence 7, Application US/09580064
; Patent No. 6200792
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Joan Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Pakkar, Shankant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Amino-peptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: No. 6200792 No. 6200792disk of No. 6200792th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,064
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/929,922
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; US-09-580-064-7

Query Match 26.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12
Db 4 VEPF 7

RESULT 20
US-09-540-448-25
; Sequence 25 Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGRI592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
; US-09-540-448-25

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14
|||||
```



; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-496-761-1

Query Match 26.7%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
Db 3 PFPF 6

RESULT 25

US-09-496-761-4  
; Sequence 4, Application US/09496761  
; Patent No. 6444660  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; APPLICANT: Shen, De Kang  
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs  
; FILE REFERENCE: UNGR-1586  
; CURRENT APPLICATION NUMBER: US/09/496,761  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 08/851,780  
; PRIOR FILING DATE: 1997-05-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-496-761-4

Query Match 26.7%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
Db 3 PFPF 6

RESULT 26

US-09-496-761-6  
; Sequence 6, Application US/09496761  
; Patent No. 6444660  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; APPLICANT: Shen, De Kang  
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs  
; FILE REFERENCE: UNGR-1586  
; CURRENT APPLICATION NUMBER: US/09/496,761  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 08/851,780  
; PRIOR FILING DATE: 1997-05-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-496-761-6

Query Match 26.7%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14

Db 3 PFPF 6

RESULT 27

US-09-496-761-10  
; Sequence 10, Application US/09496761  
; Patent No. 6444660  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; APPLICANT: Shen, De Kang  
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs  
; FILE REFERENCE: UNGR-1586  
; CURRENT APPLICATION NUMBER: US/09/496,761  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 08/851,780  
; PRIOR FILING DATE: 1997-05-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-09-496-761-10

Query Match 26.7%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
Db 3 PFPF 6

RESULT 28

US-09-324-782-12  
; Sequence 12, Application US/09324782  
; Patent No. 6448071  
; GENERAL INFORMATION:  
; APPLICANT: Schneck, Jonathan P.  
; APPLICANT: O'Heslin, Sean  
; TITLE OF INVENTION: Soluble Divalent and Multivalent  
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/324,782  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,712  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.73713  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)508-9100  
; TELEFAX: (202)508-9299  
; INFORMATION FOR SEQ ID NO: 12:



```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
US-09-324-782-12

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 29
US-09-668-143-12
; Sequence 12, Application US/09668143
; Patent No. 6458354
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan P.
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Soluble Divalent and Multivalent
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,143
; FILING DATE: 25-SEP-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,712
; FILING DATE: 28-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
US-09-668-143-12

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 30
US-08-913-612A-46
; Sequence 46, Application US/08913612A
; Patent No. 6461867
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
; TITLE OF INVENTION: ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6461867th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,612A
; FILING DATE: 08-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cepuritis, Talivaldis
; REGISTRATION NUMBER: 20,818
; REFERENCE/DOCKET NUMBER: 471.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-913-612A-46

Query Match 26.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFPF 14
Db 3 PFPF 6

RESULT 31
US-08-929-847-26
; Sequence 26, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
```

; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely synthetic sequence  
 US-08-929-847-26

Query Match 26.7%; Score 4; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
 ||||  
 Db 3 PFPF 6

RESULT 32  
 US-08-929-847-29  
 ; Sequence 29, Application US/08929847  
 ; Patent No. 6548047  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Unger, Evan C.  
 ; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions  
 ; FILE REFERENCE: BMS0441  
 ; CURRENT APPLICATION NUMBER: US/08/929,847  
 ; CURRENT FILING DATE: 1997-09-15  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 29  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely synthetic sequence  
 US-08-929-847-29

Query Match 26.7%; Score 4; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
 ||||  
 Db 3 PFPF 6

RESULT 33  
 US-08-929-847-34  
 ; Sequence 34, Application US/08929847  
 ; Patent No. 6548047  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Unger, Evan C.  
 ; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions  
 ; FILE REFERENCE: BMS0441  
 ; CURRENT APPLICATION NUMBER: US/08/929,847  
 ; CURRENT FILING DATE: 1997-09-15  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 34  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely synthetic sequence  
 US-08-929-847-34

Query Match 26.7%; Score 4; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFPF 14  
 ||||  
 Db 3 PFPF 6

RESULT 34  
 US-08-340-283-81  
 ; Sequence 81, Application US/08340283  
 ; Patent No. 5861318  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elhammer, Ake P.  
 ; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR  
 ; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY  
 ; NUMBER OF SEQUENCES: 205  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law  
 ; ADDRESS: (1920-32-1)  
 ; STREET: 301 Henrietta Street  
 ; CITY: Kalamazoo  
 ; STATE: Michigan  
 ; COUNTRY: U.S.A.  
 ; ZIP: 49001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/340,283  
 ; FILING DATE:  
 ; CLASSIFICATION: 436  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wootton, Thomas A.  
 ; REGISTRATION NUMBER: 35,004  
 ; REFERENCE/DOCKET NUMBER: 4828  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (616) 385-7914  
 ; TELEFAX: (616) 385-6897  
 ; TELEX: 224401  
 ; INFORMATION FOR SEQ ID NO: 81:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 US-08-340-283-81

Query Match 26.7%; Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLFP 8  
 ||||  
 Db 1 PVLFP 4

RESULT 35  
 US-08-828-712-13  
 ; Sequence 13, Application US/08828712  
 ; Patent No. 6015884  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schneck, Jonathan P.  
 ; APPLICANT: O'Herrin, Sean  
 ; TITLE OF INVENTION: Soluble Divalent and Multivalent  
 ; TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Banner & Witcoff, Ltd.  
 ; STREET: 1001 G Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,712  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.73713  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)508-9100  
TELEFAX: (202)508-9299  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide QL9  
US-08-828-712-13

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 11 PFPF 14  
DB 4 PFPF 7

RESULT 36  
US-08-828-712-14  
Sequence 14, Application US/08828712  
Patent No. 6015884  
GENERAL INFORMATION:  
APPLICANT: Schneck, Jonathan P.  
TITLE OF INVENTION: Soluble Divalent and Multivalent  
TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,712  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.73713  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)508-9100  
TELEFAX: (202)508-9299  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids

TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide SL9  
US-08-828-712-14

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 11 PFPF 14  
DB 3 PFPF 6

RESULT 37  
US-08-993-165-29  
Sequence 29, Application US/08993165A  
Patent No. 6123923  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C  
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use  
FILE REFERENCE: UNGR1224  
CURRENT APPLICATION NUMBER: US/08/993,165A  
CURRENT FILING DATE: 1997-12-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 9  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923e1 Sequence  
US-08-993-165-29

Query Match 26.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 11 PFPF 14  
DB 2 PFPF 5

RESULT 38  
US-09-063-276-13  
Sequence 13, Application US/09063276  
Patent No. 6140113  
GENERAL INFORMATION:  
APPLICANT: Schneck, Jonathan  
APPLICANT: O'Herrin, Sean  
TITLE OF INVENTION: Molecular Complexes Which  
TITLE OF INVENTION: Modify Immune Responses  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff  
STREET: 1001 G Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/063,276  
FILING DATE: 21-APR-1998

```
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
; US-09-063-276-13

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 4 PPPP 7

RESULT 39
US-09-063-276-14
; Sequence 14, Application US/09063276
; Patent No. 6140113
; GENERAL INFORMATION:
; APPLICANT: Schneek, Jonathan
; TITLE OF INVENTION: Molecular Complexes Which
; TITLE OF INVENTION: Modify Immune Responses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bannar & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,276
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
; US-09-063-276-14

Query Match 26.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 2 PPPP 5

RESULT 40
US-09-540-448-29
; Sequence 29, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 29
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
; US-09-540-448-29

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPPP 14
Db 2 PPPP 5

RESULT 41
US-09-496-761-5
; Sequence 5, Application US/09496761
; Patent No. 644660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: No. 6444660el Lipid soluble steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-09-496-761-5

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 11 PFPF 14  
|||||  
Db 2 PFPF 5

RESULT 42  
US-09-324-782-13  
; Sequence 13, Application US/09324782  
; Patent No. 6448071  
; GENERAL INFORMATION:  
; APPLICANT: Schneck, Jonathan P.  
; APPLICANT: O'Herrin, Sean  
; TITLE OF INVENTION: Soluble Divalent and Multivalent  
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/324,782  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,712  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.73713  
; TELEPHONE: (202)508-9100  
; TELEFAX: (202)508-9299  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: peptide QL9

US-09-324-782-13  
Query Match 26.7%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
QY 11 PFPF 14  
|||||  
Db 4 PFPF 7

RESULT 43  
US-09-324-782-14  
; Sequence 14, Application US/09324782  
; Patent No. 6448071  
; GENERAL INFORMATION:  
; APPLICANT: Schneck, Jonathan P.  
; APPLICANT: O'Herrin, Sean  
; TITLE OF INVENTION: Soluble Divalent and Multivalent  
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/324,782  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,712  
; FILING DATE: 28-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.73713  
; TELEPHONE: (202)508-9100  
; TELEFAX: (202)508-9299  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: peptide SL9

US-09-324-782-14  
Query Match 26.7%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 11 PFPF 14  
|||||  
Db 3 PFPF 6

RESULT 44  
US-09-668-143-13  
; Sequence 13, Application US/09668143  
; Patent No. 6458354  
; GENERAL INFORMATION:  
; APPLICANT: Schneck, Jonathan P.  
; APPLICANT: O'Herrin, Sean  
; TITLE OF INVENTION: Soluble Divalent and Multivalent  
; TITLE OF INVENTION: Heterodimeric Analogs of Proteins  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/668,143  
; FILING DATE: 25-SEP-2000  
; PRIOR APPLICATION DATA:



```

; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-30

Query Match 26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PPF 14
Db 2 PPF 5

RESULT 48
US-09-001-984C-92
; Sequence 92, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-92

Query Match 26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

RESULT 49
US-09-001-984C-97
; Sequence 97, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-92

Query Match 26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

RESULT 50
US-09-001-984C-101
; Sequence 101, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-101

Query Match 26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

RESULT 51
US-09-220-528-111
; Sequence 111, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Balch, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/219,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-111

Query Match 26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

RESULT 52
US-09-220-528-111
; Sequence 111, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Balch, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/219,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-528-111

Query Match 26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10
Db 6 LPVE 9

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
|||||  
Db 2 VLPV 5

## RESULT 52

US-09-396-347F-92  
; Sequence 92, Application US/09396347F  
; Patent No. 6506384  
; GENERAL INFORMATION:  
; APPLICANT: Laal, Suman  
; APPLICANT: Zolla-Pazner, Susan  
; APPLICANT: Belisle, John T  
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE  
; FILE REFERENCE: 32004-169276  
; CURRENT APPLICATION NUMBER: US/09/396,347F  
; CURRENT FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/001,984  
; PRIOR FILING DATE: 1997-12-31  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis strain H37Rv  
US-09-396-347F-92

Query Match 26.7%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10  
|||||  
Db 6 LPVE 9

## RESULT 53

US-09-396-347F-97  
; Sequence 97, Application US/09396347F  
; Patent No. 6506384  
; GENERAL INFORMATION:  
; APPLICANT: Laal, Suman  
; APPLICANT: Zolla-Pazner, Susan  
; APPLICANT: Belisle, John T  
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE  
; FILE REFERENCE: 32004-169276  
; CURRENT APPLICATION NUMBER: US/09/396,347F  
; CURRENT FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/001,984  
; PRIOR FILING DATE: 1997-12-31  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis strain H37Rv  
US-09-396-347F-97

Query Match 26.7%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10  
|||||  
Db 6 LPVE 9

## RESULT 54

US-09-396-347F-101  
; Sequence 101, Application US/09396347F  
; Patent No. 6506384

; GENERAL INFORMATION:  
; APPLICANT: Laal, Suman  
; APPLICANT: Zolla-Pazner, Susan  
; APPLICANT: Belisle, John T  
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE  
; FILE REFERENCE: 32004-169276  
; CURRENT APPLICATION NUMBER: US/09/396,347F  
; CURRENT FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/001,984  
; PRIOR FILING DATE: 1997-12-31  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 101  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis strain H37Rv  
US-09-396-347F-101

Query Match 26.7%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVE 10  
|||||  
Db 6 LPVE 9

## RESULT 55

US-08-338-992B-29  
; Sequence 29, Application US/08338992B  
; Patent No. 5736524  
; GENERAL INFORMATION:  
; APPLICANT: CONTENT, JEAN  
; APPLICANT: HUYGEN, KRIS  
; APPLICANT: LIU, MARGARET A.  
; APPLICANT: MONTGOMERY, DONNA  
; APPLICANT: ULMER, JEFFREY  
; TITLE OF INVENTION: A POLYNUCLEOTIDE TUBERCULOSIS VACCINE  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MICHAEL D. YABLONSKY - MERCK & CO., INC.  
; STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/338,992B  
; FILING DATE: 14-NOV-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YABLONSKY, MICHAEL D.  
; REGISTRATION NUMBER: 40,407  
; REFERENCE/DOCKET NUMBER: 19342  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-4678  
; TELEFAX: 908-594-4720  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
US-08-338-992B-29

Query Match

26.7%; Score 4; DB 1; Length 12;



Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVE 10  
|  
|  
|  
|  
Db 8 LPVE 11

RESULT 56  
US-08-637-759B-103  
; Sequence 103, Application US/08637759B  
; Patent No. 5876931  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS: 501  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,759B  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-637-759B-103

Query Match 26.7%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
|  
|  
|  
|  
Db 7 MPVL 10

RESULT 57  
US-08-871-355A-103  
; Sequence 103, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101 CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-871-355A-103

Query Match 26.7%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7  
|  
|  
|  
|  
Db 7 MPVL 10

RESULT 58  
US-09-365-581A-5  
; Sequence 5, Application US/09365581A  
; Patent No. 6287776  
; GENERAL INFORMATION:  
; APPLICANT: Hart, L P  
; APPLICANT: Pestka, James J  
; APPLICANT: Yuan, Qiaoping  
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: MSU 4.1-447  
; CURRENT APPLICATION NUMBER: US/09/365,581A  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,643  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 12  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: C430, the  
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a  
; OTHER INFORMATION: cysteine residue  
US-09-365-581A-5

Query Match 26.7%; Score 4; DB 3; Length 12;

```
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 11 PPF 14
Db 4 PPF 7

RESULT 59
US-09-147-208-55
; Sequence 55, Application US/09147208
; Patent No. 633303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,208
; FILING DATE: 02-MAR-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-147-208-55

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 5 VLPV 8

RESULT 60
US-09-201-945-103
; Sequence 103, Application US/09201945
; Patent No. 6342315
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9
Db 5 VLPV 8

RESULT 61
US-09-550-117A-55
; Sequence 55, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; FILE REFERENCE: 10447-106
; CURRENT APPLICATION NUMBER: US/09/550,117A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/147,208
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-205/PAP-206 linker
; US-09-550-117A-55

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPVL 7
Db 7 MPVL 10

RESULT 62
US-09-626-821A-5
; Sequence 5, Application US/09626821A
```

```
; Patent No. 6537762
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/626,821A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 12
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DMP2.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-09-626-821A-5

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 11 PFPF 14
Db 4 FFPF 7

RESULT 63
US-07-794-288D-22
; Sequence 22, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S.L. GAETA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEKIMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duff, Bradford, J.
; REGISTRATION NUMBER: 32,219

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 11 PFPF 14
Db 4 FFPF 7

RESULT 63
US-07-794-288D-22
; Sequence 22, Application US/07794288D
; Patent No. 5580953
; GENERAL INFORMATION:
; APPLICANT: ELISABETH ALBRECHT,
; APPLICANT: HOWARD JONES,
; APPLICANT: LAURA S.L. GAETA,
; APPLICANT: KATHRYN S. PRICKETT and
; APPLICANT: KEVIN BEKIMONT
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: First Interstate World
; STREET: Center
; STREET: 633 West Fifth Street,
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM M.S. DOS (Version
; OPERATING SYSTEM: 5.0)
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/794,288D
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/794,288
; FILING DATE: 19-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Duff, Bradford, J.
; REGISTRATION NUMBER: 32,219
```

```
; REFERENCE/DOCKET NUMBER: 193/153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
US-07-794-288D-22

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 PVLV 8
Db 1 PVLV 4

RESULT 64
US-08-471-033-11
; Sequence 11, Application US/08471033
; Patent No. 5770696
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael A
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Malini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,033
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: P-40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SQLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORGANISM: Bacillus thuringiensis  
US-08-471-033-11

Query Match 26.7%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 VEPP 12  
DB 6 VEPP 9

## RESULT 65

US-08-471-044-11  
Sequence 11, Application US/08471044  
Patent No. 5840868

## GENERAL INFORMATION:

APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,044  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800

PRIOR APPLICATION NUMBER: US 08/463,483

## APPLICATION DATA:

FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/cip3/DIV6 - SOLV3  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689

## INFORMATION FOR SEQ ID NO:

11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
US-08-471-044-11

Query Match 26.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 9 VEPP 12  
DB 6 VEPP 9

## RESULT 66

US-08-463-483A-11  
Sequence 11, Application US/08463483A  
Patent No. 5849870

## GENERAL INFORMATION:

APPLICANT: Warren, Gregory W  
APPLICANT: Koziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalini M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,483A  
FILING DATE:  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994

## APPLICATION DATA:

APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: CGC 1695/cip3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8615  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 11:

## SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
US-08-463-483A-11

Query Match 26.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12  
|  
|  
|  
|  
Db 6 VEPF 9

RESULT 67  
US-08-471-046A-11  
; Sequence 11, Application US/08471046A  
; Patent No. 5866326  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Gregory W  
; APPLICANT: Kozziel, Michael G  
; APPLICANT: Mullins, Martha A  
; APPLICANT: Nye, Gordon J  
; APPLICANT: Carr, Brian  
; APPLICANT: Desai, Nalini M  
; APPLICANT: Kostichka, N. Kristy  
; APPLICANT: Duck, Nicholas B  
; APPLICANT: Estruch, Juan J  
; TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5866326artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION NUMBER: US/08/471,046A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/463,483  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,594  
; FILING DATE: 09-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/218,018  
; FILING DATE: 23-MAR-1994  
; APPLICATION NUMBER: US 08/037,057  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLv4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORGANISM: Bacillus thuringiensis

US-08-471-046A-11  
Query Match 26.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 VEPF 12  
|  
|  
|  
|  
Db 6 VEPF 9

RESULT 68  
US-08-470-566B-11  
; Sequence 11, Application US/08470566B  
; Patent No. 5872212  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Gregory W  
; APPLICANT: Kozziel, Michael G  
; APPLICANT: Mullins, Martha A  
; APPLICANT: Nye, Gordon J  
; APPLICANT: Carr, Brian  
; APPLICANT: Desai, Nalini M  
; APPLICANT: Kostichka, N. Kristy  
; APPLICANT: Duck, Nicholas B  
; APPLICANT: Estruch, Juan J  
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5872212artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION NUMBER: US/08/470,566B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/463,483  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,594  
; FILING DATE: 09-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/218,018  
; FILING DATE: 23-MAR-1994  
; APPLICATION NUMBER: US 08/037,057  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV4 - SOLv4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORGANISM: Bacillus thuringiensis

US-08-470-566B-11  
Query Match 26.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEPF 12



```

; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,334
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,483
; FILING DATE:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-469-334-11

```

```

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 VEPF 12
 |||||
Db 6 VEPF 9

```

```

RESULT 72
US-09-300-529-11
; Sequence 11, Application US/09300529
; Patent No. 6066783
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066783artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,529
; FILING DATE: TBA
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,334
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19506L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-09-300-529-11

```

```

Query Match 26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 VEPF 12
 |||||
Db 6 VEPF 9

```

```

RESULT 73
US-09-233-336A-11
; Sequence 11, Application US/09233336A
; Patent No. 6107279
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
; CONTROL OF PLANT PESTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA

```

```

; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,336A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-09-233-336A-11

```

```

Query Match 26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 9 VEPF 12
Db 6 VEPF 9

```

```

RESULT 74
US-09-233-752A-11
; Sequence 11, Application US/09233752A
; Patent No. 6137033
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kosiel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
; CONTROL OF PLANT PESTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,752A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,219
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-09-233-752A-11

```

```

Query Match 26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 9 VEPF 12
Db 6 VEPF 9

```

```

RESULT 75
US-09-027-998A-29
; Sequence 29, Application US/09027998A
; Patent No. 6284949
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A
; APPLICANT: Fuchs, Roy L
; APPLICANT: Perlak, Frederick J
; TITLE OF INVENTION: Insect Resistant Plants
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White and Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,998A
; FILING DATE: 23-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```



```
; NAME: Patterson, Melinda L
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-09-027-998A-29

Query Match 26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPFV 15
 |||
Db 7 PPFV 10
```

```
Search completed: November 25, 2003, 20:16:01
Job time : 17.3564 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 10.1223 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-6  
Perfect score: 11  
Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR\_76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 4     | 36.4        | 12     | 2 PH1454 | T-cell receptor al |
| 2          | 4     | 36.4        | 13     | 2 PH0787 | hypothetical prote |
| 3          | 3     | 27.3        | 6      | 2 A17765 | hypothetical prote |
| 4          | 3     | 27.3        | 8      | 2 S16324 | prealbumin - weste |
| 5          | 3     | 27.3        | 8      | 2 I49404 | transforming prote |
| 6          | 3     | 27.3        | 11     | 2 A38590 | 214K exoantigen (v |
| 7          | 3     | 27.3        | 11     | 2 F33098 | probable minor cap |
| 8          | 3     | 27.3        | 12     | 2 E45691 | protein QAL00045 - |
| 9          | 3     | 27.3        | 12     | 2 PA0047 | photosystem II pro |
| 10         | 3     | 27.3        | 13     | 2 S01119 | GTP-binding protei |
| 11         | 3     | 27.3        | 13     | 2 S29488 | hypothetical prote |
| 12         | 3     | 27.3        | 14     | 2 B36079 | GTP-binding protei |
| 13         | 3     | 27.3        | 14     | 2 S29486 | hypothetical 1.5K  |
| 14         | 3     | 27.3        | 14     | 2 JS0272 | dehydrin 4.5K poly |
| 15         | 3     | 27.3        | 14     | 2 PC4382 | gene c-Ki-ras prot |
| 16         | 3     | 27.3        | 15     | 2 IS2734 | T cell receptor al |
| 17         | 3     | 27.3        | 15     | 2 PH1782 | T cell receptor be |
| 18         | 3     | 27.3        | 15     | 2 PQ0073 | c-Ki-ras - hamster |
| 19         | 3     | 27.3        | 15     | 2 I65478 | cytochrome P450K-2 |
| 20         | 3     | 27.3        | 15     | 2 S08282 | mannose-specific 1 |
| 21         | 3     | 27.3        | 16     | 2 C39509 | cob protein - comm |
| 22         | 3     | 27.3        | 16     | 2 S22040 | T cell receptor al |
| 23         | 3     | 27.3        | 16     | 2 PH1778 | hemoglobin beta-x  |
| 24         | 3     | 27.3        | 16     | 2 I46275 | interferon alpha ( |
| 25         | 3     | 27.3        | 17     | 2 I42753 | beta-Gliadine 13 - |
| 26         | 3     | 27.3        | 18     | 2 PN0149 | alkanal monooxygen |
| 27         | 3     | 27.3        | 18     | 2 B44995 | alpha-macroglobuli |
| 28         | 3     | 27.3        | 18     | 2 S03971 | oviductin - golden |
| 29         | 3     | 27.3        | 18     | 2 S39009 |                    |

|     |   |      |    |          |                     |
|-----|---|------|----|----------|---------------------|
| 30  | 3 | 27.3 | 19 | 2 S60633 | Ha-transporting tw  |
| 31  | 3 | 27.3 | 19 | 2 S59486 | cell wall protein,  |
| 32  | 3 | 27.3 | 20 | 2 S08605 | hypothetical prote  |
| 33  | 3 | 27.3 | 20 | 2 A34859 | heliothermine - Mex |
| 34  | 3 | 27.3 | 20 | 2 S10876 | hypothetical prote  |
| 35  | 3 | 18.2 | 3  | 3 I78890 | tyrosine protein k  |
| 36  | 2 | 18.2 | 3  | 3 S68328 | blood cell protein  |
| 37  | 2 | 18.2 | 4  | 2 T46627 | hypothetical prote  |
| 38  | 2 | 18.2 | 5  | 1 HOR08A | proctolin - Americ  |
| 39  | 2 | 18.2 | 5  | 2 JN0860 | peptidyl-dipectida  |
| 40  | 2 | 18.2 | 5  | 2 C41225 | copper resistance   |
| 41  | 2 | 18.2 | 5  | 2 E42364 | flagellar protein   |
| 42  | 2 | 18.2 | 5  | 2 A60411 | proctolin - Atlant  |
| 43  | 2 | 18.2 | 5  | 2 S53595 | hypothetical prote  |
| 44  | 2 | 18.2 | 5  | 2 B44823 | synaptosomal-assoc  |
| 45  | 2 | 18.2 | 6  | 2 S11556 | hydrogensulfite re  |
| 46  | 2 | 18.2 | 6  | 2 PC4127 | hypothetical 6 pro  |
| 47  | 2 | 18.2 | 6  | 2 I48126 | alpha-tubulin 6 Ch  |
| 48  | 2 | 18.2 | 6  | 2 B33532 | ig mu chain D regi  |
| 49  | 2 | 18.2 | 6  | 2 I67345 | MHC H2-K-K cell su  |
| 50  | 2 | 18.2 | 6  | 2 I49424 | cytotoxic T-lympho  |
| 51  | 2 | 18.2 | 6  | 2 A43129 | neuropeptide GNFR   |
| 52  | 2 | 18.2 | 6  | 4 A35039 | hypothetical colla  |
| 53  | 2 | 18.2 | 7  | 1 XEYDGD | galactose oxidase   |
| 54  | 2 | 18.2 | 7  | 1 NYPG7  | hypothalamic hepta  |
| 55  | 2 | 18.2 | 7  | 2 JN0859 | peptidyl-dipectida  |
| 56  | 2 | 18.2 | 7  | 2 ECMUCR | catch-relaxing pep  |
| 57  | 2 | 18.2 | 7  | 2 PT0087 | ribulose-bisphosph  |
| 58  | 2 | 18.2 | 7  | 2 S71299 | ICL2 protein - Par  |
| 59  | 2 | 18.2 | 7  | 2 S33246 | neuromodulatory pe  |
| 60  | 2 | 18.2 | 7  | 2 B44787 | calliPRFamide 11    |
| 61  | 2 | 18.2 | 7  | 2 B39040 | calsequestrin, fas  |
| 62  | 2 | 18.2 | 7  | 2 B33932 | ig mu chain D regi  |
| 63  | 2 | 18.2 | 7  | 2 PX0008 | glucuronosyltransf  |
| 64  | 2 | 18.2 | 7  | 2 S68442 | glutathione S-tran  |
| 65  | 2 | 18.2 | 7  | 2 S45648 | Nat-transporting A  |
| 66  | 2 | 18.2 | 7  | 2 S15597 | orf 4 rara 5'-regi  |
| 67  | 2 | 18.2 | 8  | 2 A61348 | red pigment-concen  |
| 68  | 2 | 18.2 | 8  | 2 A28004 | adipokinetic hormo  |
| 69  | 2 | 18.2 | 8  | 2 S08995 | hypertrehalosemic   |
| 70  | 2 | 18.2 | 8  | 2 S10596 | adipokinetic hormo  |
| 71  | 2 | 18.2 | 8  | 2 A49823 | adipokinetic hormo  |
| 72  | 2 | 18.2 | 8  | 2 A44960 | neuropeptide led-C  |
| 73  | 2 | 18.2 | 8  | 2 A43976 | hypertrehalosemic   |
| 74  | 2 | 18.2 | 8  | 2 B43976 | hypertrehalosemic   |
| 75  | 2 | 18.2 | 8  | 2 S55310 | adipokinetic hormo  |
| 76  | 2 | 18.2 | 8  | 2 A58620 | adipokinetic hormo  |
| 77  | 2 | 18.2 | 8  | 2 B24749 | neuropeptide B - b  |
| 78  | 2 | 18.2 | 8  | 2 S43971 | tumor-associated a  |
| 79  | 2 | 18.2 | 8  | 2 S43972 | tumor-associated a  |
| 80  | 2 | 18.2 | 8  | 2 PL0184 | capsid protein vp   |
| 81  | 2 | 18.2 | 8  | 2 S70727 | ipgf protein - Shi  |
| 82  | 2 | 18.2 | 8  | 2 S63493 | disimilatory sulf   |
| 83  | 2 | 18.2 | 8  | 2 S68802 | nitrate reductase   |
| 84  | 2 | 18.2 | 8  | 2 A05169 | neuropeptide M-I -  |
| 85  | 2 | 18.2 | 8  | 2 JS0318 | leucokinin VIII -   |
| 86  | 2 | 18.2 | 8  | 2 A14683 | aspartate transami  |
| 87  | 2 | 18.2 | 8  | 2 S10783 | enamelin f - bovin  |
| 88  | 2 | 18.2 | 8  | 2 I57018 | gene Cfr protein    |
| 89  | 2 | 18.2 | 8  | 2 S65381 | cytochrome-c oxida  |
| 90  | 2 | 18.2 | 8  | 2 I57532 | MHC class I histoc  |
| 91  | 2 | 18.2 | 8  | 2 A59028 | oxytocin - hippopo  |
| 92  | 2 | 18.2 | 9  | 2 A91466 | oxytocin - spotted  |
| 93  | 2 | 18.2 | 9  | 2 A92774 | oxytocin - finback  |
| 94  | 2 | 18.2 | 9  | 2 A33147 | oxytocin - Austral  |
| 95  | 2 | 18.2 | 9  | 2 A34408 | oxytocin - rabbit   |
| 96  | 2 | 18.2 | 9  | 2 S90667 | ribosomal protein   |
| 97  | 2 | 18.2 | 9  | 2 S35538 | calsequestrin, car  |
| 98  | 2 | 18.2 | 9  | 2 A61230 | translation elonga  |
| 99  | 2 | 18.2 | 9  | 2 D58503 |                     |
| 100 | 2 | 18.2 | 9  | 2        |                     |

## ALIGNMENTS

```

RESULT 1
PHI454
T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1454
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1454
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 36.4%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 3 QNFY 6
 ||||
Db 7 QNFY 10

RESULT 2
PH0787
T-cell receptor alpha chain (F8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0787
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-2
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0787
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60891
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
 ||||
Db 8 QNFY 11

RESULT 3
A37765
hypothetical protein (csma 5' region) - Chloroflexus aurantiacus (fragment)
C:Species: Chloroflexus aurantiacus
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
C:Accession: A37765
R/Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
J. Bacteriol. 172, 4497-4504, 1990
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus
A:Reference number: A37765; MUID:90330558; PMID:2376566
A:Accession: A37765
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <THE>
A:Cross-references: GB:M33964

Query Match 27.3%; Score 3; DB 2; Length 6;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
SI6324
hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: SI6324
R/Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked
A:Reference number: SI6323; MUID:91266907; PMID:1675603
A:Accession: SI6324
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
 |||
Db 3 YKL 5

RESULT 5
I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:g497008; PIDN:AAB60461.1; PID:g642825

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
 |||
Db 6 PQN 8

RESULT 6
A38590
transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-Sep-1993
C:Accession: A38590
R/Esch, R.K.; Firtel, R.A.
Genes Dev. 5, 9-21, 1991
A:Title: cAMP and cell sorting control the spatial expression of a developmentally essen
A:Reference number: A38590; MUID:91115102; PMID:1703508
A:Accession: A38590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <ESC>
A:Cross-references: GB:Z11804; GB:K02114; GB:X58190

```

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11
 |||
Db 1 PQM 3

RESULT 4
SI6324
hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: SI6324
R/Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked
A:Reference number: SI6323; MUID:91266907; PMID:1675603
A:Accession: SI6324
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
 |||
Db 3 YKL 5

RESULT 5
I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:g497008; PIDN:AAB60461.1; PID:g642825

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
 |||
Db 6 PQN 8

RESULT 6
A38590
transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)
C:Species: Dictyostelium discoideum
C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-Sep-1993
C:Accession: A38590
R/Esch, R.K.; Firtel, R.A.
Genes Dev. 5, 9-21, 1991
A:Title: cAMP and cell sorting control the spatial expression of a developmentally essen
A:Reference number: A38590; MUID:91115102; PMID:1703508
A:Accession: A38590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <ESC>
A:Cross-references: GB:Z11804; GB:K02114; GB:X58190

```

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
 |||  
 Db 4 YKL 6

RESULT 7  
 F33098  
 24k exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: F33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: F33098  
 A:Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <NIC>

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 |||  
 Db 3 LPQ 5

RESULT 8  
 E45691  
 probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact  
 C:Species: Lactobacillus delbrueckii subsp. lactis phage LL-H  
 C>Date: 24-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 28-Jul-2000  
 C:Accession: E45691  
 R:Vasala, A.; Dupont, L.; Baumann, M.; Ritzenthaler, P.; Alatosava, T.  
 J. Virol. 67, 3061-3066, 1993  
 A:Title: Molecular comparison of the structural proteins encoding gene clusters of two  
 A:Reference number: A45691; MUID:93267750; PMID:8497043  
 A:Accession: E45691  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-12 <VAS>  
 A>Note: sequence extracted from NCBI backbone (NCBIN:132363, NCBIPI:132373)

Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 2 KLP 4

RESULT 9  
 PA0047  
 protein QAL00045 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C:Accession: PA0047  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JPIB, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
 A:Reference number: PA0001  
 A:Accession: PA0047  
 A:Molecule type: Protein  
 A:Residues: 1-12 <KAM>

Query Match 27.3%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 7 KLP 9

RESULT 10  
 S01119  
 photosystem II protein psbK - spinach chloroplast (fragment)  
 C:Species: chloroplast Spinacia oleracea (spinach)  
 C>Date: 30-Jun-1989 #sequence\_revision 31-Dec-1990 #text\_change 19-Jan-1996  
 C:Accession: S01119  
 R:Murata, N.; Miyao, M.; Hayaashida, N.; Hidaka, T.; Sugiura, M.  
 FEBS Lett. 235, 283-288, 1988  
 A:Title: Identification of a new gene in the chloroplast genome encoding a low-molecular  
 A:Reference number: S01119  
 A:Accession: S01119  
 A:Molecule type: protein  
 A:Residues: 1-13 <MUR>  
 C:Genetics:  
 A:Gene: psbK  
 A:Genome: chloroplast  
 C:Superfamily: photosystem II protein psbK  
 C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; th

Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 1 KLP 3

RESULT 11  
 S29488  
 GTP-binding protein o-rab3 - marbled electric ray (fragment)  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C>Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
 C:Accession: S29488  
 R:Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.  
 PNAS Lett. 317, 53-56, 1993  
 A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic  
 A:Reference number: S29485; MUID:93154521; PMID:8428634  
 A:Accession: S29488  
 A:Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 <VOL>

Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5  
 |||  
 Db 6 QNF 8

RESULT 12  
 B36079  
 hypothetical protein insulin-like growth factor I 5'-region - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 30-Nov-1990 #sequence\_revision 13-Sep-1991 #text\_change 18-Aug-2000  
 C:Accession: B36079  
 R:Kajimoto, Y.; Rotwein, P.  
 Mol. Endocrinol. 4, 217-226, 1990  
 A:Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of  
 A:Reference number: A36079; MUID:90231335; PMID:2330002  
 A:Accession: B36079  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <KAJ>

A;Cross-References: GB:M29857; NID:g214287; PIDN:AAA70329.1; PID:g903887  
 A;Note: the authors translated the codon CAG for residue 4 as Gly  
 C;Superfamily: unassigned leader peptides

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 |||  
 Db 2 LPQ 4

## RESULT 13

S29486  
 GTP-binding protein o-rab3 - electric ray (Discothyoe ommata) (fragment)

C;Species: Discothyoe ommata  
 C;Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
 C;Accession: S29486  
 R;Volkmann, W.; Pevsner, J.; Eiferink, L.A.; Scheller, R.H.  
 FEBS Lett. 317, 53-56, 1993

A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle

A;Reference number: S29486; MUID:93154521; PMID:8428634

A;Accession: S29486

A;Status: preliminary

A;Molecule type: Protein

A;Residues: 1-14 <VOL>

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5  
 |||  
 Db 7 QNF 9

## RESULT 14

JS0272

hypothetical 1.5K protein - Chinese hamster

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 28-Apr-1995

C;Accession: JS0272

R;Andrulis, I.L.; Shotwell, M.; Evans-Blackler, S.; Zalkin, H.; Siminovich, L.; Ray, P.

Gene 80, 75-85, 1989

A;Title: Fine structure analysis of the Chinese hamster AS gene encoding asparagine synthetase

A;Reference number: A91619; MUID:90006788; PMID:2477309

A;Accession: JS0272

A;Molecule type: DNA

A;Residues: 1-14 <AND>

A;Experimental source: ovary

C;Comment: This open reading frame is located in the 5'-flanking region of the gene encoding

C;Genetics:

A;Gene: AS

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 3 KLP 5

## RESULT 15

PC4382

dehydrin 4.5K polypeptide - Soybean (fragment)

N;Alternate names: acid soluble 26K protein

C;Species: Glycine max

C;Date: 06-Nov-1997 #sequence\_revision 06-Nov-1997 #text\_change 18-Jul-2001

C;Accession: PC4382

R;Moma, M.; Haraguchi, K.; Saito, M.; Chikuni, K.; Harada, K.

Biosci. Biotechnol. Biochem. 61, 1286-1291, 1997

A;Title: Purification and characterization of the acid soluble 26-kDa polypeptide from soybean

A;Reference number: PC4380; MUID:97446521; PMID:9301109

A;Accession: PC4382

A;Molecule type: protein

A;Residues: 1-14 <MOM>

A;Experimental source: seed

C;Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 27.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 7 KLP 9

## RESULT 16

IS2734

Gene C-Ki-ras protein - hamster (fragment)

C;Species: Cricetinae gen. sp. (hamster)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-May-1999

C;Accession: IS2734

R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, C.

Cardiogenesis 16, 931-939, 1995

A;Title: Differences in molecular biological, biological and growth characteristics between C-Ki-ras and H-Ras

A;Reference number: IS2734; MUID:95246257; PMID:7728976

A;Accession: IS2734

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-15 <RES>

A;Cross-References: GB:S77068; NID:g914176

C;Genetics:

A;Gene: C-Ki-ras

C;Superfamily: ras transforming protein; translation elongation factor Tu homology

C;Keywords: GTP binding

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
 |||  
 Db 4 YKL 6

## RESULT 17

PH1742

T cell receptor alpha chain V region (clone IV alpha 23-1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: PH1762

R;Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1762

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <POR>

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
 |||  
 Db 10 YKL 12

## RESULT 18

PQ0073

```

T-cell receptor beta chain (BTB48) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0073
R: Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0073
A:Molecule type: mRNA
A:Residues: 1-15 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB48
C:Keywords: receptor

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 QNF 5
 |||
Db 4 QNF 6
 |||

RESULT 19
165478
C:Ki-ras - hamster (fragment)
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-Feb-1997
C:Accession: 165478
R: Rakanashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,
Carcinogenesis 16, 931-939, 1995
A:Title: Differences in molecular biological, biological and growth characteristics between
A:Reference number: 152734; MUID:95246257; PMID:7728976
A:Accession: 165478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-15 <RBS>
A:Cross-references: GB:S77069; NID:g914177
C:Genetics:
A:Gene: c-Ki-ras

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 6 YKL 8
 |||
Db 4 YKL 6
 |||

RESULT 20
S08282
cytochrome P450K-2 - rat (tentative sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Mar-2000
C:Accession: S08282
R: Inaoka, S.; Nagashima, K.; Funae, Y.
Arch. Biochem. Biophys. 276, 473-480, 1990
A:Title: Characterization of three cytochrome P450s purified from renal microsomes of un
A:Reference number: S08282; MUID:90165442; PMID:2306108
A:Accession: S08282
A:Molecule type: protein
A:Residues: 1-15 <IMA>
C:Keywords: heme; monooxygenase

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 7 KLP 9
 |||

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778
R: Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>

Query Match 27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 NFY 6
 |||
Db 3 NFY 5
 |||

RESULT 23
PH1778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778
R: Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>

Query Match 27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 NFY 6
 |||
Db 3 NFY 5
 |||

RESULT 24
S22040
cob protein - common sunflower
C:Species: Helianthus annuus (common sunflower)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C:Accession: S22040
R: Koehler, R.H.
submitted to the EMBL Data Library, October 1991
A:Reference number: S22040
A:Accession: S22040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <KOE>
A:Cross-references: EMBL:X62592; NID:g12990; PID:g12991

Query Match 27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 NFY 6
 |||
Db 3 NFY 5
 |||

RESULT 25
PH1778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1778
R: Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1778
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <FOR>

Query Match 27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 6 YKL 8
 |||

```

```

Db 12 YKL 14
RESULT 24
146275
hemoglobin beta-x chain - goat (fragment)
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46275
R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burke, D.J.; Smith, K.; Lin
J. Biol. Chem. 255:6355-6367, 1980
A>Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive
A:Reference number: I46275; MUID:80227766; PMID:6248519
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <HAY>
A:Cross-references: GB:K00659; NID:gl64151; PIDN:AAA30919.1; PID:gl64156

Query Match 27.3%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
Db 12 QNF 14

RESULT 25
142753
interferon alpha (component 1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
C:Accession: I42753
R:Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
J. Biol. Chem. 267: 15210-15216, 1992
A>Title: Purification and characterization of multiple components of human lymphoblastoid
A:Reference number: A42753; MUID:92340576; PMID:1634550
A:Accession: I42753
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <ZOO>

Query Match 27.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
Db 3 LPQ 5

RESULT 26
PN0149
beta-Gliadin 13 - Aegilops longissima (fragment)
C:Species: Aegilops longissima
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PN0149
R:Odintsova, T. I.; Egorov, T. A.
Biokhimiya 55: 509-516, 1990
A>Title: N-terminal sequences of omega-gliadins of Aegilops longissima: On the origin of
A:Reference number: PN0146; MUID:90283493; PMID:2354218
A:Accession: PN0149
A:Molecule type: protein
A:Residues: 1-18 <ODI>
A:Experimental source: strain K-202
C:Superfamily: gliadin

Query Match 27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4

Db 10 PQN 12
RESULT 27
B44995
alkanal monooxygenase (PMN-linked) (EC 1.14.14.3) beta chain - flashlight fish symbiont
C:Species: flashlight fish symbiont bacterium
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C:Accession: B44995
R:Haygood, M.G.
Arch. Microbiol. 154: 496-503, 1990
A>Title: Relationship of the luminous bacterial symbiont of the Caribbean flashlight fish
genes.
A:Reference number: A44995; MUID:91076680; PMID:2256783
A:Accession: B44995
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <HAY>
A:Cross-references: GB:M36597; NID:g213345; PIDN:AAA91214.1; PID:gl204253
C:Keywords: PMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
Db 8 QNF 10

RESULT 28
S23971
alpha-macroglobulin proteinase inhibitor - common octopus
C:Species: Octopus vulgaris (common octopus)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S23971
R:Thøgersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Engild, J.J.
Biochem. J. 285: 521-527, 1992
A>Title: Purification and characterization of an alpha-macroglobulin proteinase inhibitor
A:Reference number: S23971; MUID:92344633; PMID:1379044
A:Accession: S23971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <THO>

Query Match 27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
Db 12 NFY 14

RESULT 29
S39009
oviductin - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 19-Mar-1997 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S39009
R:Maletier, B.; Bleau, G.
Biochem. J. 295: 437-445, 1993
A>Title: Biochemical characterization of hamster oviductin as a sulphated zona pellucida
A:Reference number: S39009; MUID:94059881; PMID:8240241
A:Accession: S39009
A:Molecule type: protein
A:Residues: 1-18 <MAL>
C:Keywords: glycoprotein

Query Match 27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 6 YKL 8  
 Db 1 YKL 3

RESULT 30  
 S0633  
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion  
 C:Species: mitochondrion Artemia sp. (brine shrimp)  
 A:Variety: Strain La Mata  
 C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
 C:Accession: S0633  
 R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.  
 J. Mol. Evol. 38, 156-168, 1994  
 A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic populations  
 A:Reference number: S0624; MUID:194223692; PMID:8169960  
 A:Accession: S0633  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-19 <PER>  
 A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211  
 A:Experimental source: strain La Mata  
 A:Note: the source is designated as Artemia parthenogenetica  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
 C:Genetics:  
 A:Gene: ATP8  
 A:Genome: mitochondrion  
 A:Genetic code: SGC4  
 C:Superfamily: H+-transporting ATP synthase protein 8  
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11  
 Db 2 PQM 4

RESULT 31  
 S59486  
 cell wall protein, 22K - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C:Accession: S59486  
 R:Wojtaszek, P.; Tretow, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A:Title: Specificity in the immobilisation of cell wall proteins in response to different elicitors  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59486  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <WOJ>

Query Match 27.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQM 4  
 Db 14 PQM 16

RESULT 32  
 S08605  
 hypothetical protein 1 estrogen receptor 5'-region - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Aug-2000  
 C:Accession: S08605  
 R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.  
 EMBO J. 5, 891-897, 1986

A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes  
 A:Reference number: S07192; MUID:86247578; PMID:3755102  
 A:Accession: S08605  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-20 <KRU>  
 A:Cross-references: EMBL:X03805; NID:963378; PIDN:CAA27431.1; PID:963379  
 A:Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue 16  
 C:Superfamily: unassigned leader peptides

Query Match 27.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQM 4  
 Db 12 PQM 14

RESULT 33  
 A34859  
 heliothermine - Mexican beaded lizard (fragment)  
 C:Species: Heloderma horridum (Mexican beaded lizard)  
 C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 30-Sep-1993  
 C:Accession: A34859  
 R:Mochca-Morales, J.; Martin, B.M.; Possani, L.D.  
 Toxicon 28, 299-309, 1990  
 A:Title: Isolation and characterization of heliothermine, a novel toxin from Heloderma horridum  
 A:Reference number: A34859; MUID:90260878; PMID:1693019  
 A:Accession: A34859  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <MOC>

Query Match 27.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 5 KLP 7

RESULT 34  
 S10876  
 hypothetical protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 18-Nov-1994  
 C:Accession: S10876  
 R:Assouline, Z.; Kerbirou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D.  
 Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988  
 A:Title: The human gene for von Willebrand factor. Identification of repetitive Alu sequ  
 A:Reference number: S10876; MUID:88268889; PMID:3260493  
 A:Accession: S10876  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-20 <ASS>  
 A:Cross-references: EMBL:X07258

Query Match 27.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 Db 8 LPQ 10

RESULT 35  
 I78890  
 tyrosine protein kinase - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001



C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protei  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:I33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 18.2%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MP 2  
||  
Db 1 MP 2

RESULT 36  
S68328  
blood cell protein A - Molgula manhattensis (fragment)  
C;Species: Molgula manhattensis  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: S68328  
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.  
Arch. Biochem. Biophys. 324, 228-240, 1995  
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th  
A;Reference number: S68325; MUID:96132650; PMID:9554314  
A;Accession: S68328  
A;Molecule type: protein  
A;Residues: 1-3 <TAY>

Query Match 18.2%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FY 6  
||  
Db 2 FY 3

RESULT 37  
T46627  
hypothetical protein c4 - loblolly pine  
C;Species: Pinus taeda (loblolly pine)  
C;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
C;Accession: T46627  
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.  
submitted to the EMBL Data Library, July 1995  
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is d  
A;Reference number: 223105  
A;Accession: T46627  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-4 <CHA>  
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292  
A;Experimental source: strain s6PTx56PT3; 8 month seedlings

Query Match 18.2%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KL 8  
||  
Db 2 KL 3

RESULT 38  
HORCHA

proctolin - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 29-Jul-1991 #sequence\_revision 29-Jul-1991 #text\_change 23-Aug-1996  
C;Accession: A01644  
R;Starratt, A.N.; Brown, B.E.  
Life Sci. 17, 1253-1256, 1975  
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects  
A;Reference number: A93048; MUID:76074708; PMID:576  
A;Accession: A01644  
A;Molecule type: protein  
A;Residues: 1-5 <STA>  
A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac  
R;O'Shea, M.; Adams, M.E.  
Science 213, 567-569, 1981  
A;Title: Pentapeptide (proctolin) associated with an identified neuron.  
A;Reference number: A94260; MUID:91225865; PMID:6113690  
A;Contents: annotation; biological source  
C;Comment: this peptide is found in the lateral white neurons, which occur (in the cockr  
innervate the striated hindgut muscles in insects and stimulate contraction of these mus  
C;Superfamily: proctolin  
C;Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9  
||  
Db 3 LP 4

RESULT 39  
JN0860  
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
C;Species: Sarda orientalis (striped bonito)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: JN0860  
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
A;Reference number: JN0859; MUID:94080036; PMID:7764272  
A;Accession: JN0860  
A;Molecule type: protein  
A;Residues: 1-5 <MAT>  
A;Experimental source: intestine  
C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensi  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9  
||  
Db 2 LP 3

RESULT 40  
C41225  
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
C;Species: Pseudomonas syringae pv. tomato  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C;Accession: C41225  
R;Cha, J.-S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem  
A;Reference number: A41225; MUID:92020961; PMID:1924351  
A;Accession: C41225  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <CHA>

## A;Cross-references: EMBL:X66844

Query Match 18.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2  
 ||  
 Db 1 MP 2

## RESULT 44

B44823 synaptonemal-associated protein SNAP-25 peptide 10A - rabbit (fragment)

N;Alternate names: superprotein peptide 10A  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
 C;Accession: B44823  
 R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
 J. Neurosci. 11, 3412-3421, 1991  
 A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
 A;Reference number: A44823; MUID:92044785; PMID:1941090  
 A;Accession: B44823  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-5 <LO>  
 A;Experimental source: visual tissue  
 A;Note: sequence extracted from NCBI backbone (NCBI:P.64255)  
 C;Keywords: membrane trafficking

Query Match 18.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11  
 ||  
 Db 2 QM 3

## RESULT 45

S11556 hydroxynitrile reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)  
 N;Alternate names: bisulfite reductase; desulfofusicidin  
 C;Species: Desulfovibrio thermophilus  
 C;Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
 C;Accession: S11556  
 R;Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; L  
 Biochim. Biophys. Acta 1040, 112-118, 1990  
 A;Title: Purification and characterization of bisulfite reductase (desulfofusicidin) from  
 A;Reference number: S11024; MUID:90335276; PMID:2165817  
 A;Accession: S11556  
 A;Molecule type: protein  
 A;Residues: 1-6 <FAU>  
 C;Keywords: oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YK 7  
 ||  
 Db 5 YK 6

## RESULT 46

PC4127 hypothetical 6 protein - Streptomyces clavuligerus (fragment)

C;Species: Streptomyces clavuligerus  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C;Accession: PC4127  
 R;Rodriguez-Garcia, A.; Martin, J.F.; Liras, P.  
 Gene 167, 9-15, 1995  
 A;Title: The argG gene of Streptomyces clavuligerus has low homology to unstable argG fr

Query Match 18.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8  
 ||  
 Db 3 KL 4

## RESULT 41

E42364 flagellar protein flir - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium  
 C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
 C;Accession: E42364  
 R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
 J. Bacteriol. 173, 3564-3572, 1991  
 A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seg  
 A;Reference number: A42364; MUID:91258342; PMID:1646201  
 A;Accession: E42364  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5 <VO>  
 A;Cross-references: GB:M62408

Query Match 18.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 ||  
 Db 4 LP 5

## RESULT 42

A60411

proctolin - Atlantic horseshoe crab

C;Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
 C;Accession: A60411  
 R;Groome, J.R.; Killingham, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D  
 Peptides 11, 205-211, 1990  
 A;Title: Identification of proctolin in the central nervous system of the horseshoe crab  
 A;Reference number: A60411; MUID:90287800; PMID:2356151  
 A;Accession: A60411  
 A;Molecule type: protein  
 A;Residues: 1-5 <GRO>  
 C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
 C;Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 ||  
 Db 3 LP 4

## RESULT 43

S53595 hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken

C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C;Accession: S53595  
 R;Calhoun, C.F.; Bowman, P.R.J.; Snippe, L.; Ab, G.  
 Nucleic Acids Res. 22, 5540-5547, 1994

A;Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha  
 A;Reference number: S53595; MUID:95140613; PMID:7838705  
 A;Accession: S53595  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5 <CAL>

A:Reference number: JC4548; MUID:96144242; PMID:8566818

A:Accession: FC4127

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <RD>

A:Cross-references: EMBL:Z49111

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4

DB 2 QN 3

RESULT 47

I48126

alpha-tubulin - Chinese hamster (fragment)

C:Species: Crictulus griseus (Chinese hamster)

C>Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999

C:Accession: I48126

R:Elliot, E.M.; Sarangi, F.; Henderson, G.; Ling, V.

Can. J. Biochem. Cell Biol. 63, 511-519, 1985

A:Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster

A:Reference number: I48126; MUID:86001952; PMID:2931165

A:Accession: I48126

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M25895; NID:g341417; PIDN:AAA74493.1; PID:g516601

C:Genetics:

A:Introns: 3/3

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 2 KL 3

RESULT 48

B3932

Ig mu chain D region (D23) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996

C:Accession: B3932

R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A:Title: Two murine natural polyclonal antibodies are encoded by nonmutated germ-

A:Reference number: A33932; MUID:89282823; PMID:2499887

A:Accession: B3932

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-6 <BAC>

A:Cross-references: GB:M27107

C:Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 2 KL 3

RESULT 49

I67345

MHC H2-K-k cell surface glycoprotein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C:Accession: I67345

R:Archibald, A.L.; Thompson, N.A.; Kvist, S.

EMBO J. 5, 957-965, 1986

A:Title: A single nucleotide difference at the 3' end of an intron causes differential s

A:Reference number: I53243; MUID:86247587; PMID:3013627

A:Accession: I67345

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458

C:Genetics:

A:Introns: 6/1

C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9

DB 1 LP 2

RESULT 50

I49424

cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I49424

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maizaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I49424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:U05745; NID:g497084; PIDN:AAB60481.1; PID:g642831

C:Keywords: hydrolase; serine proteinase

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8

DB 4 KL 5

RESULT 51

A43129

neuropeptide GNFRamide - tapeworm (Moniezia expansa)

C:Species: Moniezia expansa

C>Date: 10-Nov-1997 #sequence\_revision 14-Nov-1997 #text\_change 14-Nov-1997

C:Accession: A43129

R:Maule, A.; Shaw, C.; Halton, D.; Thim, L.

Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993

A:Title: GNFRamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t

A:Reference number: A43129; MUID:93312289; PMID:8323531

A:Accession: A43129

A:Molecule type: protein

A:Residues: 1-6 <MAU>

C:Keywords: amidated carboxyl end; neuropeptide

F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5

DB 2 NF 3

RESULT 52  
 A35039  
 hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: A35039  
 R:Bernmetz, V.D.; Adams, S.L.  
 J. Biol. Chem. 265, 2223-2230, 1990  
 A>Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 2(I) collagen gene  
 A:Reference number: A35039; MUID:190130479; PMID:1688851  
 A:Accession: A35039  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <BN>  
 A:Cross-references: GB:M33382; NID:g211043  
 A>Note: This ORF is not translated in GenBank entry CHKA21CG  
 C:Comment: This sequence is the translation of a cartilage specific alternative transcript  
 C:Keywords: alternative splicing; cartilage  
 Query Match 18.2%; Score 2; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LP 9  
 DB 4 LP 5  
 RESULT 53  
 XYDGD  
 galactose oxidase inhibitor - fungus (Cladobotryum dendroides)  
 C:Species: Cladobotryum dendroides  
 C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 31-Dec-1993  
 C:Accession: A01341  
 R:Avigad, G.; Markus, Z.  
 Fed. Proc. 31, 447, 1972  
 A:Reference number: A01341  
 A:Accession: A01341  
 A:Molecule type: protein  
 A:Residues: 1-7 <AVI>  
 C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, which is inactivated by the enzyme by binding to its prosthetic copper group.  
 C:Superfamily: galactose oxidase inhibitor  
 C:Keywords: copper  
 Query Match 18.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QN 4  
 DB 3 QN 4  
 RESULT 54  
 NYEG7  
 hypothalamic heptapeptide - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 23-Aug-1996  
 C:Accession: A01417  
 R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, H.M. Metab. Res. 13, 228-232, 1981  
 A>Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity  
 A:Reference number: A01417; MUID:81213980; PMID:6263778  
 A:Accession: A01417  
 A:Molecule type: protein  
 A:Residues: 1-7 <CH>  
 A:Superfamily: hypothalamic heptapeptide  
 C:Keywords: hypothalamus  
 Query Match 18.2%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QN 4  
 DB 3 QN 4  
 RESULT 55  
 JN0859  
 peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: JN0859  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A>Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the bonito  
 A:Reference number: JN0859; MUID:194080036; PMID:7764272  
 A:Accession: JN0859  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAT>  
 A:Experimental source: intestine  
 A:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor  
 Query Match 18.2%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KL 8  
 DB 4 KL 5  
 RESULT 56  
 ECMUCR  
 catch-relaxing peptide - blue mussel  
 N:Alternate names: CARP  
 C:Species: Mytilus edulis (blue mussel)  
 C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C:Accession: A29342  
 R:Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Munesaka, Y.  
 Brain Res. 422, 374-376, 1987  
 A>Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.  
 A:Reference number: A29342; MUID:58052022; PMID:3676797  
 A:Accession: A29342  
 A:Molecule type: protein  
 A:Residues: 1-7 <HR>  
 C:Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) activities  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hormone; retractor muscle  
 F:7/Modified site: amidated carboxyl end (Leu) #status experimental  
 Query Match 18.2%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MP 2  
 DB 2 MP 3  
 RESULT 57  
 PT0087  
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (fragaria)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 24-Nov-1999  
 C:Accession: PT0087  
 R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
 submitted to JIPID, December 1995  
 A:Description: Two dimensional electrophoresis of plant proteins and standardization of  
 A:Reference number: PNO173  
 A:Accession: PT0087

A;Molecule type: protein  
A;Residues: 1-7 <TSU>  
A;Experimental source: leaf  
C;Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase  
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3  
||  
2 PQ 3

Db

RESULT 58  
S71299  
ICL2 protein - Paramecium tetraurelia (fragment)  
C;Species: Paramecium tetraurelia  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
C;Accession: S71299  
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
Eur. J. Biochem. 238, 121-128, 1996  
A;Title: Characterization of centrin genes in Paramecium.  
A;Reference number: S71298; MUID:96248429; PMID:8665928  
A;Accession: S71299  
A;Molecule type: protein  
A;Residues: 1-7 <WAD>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGC5

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3  
||  
5 PQ 6

Db

RESULT 59  
S3246  
neuromodulatory peptide Wamide-3 - giant African snail  
C;Species: Achatina fulica (giant African snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C;Accession: S3246  
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323, 104-108, 1993  
A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t  
A;Reference number: S3244; MUID:93265912; PMID:8495720  
A;Accession: S3246  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIN>

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11  
||  
3 QM 4

Db

RESULT 60  
B44787  
calliphorinamide 11 - bluebottle fly (Calliphora vomitoria)  
C;Species: Calliphora vomitoria  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C;Accession: B44787  
R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi-  
A;Reference number: A41978; MUID:92196111; PMID:1549595  
A;Accession: B44787  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <DUV>  
C;Keywords: amidated carboxyl end; neuropeptide  
F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5  
||  
3 NF 4

Db

RESULT 61  
B39040  
calsequestrin, fast skeletal muscle - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997  
C;Accession: B39040  
R;Cala, S.E.; Jones, L.R.  
J. Biol. Chem. 266, 391-398, 1991  
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein  
A;Reference number: A39040; MUID:91093153; PMID:1985907  
A;Accession: B39040  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <CAL>  
C;Keywords: phosphoprotein; skeletal muscle

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
||  
6 LP 7

Db

RESULT 62  
E33932  
I9 mu chain D region (E7) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996  
C;Accession: E33932  
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l  
A;Reference number: A33932; MUID:89282823; PMID:2499887  
A;Accession: E33932  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-7 <BAC>  
A;Cross-references: GB:M27106  
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6  
||  
3 FY 4

Db

RESULT 63  
PX0008  
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)  
N;Alternate names: UDP-glucuronyltransferase

```

C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C:Accession: PX0008
R:Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver
A:Reference number: PX0008; MUID:89197852; PMID:3149280
A:Accession: PX0008
A:Molecule type: protein
A:Residues: 1-7 <YOK>
C:Keywords: Glycosyltransferase; hexosyltransferase; liver

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
 ||
Db 2 KL 3

RESULT 64
S66442
glutathione S-transferase P - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66442
R:Nishibira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
Eur. J. Biochem. 232, 106-110, 1995
A:Title: Identification of the electrophilic substrate-binding site of glutathione S-transferase
A:Reference number: S66442; MUID:96048035; PMID:7556138
A:Accession: S66442
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NIS>

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
Db 2 LP 3

RESULT 65
S45648
Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fragment)
N:Alternate names: ATPase alpha chain
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S45648
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S45648
A:Molecule type: protein
A:Residues: 1-3; 4-7 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
Db 3 LP 4

RESULT 66
S15597
orf 4 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15597
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-.
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15597
A:Molecule type: DNA
A:Residues: 1-7 <BRA>
A:Cross-references: EMBL:X56058; NID:935876
A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA
A:Cross-references: GDB:120337; OMIM:180240
A:Map position: 17q12-17q12

Query Match 18.2%; Score 2; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
 ||
Db 1 MP 2

RESULT 67
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738; PMID:5041363
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis
A:Reference number: S07139; MUID:75054965; PMID:4433569
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'B', 2-8 <FER2>
A:Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi-
red pigment-containing cells.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
 ||
Db 3 NF 4

RESULT 68
A28004
adipokinetic hormone G - two-spotted cricket
N:Alternate names: AKH-G
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C:Accession: A28004

```

R;Gaede, G.; Rinehart, K.L.  
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
 A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide  
 A;Reference number: A28004; MUID:88106553; PMID:3426616  
 A;Accession: A28004  
 A;Molecule type: protein  
 A;Residues: 1-8 <GAE>  
 A;Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 3 NF 4

RESULT 69  
 S10595  
 Hypertrehalosemic hormone I - oriental cockroach  
 N;Alternate names: Pea-CAH-I  
 C;Species: Blatta orientalis (oriental cockroach)  
 C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
 C;Accession: S08995  
 R;Gaede, G.; Rinehart, K.L.  
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
 A;Reference number: S08995; MUID:90253659; PMID:2340112  
 A;Accession: S08995  
 A;Molecule type: protein  
 A;Residues: 1-8 <GAE>  
 A;Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 3 NF 4

RESULT 70  
 S10596  
 Adipokinetic hormone - pond skimmer  
 C;Species: Libellula auripennis  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 14-Nov-1997  
 C;Accession: S10596  
 R;Gaede, G.  
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990  
 A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho  
 A;Reference number: S10596; MUID:90359055; PMID:2390213  
 A;Accession: S10596  
 A;Molecule type: protein  
 A;Residues: 1-8 <BIO>  
 C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Qy 4 NF 5  
 ||  
 Db 3 NF 4

RESULT 71  
 A49823  
 Adipokinetic hormone I - American cockroach  
 N;Alternate names: Periplaneta americana CC-1  
 C;Species: Periplaneta americana (American cockroach)  
 C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C;Accession: A49823  
 R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 5575-5579, 1994  
 A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp  
 A;Reference number: A49823; MUID:84298179; PMID:6591205  
 A;Accession: A49823  
 A;Molecule type: protein  
 A;Residues: 1-8 <SCA>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 3 NF 4

RESULT 72  
 A44960  
 Neuropeptide Led-CC-I - Colorado potato beetle  
 C;Species: Leptinotarsa decemlineata (Colorado potato beetle)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: A44960  
 R;Gaede, G.; Kellner, R.  
 Peptides 10, 1287-1289, 1989  
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and  
 A;Reference number: A44960; MUID:90160053; PMID:2576128  
 A;Accession: A44960  
 A;Molecule type: protein  
 A;Residues: 1-8 <GAE>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 3 NF 4

RESULT 73  
 A43976  
 Hypertrehalosemic hormone - yellow mealworm  
 C;Species: Tenebrio molitor (yellow mealworm)  
 C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C;Accession: A43976  
 R;Gaede, G.; Rosinski, G.  
 Peptides 11, 455-459, 1990  
 A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be  
 A;Reference number: A43976; MUID:90341081; PMID:2381871  
 A;Accession: A43976

A:Molecule type: protein  
 A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 0;

QY 4 NF 5  
 ||  
 DB 3 NF 4

## RESULT 74

B43976  
 hypertrehalosemic hormone - beetle (Zophobas rugipes)  
 C:Species: Zophobas rugipes  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C:Accession: B43976  
 R:Gaede, G.; Rosinski, G.  
 Peptides 11; 455-459, 1990  
 A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
 A:Reference number: A43976; PMID:90341031; PMID:2381871  
 A:Accession: B43976  
 A:Molecule type: protein

A:Residues: 1-8 <GAE>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 0;

QY 4 NF 5  
 ||  
 DB 3 NF 4

## RESULT 75

S55310  
 adipokinetic hormone - damselfly (Pseudagrion inconspicuum)  
 N:Alternate names: Psi-AKH  
 C:Species: Pseudagrion inconspicuum  
 C:Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-May-1999  
 C:Accession: S55310  
 R:Janssens, M.P.E.; Kellner, R.; Gaede, G.  
 Biochem. J. 302, 539-543, 1994

A:Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum  
 A:Reference number: S55310; PMID:94379987; PMID:8093008  
 A:Accession: S55310  
 A:Molecule type: protein  
 A:Residues: 1-8 <JAN>  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 0;

QY 4 NF 5  
 ||  
 DB 3 NF 4

Search completed: November 25, 2003, 18:28:17  
 Job time : 10.1223 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 5.32447 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-6  
Perfect score: 11  
Sequence: 1 MPONFYKLPQM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 3     | 27.3        | 9      | 1     | BUK_CLOPA   |
| 2          | 3     | 27.3        | 11     | 1     | CXLI_CONMR  |
| 3          | 3     | 27.3        | 13     | 1     | CXLI_CONMR  |
| 4          | 3     | 27.3        | 15     | 1     | GTS_ASADI   |
| 5          | 3     | 27.3        | 15     | 1     | MCA_RHOOP   |
| 6          | 3     | 27.3        | 15     | 1     | SODM_ENTAE  |
| 7          | 3     | 27.3        | 18     | 1     | A2M_OCTVU   |
| 8          | 3     | 27.3        | 18     | 1     | LUXB_KRYAS  |
| 9          | 3     | 27.3        | 20     | 1     | CATA_ACTRA  |
| 10         | 3     | 27.3        | 20     | 1     | FIBB_SHEEP  |
| 11         | 3     | 27.3        | 20     | 1     | MY17_BOVIN  |
| 12         | 2     | 18.2        | 4      | 1     | FYRI_ATEL   |
| 13         | 2     | 18.2        | 5      | 1     | PRCT_PERAM  |
| 14         | 2     | 18.2        | 6      | 1     | FARP_MONEX  |
| 15         | 2     | 18.2        | 6      | 1     | QVM_FEDDE   |
| 16         | 2     | 18.2        | 6      | 1     | TRPI_PSEPU  |
| 17         | 2     | 18.2        | 7      | 1     | CARP_MTED   |
| 18         | 2     | 18.2        | 7      | 1     | FARI_MACRS  |
| 19         | 2     | 18.2        | 7      | 1     | FARI_PROCL  |
| 20         | 2     | 18.2        | 7      | 1     | FARI_PANRE  |
| 21         | 2     | 18.2        | 7      | 1     | FARB_CALVO  |
| 22         | 2     | 18.2        | 7      | 1     | HY7_PIG     |
| 23         | 2     | 18.2        | 7      | 1     | IGAO_DACDE  |
| 24         | 2     | 18.2        | 7      | 1     | UNO6_PINPS  |
| 25         | 2     | 18.2        | 7      | 1     | WMA2_ACHFU  |
| 26         | 2     | 18.2        | 7      | 1     | AKHG_GRYBI  |
| 27         | 2     | 18.2        | 8      | 1     | AKH_LIBAU   |
| 28         | 2     | 18.2        | 8      | 1     | ALLI_CVDPO  |
| 29         | 2     | 18.2        | 8      | 1     | ALLI_CVDPO  |
| 30         | 2     | 18.2        | 8      | 1     | ALLI_CVDPO  |
| 31         | 2     | 18.2        | 8      | 1     | COM2_CONPU  |
| 32         | 2     | 18.2        | 8      | 1     | COAG_RAT    |
| 33         | 2     | 18.2        | 8      | 1     | FARI_PANRE  |

|     |   |      |    |   |             |
|-----|---|------|----|---|-------------|
| 34  | 2 | 18.2 | 8  | 1 | FARI_PENMO  |
| 35  | 2 | 18.2 | 8  | 1 | FAR2_MACRS  |
| 36  | 2 | 18.2 | 8  | 1 | FAR3_HOMAM  |
| 37  | 2 | 18.2 | 8  | 1 | FAR4_HOMAM  |
| 38  | 2 | 18.2 | 8  | 1 | HTF1_PERAM  |
| 39  | 2 | 18.2 | 8  | 1 | HTF1_PENMO  |
| 40  | 2 | 18.2 | 8  | 1 | LCK3_LEUMA  |
| 41  | 2 | 18.2 | 8  | 1 | NPB_BOVIN   |
| 42  | 2 | 18.2 | 8  | 1 | RPCH_PANBO  |
| 43  | 2 | 18.2 | 8  | 1 | UPAA_HUMAN  |
| 44  | 2 | 18.2 | 9  | 1 | AL10_CARMA  |
| 45  | 2 | 18.2 | 9  | 1 | FARI_CALVO  |
| 46  | 2 | 18.2 | 9  | 1 | FAR2_PANRE  |
| 47  | 2 | 18.2 | 9  | 1 | FAR3_MACRS  |
| 48  | 2 | 18.2 | 9  | 1 | FAR3_PENMO  |
| 49  | 2 | 18.2 | 9  | 1 | FAR8_MACRS  |
| 50  | 2 | 18.2 | 9  | 1 | FAR8_MACRS  |
| 51  | 2 | 18.2 | 9  | 1 | OXYT_CYPCA  |
| 52  | 2 | 18.2 | 9  | 1 | OXYT_RABIT  |
| 53  | 2 | 18.2 | 9  | 1 | OXYT_RAJCL  |
| 54  | 2 | 18.2 | 9  | 1 | OXYV_SQUAC  |
| 55  | 2 | 18.2 | 9  | 1 | RS10_SERMA  |
| 56  | 2 | 18.2 | 9  | 1 | TKCI_CALVO  |
| 57  | 2 | 18.2 | 9  | 1 | TKLI_LOEMI  |
| 58  | 2 | 18.2 | 10 | 1 | ANGLI_LOEMI |
| 59  | 2 | 18.2 | 10 | 1 | BPP2_BOTIN  |
| 60  | 2 | 18.2 | 10 | 1 | BPP2_BOTIN  |
| 61  | 2 | 18.2 | 10 | 1 | CATE_SHEEP  |
| 62  | 2 | 18.2 | 10 | 1 | COXK_ONCMI  |
| 63  | 2 | 18.2 | 10 | 1 | FAR6_PANRE  |
| 64  | 2 | 18.2 | 10 | 1 | FAR7_MACRS  |
| 65  | 2 | 18.2 | 10 | 1 | FAR7_MACRS  |
| 66  | 2 | 18.2 | 10 | 1 | GON3_ONCKE  |
| 67  | 2 | 18.2 | 10 | 1 | GONL_SQUAC  |
| 68  | 2 | 18.2 | 10 | 1 | HTF1_ROMMI  |
| 69  | 2 | 18.2 | 10 | 1 | HTF1_NAUCI  |
| 70  | 2 | 18.2 | 10 | 1 | MOSQ_CLYJA  |
| 71  | 2 | 18.2 | 10 | 1 | PNEU_HUMAN  |
| 72  | 2 | 18.2 | 10 | 1 | PNEU_RAT    |
| 73  | 2 | 18.2 | 10 | 1 | RL16_ACHLA  |
| 74  | 2 | 18.2 | 10 | 1 | TEMK_RANTE  |
| 75  | 2 | 18.2 | 10 | 1 | TKL2_LOEMI  |
| 76  | 2 | 18.2 | 10 | 1 | TKL3_LOEMI  |
| 77  | 2 | 18.2 | 10 | 1 | TKN1_SCYCA  |
| 78  | 2 | 18.2 | 10 | 1 | TKNE_RANCA  |
| 79  | 2 | 18.2 | 10 | 1 | TKNE_RANRI  |
| 80  | 2 | 18.2 | 10 | 1 | TKN1_FHYBI  |
| 81  | 2 | 18.2 | 10 | 1 | TKSI_ABDAA  |
| 82  | 2 | 18.2 | 10 | 1 | TKS2_ABDAA  |
| 83  | 2 | 18.2 | 10 | 1 | URA7_HUMAN  |
| 84  | 2 | 18.2 | 10 | 1 | URA6_CHLTR  |
| 85  | 2 | 18.2 | 10 | 1 | VEG6_BACSU  |
| 86  | 2 | 18.2 | 11 | 1 | BPP3_BOTIN  |
| 87  | 2 | 18.2 | 11 | 1 | BPP4_BOTIN  |
| 88  | 2 | 18.2 | 11 | 1 | BPPB_AKSHA  |
| 89  | 2 | 18.2 | 11 | 1 | CEPI_ACHFU  |
| 90  | 2 | 18.2 | 11 | 1 | FEF_CLOPA   |
| 91  | 2 | 18.2 | 11 | 1 | LPW_THSTH   |
| 92  | 2 | 18.2 | 11 | 1 | MHI_KLEPN   |
| 93  | 2 | 18.2 | 11 | 1 | NASN_PSETE  |
| 94  | 2 | 18.2 | 11 | 1 | RANC_RANPI  |
| 95  | 2 | 18.2 | 11 | 1 | TZPI_PROVU  |
| 96  | 2 | 18.2 | 11 | 1 | TINA_HOPTI  |
| 97  | 2 | 18.2 | 11 | 1 | TKN1_UPEIN  |
| 98  | 2 | 18.2 | 11 | 1 | TKN1_UPERU  |
| 99  | 2 | 18.2 | 11 | 1 | TKN2_UPERU  |
| 100 | 2 | 18.2 | 11 | 1 | TKNA_CHICK  |

## ALIGNMENTS

RESULT 1

BUK\_CLOPA  
ID - BUK\_CLOPA STANDARD; PRT; 9 AA.  
AC P81337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).  
GN BUK.  
OS Clostridium pasteurianum  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RA MEDLINE=98291870; PubMed=9629918;  
RA Flengserud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl  
phosphate to butyrate (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.  
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the acetate kinase family.  
DR HAMAP; MF\_00542; ; 1  
DR InterPro; IPR000890; Acetate kin.  
DR PROSITE; PS01075; ACETATE KINASE\_1; PARTIAL.  
DR PROSITE; PS01076; ACETATE KINASE\_2; PARTIAL.  
KW Transferase; Kinase.  
FT NON TER 9  
FT SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 27.3%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
DB 2 YKL 4

RESULT 2  
CXLI\_CONMR STANDARD; PRT; 11 AA.  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CM-VIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
RA Seow K.T., Bay B.-H.;  
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
pattern and protein folding. Isolation and characterization from the  
venom of Conus marmoreus.";  
RL J. Biol. Chem. 275:39516-39522(2000).  
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.  
CC -!- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.  
KW Neurotoxin; Toxin; Hydroxylation.  
FT DISULFID 2  
FT SEQUENCE 11 AA; 1104 MW; 055D40505727232B CRC64;

FT DISULFID 3 8  
FT MOD\_RES 10 10 HYDROXYLATION.  
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;  
Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 6.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
DB 5 YKL 7

RESULT 3  
CXLI4\_CONMR STANDARD; PRT; 13 AA.  
ID AC P58810;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda/chi-conotoxin MrIB (Chi-MrIB).  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.  
RC TISSUE=Venom;  
RX MEDLINE=21419681; PubMed=11528421;  
RA Sharpe I.A., Gehrmann U., Loughman M.L., Thomas L., Adams D.A.,  
RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,  
RA Lewis R.J.;  
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and  
noradrenaline transporter.";  
RL Nat. Neurosci. 4:902-907(2001).  
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- PTM: Exists in two forms, due to cis-trans isomerization at His-  
11-Hyp-12.  
CC -!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.  
CC -!- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.  
DR PDB; IIEO; 03-APR-02.  
KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.  
FT DISULFID 4 13  
FT DISULFID 5 10  
FT MOD\_RES 12 12 HYDROXYLATION  
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376AD2B58 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 7.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
DB 7 YKL 9

RESULT 4  
GTS\_ASADI STANDARD; PRT; 15 AA.  
ID AC P83246;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST)  
(fragment).  
OS Asaphis dichotoma.  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Tellinoidea; Psammobiidae; Asaphis.  
OX NCBI\_TaxID=184428;  
RN [1]

Query Match 27.3%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 7.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
DB 7 YKL 9

RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM  
 RP ANALYSIS.  
 RC TISSUE=Intestine, and Liver;  
 RX MEDLINE=22135252; PubMed=12139969;  
 RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;  
 RT "Purification and characterization of a novel glutathione S-  
 RL transferase from *Asaphis dichotoma*.";  
 RL Arch. Biochem. Biophys. 403:202-208(2002).  
 CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-  
 CC dinitrobenzene and etharynic acid.  
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.  
 CC -!- MISCELLANEOUS: In *A. dichotoma* there are at least two isozymes of  
 CC glutathione S-transferase.  
 CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene  
 CC as the substrate.  
 CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and  
 CC glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax  
 CC is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,  
 CC respectively.  
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.  
 DR GO; GO:0004364; F:Glutathione transferase activity; NAS.  
 DR GO; GO:0006803; P:Glutathione conjugation reaction; NAS.  
 KW Transferase.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB09 CRC64;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 YKL 8  
 DB 3 YKL 5  
 RESULT 5  
 MCA2 RHOOB  
 ID MCA2 RHOOB STANDARD; PRT; 15 AA.  
 AC P56870;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Purative maleylacetate reductase II (EC 1.3.1.32) (Fragment).  
 OS Rhodococcus opacus (Nocardia opaca).  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacteriaceae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=37919;  
 [1]  
 RN SEQUENCE.  
 RC STRAIN=ICP;  
 RX MEDLINE=98324954; PubMed=9657989;  
 RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;  
 RT "Characterization of a maleylacetate reductase encoding region from  
 RT Rhodococcus opacus ICP.";  
 RL J. Bacteriol. 180:3503-3508(1998).  
 CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P) (+) = 2-maleylacetate +  
 CC NAD(P)H.  
 CC -!- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).  
 CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC  
 CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL  
 CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.  
 CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE  
 CC FAMILY.  
 DR InterPro; IPR001670; Fe-ADH.  
 DR PROSITE; PS00013; ADH\_IRON\_1; PARTIAL.  
 DR PROSITE; PS00060; ADH\_IRON\_2; PARTIAL.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;  
 Query Match 27.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPQ 10  
 DB 8 LPQ 10  
 RESULT 6  
 SODM ENTAE  
 ID SODM ENTAE STANDARD; PRT; 15 AA.  
 AC P22739;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).  
 GN SODA.  
 OS Enterobacter aerogenes (Aerobacter aerogenes).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Enterobacter.  
 OX NCBI\_TaxID=548;  
 [1]  
 RN SEQUENCE.  
 RX MEDLINE=91248479; PubMed=1368658;  
 RA Kim S.W., Lee S.O., Lee T.H.;  
 RT "Purification and characterization of superoxide dismutase from  
 RT Aerobacter aerogenes.";  
 RL Agric. Biol. Chem. 55:101-108(1991).  
 CC -!- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems.  
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -!- COFACTOR: IRON.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE  
 CC FAMILY.  
 DR PIR; PNO615; PNO615.  
 DR InterPro; IPR001189; SODismutase.  
 DR Pfam; PF00081; sodfe; 1.  
 DR PROSITE; PS00088; SOD\_MN; PARTIAL.  
 KW Oxidoreductase; Iron.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202B642 CRC64;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPQ 10  
 DB 4 LPQ 6  
 RESULT 7  
 A2M OCTVU  
 ID A2M OCTVU STANDARD; PRT; 18 AA.  
 AC P30800;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).  
 OS Octopus vulgaris (Octopus).  
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=6645;  
 [1]  
 RN SEQUENCE.  
 RX MEDLINE=92344633; PubMed=1379044;  
 RA Thøgersen I.B., Salvesen G., Brucato P.H., Pizzo S.V., Enghild J.J.;  
 RT "Purification and characterization of an alpha-macroglobulin  
 RT proteinase inhibitor from the mollusc *Octopus vulgaris*.";  
 RL Biochem. J. 285:521-527(1992).  
 CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A  
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,

CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES  
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT  
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH  
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST  
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR  
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE  
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE  
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked.  
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,  
 CC PIR: S23971; S23971.  
 CC GO: GO:0016975; F:alpha-2 macroglobulin; NAS.  
 CC InterPro: IPR001599; MacroglblnA2.  
 CC Pfam: PF00207; A2M; 1.  
 CC PROSITE: PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
 CC Serine protease inhibitor; Glycoprotein; Plasma; Bait region;  
 CC Thioester bond.  
 CC NON TER 1 1 Isoglutamyl cysteine thioester (Cys-Gln).  
 CC CROSSLNK 5 8  
 CC NON TER 18 18  
 CC SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;  
 CC  
 CC Query Match 27.3%; Score 3; DB 1; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 4 NPY 6  
 CC DB 12 NPY 14  
 CC  
 CC RESULT 8  
 CC LUXB KYAS STANDARD; PRT; 18 AA.  
 CC ID LUXB KYAS  
 CC AC P18300;  
 CC DT 01-NOV-1990 (Rel. 16; Created)  
 CC DT 01-NOV-1990 (Rel. 16; Last sequence update)  
 CC DT 15-DEC-1998 (Rel. 37; Last annotation update)  
 CC DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase  
 CC beta chain) (Fragment).  
 CC GN LUXB  
 CC OS Kryptophanaron alfredi symbiont.  
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 CC OC Vibrionaceae; light emitting symbionts of fish.  
 CC OX NCBI\_TaxID=28177;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=91076680; PubMed=2256783;  
 CC RA Haygood M.G.;  
 CC RT "Relationship of the luminous bacterial symbiont of the Caribbean  
 CC flashlight fish, Kryptophanaron alfredi (family Anomalopidae) to  
 CC other luminous bacteria based on bacterial luciferase (luxA) genes.";  
 CC Arch. Microbiol. 154:496-503(1990).  
 CC -1- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE  
 CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY  
 CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +  
 CC light.  
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M36597; AAA91214.1; ..  
 CC InterPro: IPR002103; Bac luciferase.  
 CC DR PROSITE: PS00494; BACTERIAL LUCIFERASE; PARTIAL.  
 CC KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;

KW Flavoprotein; FMN.  
 FT NON TER 18  
 SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;  
 CC  
 CC Query Match 27.3%; Score 3; DB 1; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 QNF 5  
 CC DB 8 QNF 10  
 CC  
 CC RESULT 9  
 CC CATA ACIRA STANDARD; PRT; 20 AA.  
 CC ID CATA ACIRA  
 CC AC P81422;  
 CC DT 15-DEC-1998 (Rel. 37; Created)  
 CC DT 15-DEC-1998 (Rel. 37; Last sequence update)  
 CC DT 15-JUL-1999 (Rel. 38; Last annotation update)  
 CC DE Catechol 1,2-dioxygenase (EC 1.13.11.1) (Fragment).  
 CC OS Acinetobacter radioresistens.  
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC OC Moraxellaceae; Acinetobacter.  
 CC OX NCBI\_TaxID=40216;  
 CC RN [1]  
 CC RP SEQUENCE  
 CC RX MEDLINE=98034166; PubMed=9369233;  
 CC RA Briganti F., Pessione E., Giunta C., Scozzafava A.;  
 CC RT "Purification, biochemical properties and substrate specificity of a  
 CC catechol 1,2-dioxygenase from a phenol degrading Acinetobacter  
 CC radioresistens.";  
 CC RL FEBS Lett. 416:61-64(1997).  
 CC -1- CATALYTIC ACTIVITY: Catechol + O(2) = cis,cis-muconate.  
 CC -1- COFACTOR: FERRIC ION.  
 CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF CATECHOL TO SUCCINATE  
 CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.  
 CC -1- SUBUNIT: HOMODIMER WHICH DISSOCIATES INTO ACTIVE MONOMERIC  
 CC SUBUNITS AT HIGH IONIC STRENGTHS.  
 CC -1- SIMILARITY: BELONGS TO THE INTRADIOL RING-CLEAVAGE DIOXYGENASE  
 CC FAMILY.  
 CC InterPro: IPR000627; Dioxygenase.  
 CC DR PROSITE: PS00083; INTRADIOL DIOXYGENAS; PARTIAL.  
 CC KW Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron.  
 CC FT NON TER 20  
 CC SEQUENCE 20 AA; 2279 MW; 70E8A5038F602327 CRC64;  
 CC  
 CC Query Match 27.3%; Score 3; DB 1; Length 20;  
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
 CC Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 3 QNF 5  
 CC DB 14 QNF 16  
 CC  
 CC RESULT 10  
 CC FIBB SHEEP STANDARD; PRT; 20 AA.  
 CC ID FIBB SHEEP  
 CC AC P14470;  
 CC DT 01-JAN-1990 (Rel. 13; Created)  
 CC DT 01-JAN-1990 (Rel. 13; Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 CC DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 CC GN FGB.  
 CC OS Ovis aries (Sheep), and  
 CC OS Capra hircus (Goat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC OC Bovidae; Caprinae; Ovis.  
 CC OX NCBI\_TaxID=9940, 9925;  
 CC RN [1]  
 CC RP SEQUENCE.